

## ALIGNMENTS

RESULT 1  
513586  
triacylglycerol lipase (EC 3.1.1.3) precursor, bile salt-activated - human  
N/Alternate names: bile salt-stimulated lipase; carboxyl ester lipase; 1-paninidase; panc  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 18-Jun-1999  
C/Accession: S13586 #sequence revision 30-Sep-1993 #text change 18-Jun-1999  
R/Nielsen, J., Bjaeckberg, L., Carlsson, P., Enerback, S., Hernell, O., Bjursell, G.  
Eur. J. Biochem. 192, 543-550, 1990  
A>Title: cDNA cloning of human-milk bile-salt-stimulated lipase and evidence for its id  
A/Reference number: S13586; MUID:9106144; PMID:1698625  
A/Accession: S13586  
A/Molecule type: mRNA  
A/Residues: 1-745 <NII>  
A/Cross-references: EMBL:X54457; NID:g295C0; PIDN:CAA3a325.1; PID:g29501  
A/Accession: S34490  
A/Molecule type: protein  
A/Residues: 55-6336; 378,387-403;436-446 <NI>  
R/Hult, D.V., Kisel, J.A.  
FEBS Lett. 276, 131-134, 1990  
A>Title: Sequence identity between human pancreatic cholesterol esterase and bile salt-s  
A/Reference number: S12983; MUID:51092399; PMID:2265692  
A/Accession: S12983  
A/Molecule type: mRNA  
A/Residues: 1-745 <HUI>  
A/Cross-references: EMBL:M85201  
R/Hult, D.V., Kisel, J.A.  
Submitted to the EMBL Data Library, February 1992  
A/Description: Molecular cloning and tentative identification of the catalytic triad of  
A/Reference number: S34489  
A/Accession: S34489  
A/Molecule type: mRNA  
A/Residues: 1-715; 'CAPRYT.RLPDLPQMTPRKLRCLGSGFV' <HUI>  
A/Cross-references: EMBL:M85201; NID:G180481; PIDN:AA5202.4.1; PID:g180482  
R/Baba, T., Downs, D.; Jackson, K.W.; Tang, J.; Wang, C.S.  
Biochemistry 30, 500-510, 1991  
A>Title: Structure of human milk bile salt activated lipase.  
A/Reference number: A37916; MUID:91105134; PMID:198604  
A/Accession: A37916  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 4-745 <BAB>  
A/Cross-references: GB:M54994; GB:J05301; NID:g187249; PIDN:AAA63211.1; PID:g187150  
A/Note: It is uncertain whether Met-1 or Met-4 is the initiator  
R/Lidberg, U., Nielsen, J., Stromberg, K., Stemman, G., Sahlin, P., Enerback, S., Bjursell  
Genomics 13, 630-640, 1992  
A>Title: Genomic Organization, sequence analysis, and chromosomal localization of the hu  
A/Reference number: A42824; MUID:92347858; PMID:1639390  
A/Accession: A42824  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 433-498 <LID>  
A/Cross-references: GB:M94579  
A/Note: the authors translated the codon TAC for residue 7 as Thr  
R/Kumar, B.V.; Alman-Gomez, C.A.; Colwell, N.; Lopez-Candales, A.; Bosner, M.S.; Spilbu  
Biochemistry 31, 6077-6081, 1992  
A>Title: Structure of the human pancreatic cholesterol esterase gene.  
A/Reference number: A42864; MUID:92329425; PMID:1627550  
A/Accession: A42864  
A/Molecule type: DNA  
A/Residues: 456-485 <KUM>  
A/Cross-references: GB:540178; NID:g251572; PIDN:AA522337.1; PID:g251573  
A/Experimental source: pME 15, PTC  
A/Note: sequence extracted from NCBI Backbone (NCBI:109184, NCBI:P:109185)  
R/Christie, D.L.; Cleaverly, D.R.; O'Connor, C.J.  
FEBS Lett. 278, 193-194, 1991  
A>Title: Human milk bile-salt stimulated lipase: Sequence similarity with rat lysophosphol  
A/Reference number: S13917; MUID:91122282; PMID:1991511  
A/Accession: S13917

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A:Status: preliminary
A:Molecule type: protein
A:Residues: 24-40;115-170;278-286,'V',288-294,'L',296;305-340;534-543 <CHR>
R:Wang, C.S.
Biochem. Biophys. Res. Commun. 155, 950-955, 1988
A>Title: Purification of carboxyl ester lipase from human pancreas and the amino acid
A:Reference number: A31520; PMID:88339990; PMID:3421974
A:Accession: A31520
A:Molecule type: protein
A:Residues: 24-33 <MAN>
R:Hui, D.Y.; Hayakawa, K.; Oizumi, J.
Biochem. J. 291, 65-69, 1993
A>Title: Lipomidease activity in normal and mutagenized pancreatic cholesterol estera
A:Reference number: S32318; PMID:3328634; PMID:8471055
A:Accession: S32318
A:Status: preliminary
A:Molecule type: protein
A:Residues: 54,'X',56-75;77-79;369-377 <HU3>
R:Roudaut, S.; M'Alles, F.; Margotat, A.; Escibano, M.D.; Lombard, D.
Biochim. Biophys. Acta 1264, 141-150, 1995
A>Title: Bile salt-dependent lipase transcripts in human fetal tissues.
A:Reference number: S59907; PMID:96038831; PMID:7578248
A:Accession: S59907
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 26-729 <ROU>
R:Loomes, K.M.
Eur. J. Biochem. 230, 607-613, 1995
A>Title: Structural organisation of human bile-salt-activated lipase probed by limited
A:Reference number: S65641; PMID:95331299; PMID:7607235
A:Accession: S65641
A:Status: preliminary
A:Molecule type: protein
A:Residues: 24-30;31-32;109-110;456-459;545-552 <LOO>
C:Genetics:
A:Gene: GDB:CEL
A:Cross-references: GDB:127527; OMIM:114840
A:Map position: 9q34.3-9q34.3
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:1-23/Domain: (or 4-23) signal sequence #status predicted <SIG>
F:24-745/Product: triacylglycerol lipase, bile salt-activated #status predicted <MAT>
F:53-536/Domain: cholinesterase homology <CHE>
F:210/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:211,458/Active site: Ser, His #status predicted

Query Match 1.5%; Score 12; DB 2; length 745;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 526 YWTFNFAKGDPN 537
|||||
Db 490 YWTFNFAKGDPN 501

RESULT 2
S53372
carboxylesterase (EC 3.1.1.1) B1 - southern house mosquito
C:Species: Culex pipiens quinquefasciatus (southern house mosquito)
C>Date: 01-Aug-1995 #sequence_revision 0;-Sep-1995 #text_change 21-Jul-2000
C:Accession: S53371
R:Vaughan, A.; Rodriguez, M.; Hemingway, J.
Biochem. J. 305, 651-658, 1995
A>Title: The independent gene amplification of electrophoretically indistinguishable
A:Reference number: S53370; MUID:95134253; PMID:7530448
A:Accession: S53371
A:Molecule type: mRNA
A:Residues: 1-540 <MAN>
A:Cross-references: EMBL:Z33695; NID:9475069; P1DN:CAA83644.1; P1D:9780238
A:Experimental source: strain MRES
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

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OM protein - protein search, using sw model

Run on: November 5, 2003, 15:22:38 ; Search time 21 Seconds

(without alignments)  
3736.840 Million cell updates/sec

Title: US-09-978-423a-375

Perfect score: 816  
Sequence: 1 MENSVLWLTALAIKFTL.....TFSGGQNSTNLPHGHSTTRV 816

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database:

PIR 76:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	1.5	745	2	triacylglycerol 11
2	11	1.3	540	2	carboxylesterase 1
3	10	1.2	348	2	CAMP-regulated D2
4	10	1.2	503	2	carboxylesterase 1
5	10	1.2	540	2	carboxylesterase 1
6	10	1.2	540	2	carboxylesterase 1
7	9	1.1	157	2	esterase B1 - souc
8	9	1.1	503	2	lysyl-tRNA synthet
9	9	1.1	503	2	lysine-tRNA ligase
10	9	1.1	532	2	60K esterase (EC 3
11	9	1.1	539	2	carboxylesterase 1
12	9	1.1	540	2	carboxylesterase 1
13	9	1.1	549	2	carboxylesterase 1
14	9	1.1	554	2	carboxylesterase 1
15	9	1.1	554	2	carboxylesterase 1
16	9	1.1	557	2	esterase - Caenorh
17	9	1.1	561	2	carboxylesterase 1
18	9	1.1	561	2	carboxylesterase 1
19	9	1.1	561	2	carboxylesterase 1
20	9	1.1	561	2	carboxylesterase 1
21	9	1.1	562	2	carboxylesterase 1
22	9	1.1	562	2	esterase precursor
23	9	1.1	565	2	hypothetical prote
24	9	1.1	566	2	carboxylesterase 1
25	9	1.1	567	1	carboxylesterase 1
26	9	1.1	597	2	sterol esterase (E
27	9	1.1	620	2	acetylcholinestera
28	9	1.1	956	2	glutactin precurs
29	8	1.0	231	2	hypothetical prote

30	8	1.0	281	2	hypothetical prote
31	8	1.0	289	2	hypothetical prote
32	8	1.0	380	2	probable cysteine
33	8	1.0	450	2	hypothetical prote
34	8	1.0	506	2	cysteine proteinas
35	8	1.0	518	1	multidrug-efflux t
36	8	1.0	539	2	hypothetical prote
37	8	1.0	540	2	carboxylesterase 1
38	8	1.0	544	2	triacylglycerol 11
39	8	1.0	544	2	triacylglycerol 11
40	8	1.0	544	2	triacylglycerol 11
41	8	1.0	544	2	triacylglycerol 11
42	8	1.0	544	2	triacylglycerol 11
43	8	1.0	544	2	triacylglycerol 11
44	8	1.0	544	2	triacylglycerol 11
45	8	1.0	563	1	triacylglycerol 11
46	8	1.0	563	1	triacylglycerol 11
47	8	1.0	578	2	protein 128C12.4b
48	8	1.0	596	1	acetylcholinestera
49	8	1.0	596	1	acetylcholinestera
50	8	1.0	599	1	sterol esterase (E
51	8	1.0	599	2	acetylcholinestera
52	8	1.0	602	2	sterol esterase (E
53	8	1.0	612	2	acetylcholinestera
54	8	1.0	637	2	acetylcholinestera
55	8	1.0	656	2	hypothetical prote
56	8	1.0	658	2	hypothetical prote
57	8	1.0	672	2	hypothetical prote
58	8	1.0	730	2	hypothetical prote
59	8	1.0	782	1	probable organic s
60	8	1.0	837	2	muclin-like peptide
61	8	1.0	912	1	protein kinase C 1
62	8	1.0	918	1	protein kinase C 1
63	8	1.0	2145	2	glutamate synthase
64	7	0.9	23	2	trans-cinnamate 4-
65	7	0.9	28	2	sterol esterase (E
66	7	0.9	89	2	hypothetical prote
67	7	0.9	98	2	probable PE protei
68	7	0.9	103	2	hypothetical prote
69	7	0.9	133	2	ribosome binding f
70	7	0.9	141	2	cholesterase (EC
71	7	0.9	141	2	cholesterase (EC
72	7	0.9	141	2	cholesterase (EC
73	7	0.9	141	2	cholesterase (EC
74	7	0.9	141	2	cholesterase (EC
75	7	0.9	162	2	cholesterase (EC
76	7	0.9	166	2	cholesterase (EC
77	7	0.9	177	2	cholesterase (EC
78	7	0.9	180	2	cholesterase (EC
79	7	0.9	188	2	cholesterase (EC
80	7	0.9	199	2	cholesterase (EC
81	7	0.9	206	2	cholesterase (EC
82	7	0.9	208	2	cholesterase (EC
83	7	0.9	208	2	cholesterase (EC
84	7	0.9	208	2	cholesterase (EC
85	7	0.9	225	2	cholesterase (EC
86	7	0.9	225	2	cholesterase (EC
87	7	0.9	230	2	cholesterase (EC
88	7	0.9	240	2	cholesterase (EC
89	7	0.9	256	2	cholesterase (EC
90	7	0.9	259	2	cholesterase (EC
91	7	0.9	259	2	cholesterase (EC
92	7	0.9	259	2	cholesterase (EC
93	7	0.9	260	2	cholesterase (EC
94	7	0.9	270	2	cholesterase (EC
95	7	0.9	270	2	cholesterase (EC
96	7	0.9	274	2	cholesterase (EC
97	7	0.9	274	2	cholesterase (EC
98	7	0.9	280	2	cholesterase (EC
99	7	0.9	282	2	cholesterase (EC
100	7	0.9	291	2	cholesterase (EC



Query Match 1.3%; Score 11; DB 2; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 240 AFGGDPKRYT 250  
 |||||  
 DB 176 AFGGDPKRYT 186

## RESULT 3

C26720  
 C:Species: Dictyostelium discoideum  
 C:Date: 19-Nov-1988 #sequence\_revision 30-Jun-1991 #text\_change 16-Dec-1998  
 C:Accession: C26720  
 R:Van, S.K.O.; Firtel, R.A.  
 Mol. Cell. Biol. 7, 458-469, 1987  
 A:Title: Cyclic AMP regulation of early gene expression in Dictyostelium discoideum: mod  
 A:Reference number: A26720; MUID:87172740; PMID:3031475  
 A:Accession: C26720  
 A:Molecule type: DNA  
 A:Residues: 1-348 <MAN>  
 A:Cross-references: GB:M15966  
 C:Superfamily: cholinesterase homology  
 F:52-343/Domain: cholinesterase homology <CHE>

Query Match 1.2%; Score 10; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 0.082;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 201 TINRGLIG 210  
 |||||  
 DB 123 TINRGLIG 132

## RESULT 4

S53372  
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 20-Sep-1999  
 C:Accession: S53372; S44212  
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.  
 Biochem. J. 305, 651-658, 1995  
 A:Title: The independent gene amplification of electrophoretically indistinguishable B e  
 A:Reference number: S53370; MUID:9534253; PMID:7530448  
 A:Accession: S53372  
 A:Molecule type: mRNA  
 A:Residues: 1-503 <VAU>  
 A:Cross-references: EMBL:Z32696  
 A:Experimental source: Peiss  
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.  
 Submitted to the EMBL Data Library, April 1994  
 A:Description: The independent gene amplification of indistinguishable esterase B elect  
 A:Reference number: S44212  
 A:Accession: S44212  
 A:Molecule type: mRNA  
 A:Residues: 1-503 <VAU>  
 A:Cross-references: EMBL:Z32696; NID:9475070; PID:9475071  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase

Query Match 1.2%; Score 10; DB 2; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 AFGGDPKRYT 250  
 |||||  
 DB 140 AFGGDPKRYT 149

## RESULT 5

S53370  
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)  
 C:Date: 15-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 21-Jul-2000  
 C:Accession: S53370; S44211  
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.  
 Biochem. J. 305, 651-658, 1995  
 A:Title: The independent gene amplification of electrophoretically indistinguishable  
 A:Reference number: S53370; MUID:9534253; PMID:7530448  
 A:Accession: S53370  
 A:Molecule type: mRNA  
 A:Residues: 1-540 <VAU>  
 A:Cross-references: EMBL:Z32694; NID:9475067; PID:CAA83643.1; PID:9475068  
 A:Experimental source: strain Peiss  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase

C:Species: Culex pipiens quinquefasciatus (southern house mosquito)  
 C:Date: 15-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 21-Jul-2000  
 C:Accession: S53370; S44211  
 R:Vaughan, A.; Rodriguez, M.; Hemingway, J.  
 Biochem. J. 305, 651-658, 1995  
 A:Title: The independent gene amplification of electrophoretically indistinguishable  
 A:Reference number: S53370; MUID:9534253; PMID:7530448  
 A:Accession: S53370  
 A:Molecule type: mRNA  
 A:Residues: 1-540 <VAU>  
 A:Cross-references: EMBL:Z32694; NID:9475067; PID:CAA83643.1; PID:9475068  
 A:Experimental source: strain Peiss  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase

Query Match 1.2%; Score 10; DB 2; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 AFGGDPKRYT 250  
 |||||  
 DB 177 AFGGDPKRYT 186

## RESULT 6

A35986  
 C:Species: Culex pipiens quinquefasciatus (southern house mosquito)  
 C:Date: 16-Nov-1990 #sequence\_revision 13-Jan-1993 #text\_change 21-Jul-2000  
 C:Accession: A35986  
 R:Mouches, C.; Pauplin, Y.; Aarwal, M.; Lemieux, L.; Herzog, M.; Abador, M.; Beyssat  
 Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990  
 A:Title: Characterization of amplification core and esterase B1 gene responsible for  
 A:Reference number: A35986; MUID:90207238; PMID:2120576  
 A:Accession: A35986  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-540 <MOU>  
 A:Cross-references: GB:M32228; NID:9156687; PIDN:AAA28289.1; PID:9156688  
 A:Note: the authors translated the codon CGT for residue 213 as Ala, and CGT for resi  
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.2%; Score 10; DB 2; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 AFGGDPKRYT 250  
 |||||  
 DB 177 AFGGDPKRYT 186

## RESULT 7

T29347  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000  
 C:Accession: T29347  
 R:Wu, X.; Le, T.T.  
 Submitted to the EMBL Data Library, April 1996  
 A:Description: The sequence of C. elegans cosmid F01G12.  
 A:Reference number: Z20611  
 A:Accession: T29347  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-157 <MTX>  
 A:Cross-references: EMBL:U53342; PIDN:AAA96212.1; GSPDB:GN00028; CESP:ace-1  
 A:Experimental source: strain Bristol N2, clone F01G12  
 C:Genetics:  
 A:Gene: CESP:ace-1  
 A:Map position: X  
 A:Insertions: 46/2; 110/1; 143/2  
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.1%; Score 9; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 0.45;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 NFAKTGDPN 537  
 DB 41 NFAKTGDPN 49

## RESULT 8

C8:086

lysyl-tRNA synthetase, heat inducible NMB1425 (imported) - Neisseria meningitidis (strain  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C:Species: Neisseria meningitidis  
 C:Accession: C81086  
 R:Etzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
 et al.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiarati, V.; Pizzi, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Xoxon, E.R.; Rappaport, R.; Va  
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.  
 A:Reference number: A81000; MUID:20175755; PMID:10710307  
 A:Accession: C81086  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-503 <ET>  
 A:Cross-references: GB:AE002491; GB:AE002098; NID:97226655; PID:NAB41786.1; PID:9722666

A:Experimental source: serogroup B, strain MCS9  
 C:Genetics:  
 A:Gene: NMB1425  
 C:Superfamily: lysine-tRNA ligase

Query Match 1.1%; Score 9; DB 2; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 AADLHAQYG 464  
 DB 46 AADLHAQYG 54

## RESULT 9

B81858

lysine-tRNA ligase (EC 6.1.1.6) NMA1638 (imported) - Neisseria meningitidis (strain Z243  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 03-Jun-2002

C:Accession: B81858  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holtz, S.; Jørgensen, K.; Leather, S.; Kettle, S.; Mungall, K.; Quail, M.A.; Rajadaram,  
 Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z243.  
 A:Reference number: A81775; MUID:20222556; PMID:10761913  
 A:Accession: B81858  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-503 <PAR>  
 A:Cross-references: GB:AL16256; GB:AL157959; NID:9738029; P:DN:CA884866.1; PID:9738028

A:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 A:Gene: lysS; NMA1638  
 C:Superfamily: lysine-tRNA ligase  
 C:Keywords: ligase

Query Match 1.1%; Score 9; DB 2; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 AADLHAQYG 464  
 DB 46 AADLHAQYG 54

RESULT 10

A34329  
 60K esterase (EC 3.1.1.-) isoform 2 - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 21-Aug-1998  
 C:Accession: A34329

R:Ozols, J.  
 J. Biol. Chem. 264, 12533-12545, 1989  
 A:Title: Isolation, properties, and the complete amino acid sequence of a second form  
 A:Reference number: A34329; MUID:89308686; PMID:2745458  
 A:Accession: A34329

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-532 <OZO>  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase  
 F:32-517/Domain: cholinesterase homology <CHE>  
 F:201,430/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 532;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNLY 133  
 DB 94 EDCLYLNLY 102

## RESULT 11

A29923

carboxylesterase (EC 3.1.1.1), TCDD-induced 60K microsomal - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 08-Dec-1988 #sequence\_revision 08-Dec-1988 #text\_change 21-Aug-1998

C:Accession: A29923; A29471  
 R:Korza, G.; Ozols, J.  
 J. Biol. Chem. 263, 3486-3495, 1988  
 A:Title: Complete covalent structure of 60-kDa esterase isolated from 2,3,7,8-tetrach

A:Reference number: A29923; MUID:8819451; PMID:3343253  
 A:Accession: A29923  
 A:Molecule type: protein  
 A:Residues: 1-539 <KOR>  
 R:Ozols, J.

J. Biol. Chem. 262, 15316-15321, 1987  
 A:Title: Isolation and characterization of a 60-kDa glycoprotein esterase from  
 A:Reference number: A29471; MUID:88033124; PMID:3667634  
 A:Accession: A29471

A:Molecule type: protein  
 A:Residues: 1-71;193-209;436-446;532-539 <OZO>  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein  
 F:32-526/Domain: cholinesterase homology <CHE>  
 F:61,363/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:195,441/Active site: Ser, His #status experimental

Query Match 1.1%; Score 9; DB 2; Length 539;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNLY 133  
 DB 96 EDCLYLNLY 104

## RESULT 12

A31584

carboxylesterase (EC 3.1.1.1) precursor - rat (fingert)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 21-May-1990 #sequence\_revision 03-Aug-1992 #text\_change 18-Jun-1999

C:Accession: A31584  
 R:Long, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R.  
 Biochem. Biophys. Res. Commun. 166, 866-873, 1988  
 A:Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence for a mul  
 A:Reference number: A31584; MUID:89050119; PMID:2573315  
 A:Accession: A31584

A:Molecule type: mRNA  
A:Residues: 1-540 <LON>  
A:Cross-references: GB:M20629; GB:X13587; NID:g203279; PIDN:AAA40871.1; PID:g203280  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein  
F:1-9/Domain: signal sequence #status predicted <SIG>  
F:13-540/Product: carboxylesterase #status predicted <CAT>  
F:41-529/Domain: cholinesterase homology <CHE>  
F:70,265,266,293,467/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:212,444/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYNTY 133  
Db 105 EDCLYNTY 113

RESULT 13  
carboxylesterase (EC 3.1.1.1) E1 precursor, minor form - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Aug-1995  
C:Accession: U00354  
R:Tagaki, Y.; Morohashi, K.; Kawabata, S.; Go, M.; Omura, T.  
J. Biochem. 104, 801-806, 1988  
A:Title: Molecular cloning and nucleotide sequence of cDNA of microsomal carboxylesterase  
A:Reference number: U00354; MUID:89174514; PMID:3235453  
A:Accession: U00354  
A:Molecule type: mRNA  
A:Residues: 1-549 <TAK>  
A:Experimental source: liver  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein; microsome  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-549/Product: carboxylesterase E1 #status predicted <CAT>  
F:150-538/Domain: cholinesterase homology <CHE>  
F:79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:221,453/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 549;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYNTY 133  
Db 114 EDCLYNTY 122

RESULT 14  
carboxylesterase (EC 3.1.1.1) precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Mar-1992 #sequence\_revision 06-Mar-1992 #text\_change 18-Jun-1999  
C:Accession: A30063  
R:Ovanc, M.; Tepperman, K.; Medda, S.; Elliott, R.N.; Stephenson, D.A.; Grant, S.G.; Gar-  
tonomics 9, 344-354, 1991  
A:Title: Characterization of a murine cDNA encoding a member of the carboxylesterase mul-  
A:Reference number: A39060; MUID:91169540; PMID:1845565  
A:Accession: A39060  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-554 <OVN>  
A:Cross-references: GB:M57960; NID:g192853; PIDN:AAA63297.1; PID:g192854  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase  
F:50-540/Domain: cholinesterase homology <CHE>  
F:221,455/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 554;  
Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYNTY 133  
Db 114 EDCLYNTY 122

RESULT 15  
T31783  
hypothetical protein F13H6.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T31783  
R:Jones, K.; Wohldmann, P.  
Submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid F13H6.  
A:Reference number: Z21085  
A:Accession: T31783  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-554 <JON>  
A:Cross-references: EMBL:AF016437; PIDN:AA65887.1; GSPDB:GN00023; CESP:F13H6.3  
A:Experimental source: strain Bristol N2; clone F13H6  
C:Genetics:  
A:Gene: CESP:F13H6.3  
A:Map position: 5  
A:Insertions: 31/3; 84/3; 113/3; 143/2; 225/1; 443/1; 486/2  
C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.1%; Score 9; DB 2; Length 554;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 PVMVYIHGG 176  
Db 118 PVMVYIHGG 126

RESULT 16  
A56690  
esterase - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Jul-2000  
C:Accession: A56690; S21556  
R:Fedon, Y.; Cousin, X.; Toulant, J.P.; Thierry-Mieg, D.; Atyagaus, M.  
DNA Seq. 3, 347-355, 1993  
A:Title: cDNA sequence, gene structure, and cholinesterase-like domains of an esterase  
A:Reference number: A56690; MUID:94033620; PMID:8219278  
A:Accession: A56690  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-557 <FED>  
A:Cross-references: EMBL:X66104; NID:g6703; PIDN:CAA46899.1; PID:g6704  
C:Genetics:  
A:Insertions: 31/3; 84/3; 113/3; 143/2; 225/1; 443/1; 486/2  
C:Superfamily: cholinesterase; cholinesterase homology  
F:39-537/Domain: cholinesterase homology <CHE>

Query Match 1.1%; Score 9; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 PVMVYIHGG 176  
Db 118 PVMVYIHGG 126

RESULT 17  
S62788  
carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat  
N:Alternate names: hydrolase B  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999

C:Accession: S62788; S51203; A55304; S49257  
 R:Robbi, M.; van Schaftingen, E.; Beaufay, H.  
 B:Biochem. J. 313, 821-826, 1996  
 A:Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal, palmitoyl-  
 A:Reference number: S62788; MUID:96590723; PMID:8611161  
 A:Accession: S62788  
 A:Molecule type: mRNA  
 A:Residues: 1-561 <ROB>  
 A:Cross-references: EMBL:X81825; NID:9550417; PIDN:CA57419.1; PID:9550418  
 A:Experimental source: liver  
 R:Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.  
 Arch Biochem Biophys 315, 495-512, 1994  
 A:Title: Purification and characterization of two rat liver microsomal carboxylesterases  
 A:Reference number: S51203; MUID:95077430; PMID:7986098  
 A:Accession: S51203  
 A:Molecule type: protein  
 A:Residues: 19-48 <MOR>  
 A:Experimental source: liver  
 R:Yan, B.; Yang, D.; Brady, M.; Parkinson, A.  
 J. Biol. Chem. 269, 29688-29696, 1994  
 A:Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re  
 A:Reference number: A55304; MUID:95050819; PMID:7961958  
 A:Accession: A55304  
 A:Molecule type: mRNA  
 A:Residues: 1-6, 'F', 8-59, 'P', 61-212, 'A', 214-252, 'T', 254-309, 'T', 312-341, 'N', 343-424, 'F'  
 A:Cross-references: GB:U0697; NID:9562007  
 A:Note: the sequence in GenBank entry R010697, release 107, (PID:9562008) has the codon  
 R:Robbi, M.; Beaufay, H.  
 submitted to the EMBL Data Library, September 1994  
 A:Accession: S49257  
 A:Reference number: S49257  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-561 <RO2>  
 A:Cross-references: EMBL:X81825; NID:9550417; PIDN:CA57419.1; PID:9550418  
 A:Function:  
 A:Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion  
 C:Superfamily: cholinesterase; cholinesterase, homology  
 C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-561/Product: carboxylesterase ES-4 #status experimental <MAT>  
 F:50-551/Domain: cholinesterase homology <CHE>  
 F:221-466/Active site: Ser, His #status predicted  
 F:301/Binding site: carboxylate (asn) (covalent) #status predicted  
 Query Match 1.1%; Score 9; DB 2; Length 561;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCLYLNTY 133  
 Db 114 EDCLYLNTY 122  
 RESULT 18  
 S71597  
 carboxylesterase (EC 3.1.1.1) precursor, liver - rat  
 N:Alternate names: hydrolase C  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 13-Sep-1998  
 C:Accession: S71597  
 R:Yan, B.; Yang, D.; Parkinson, A.  
 Arch. Biochem. Biophys. 317, 222-234, 1995  
 A:Title: Cloning and expression of hydrolase C, a member of the rat carboxylesterase fam  
 A:Reference number: S71597; MUID:95177656; PMID:7872788  
 A:Accession: S71597  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-561 <YAN>  
 A:Experimental source: liver; endoplasmic reticulum  
 A:Function:  
 A:Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion  
 C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-561/Product: carboxylesterase #status predicted <MAT>  
 F:50-551/Domain: cholinesterase homology <CHE>  
 F:558-561/Region: endoplasmic reticulum retention signal  
 F:79,301/Binding site: carboxylate (asn) (covalent) #status predicted  
 F:221,466/Active site: Ser, His #status predicted  
 Query Match 1.1%; Score 9; DB 2; Length 561;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCLYLNTY 133  
 Db 114 EDCLYLNTY 122  
 RESULT 19  
 JC2447  
 carboxylesterase (EC 3.1.1.1) ES-3 precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 29-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 18-Jun-1995  
 C:Accession: JC2447; S23462  
 R:Robbi, M.; Beaufay, H.  
 Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994  
 A:Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (ECASIN).  
 A:Reference number: JC2447; MUID:95032008; PMID:7945287  
 A:Accession: JC2447  
 A:Molecule type: mRNA  
 A:Residues: 1-561 <ROB>  
 A:Cross-references: GB:X81995; NID:9550146; PIDN:CA57158.1; PID:9550147  
 A:Experimental source: liver  
 R:Meda, S.; Proia, R.L.  
 Eur. J. Biochem. 206, 801-806, 1992  
 A:Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting  
 A:Reference number: S23460; MUID:92299009; PMID:1606962  
 A:Accession: S23462  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 503-554, 'R', 556-563 <MED>  
 A:Cross-references: EMBL:X65295; NID:957557; PIDN:CA446390.1; PID:957558  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-561/Product: carboxylesterase ES-3 #status predicted <MAT>  
 F:50-551/Domain: cholinesterase homology <CHE>  
 F:79,107,499/Binding site: carboxylate (asn) (covalent) #status predicted  
 F:221,466/Active site: Ser, His #status predicted  
 Query Match 1.1%; Score 9; DB 2; Length 561;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCLYLNTY 133  
 Db 114 EDCLYLNTY 122  
 RESULT 20  
 S47655  
 carboxylesterase (EC 3.1.1.1) precursor - golden hamster  
 C:Species: Mesocricetus auratus (golden hamster)  
 C:Date: 26-Dec-1994 #sequence\_revision 03-Aug-1995 #text\_change 20-Jun-2000  
 C:Accession: S47655  
 R:Stone, T.; Isobe, M.; Takabatake, E.; Wang, C.Y.  
 Biochem. Biophys. Acta 1207, 138-142, 1994  
 A:Title: Cloning and sequence analysis of a hamster liver cDNA encoding a novel putat  
 A:Reference number: S47655; MUID:94318665; PMID:8043605  
 A:Accession: S47655  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-561 <SON>  
 A:Cross-references: EMBL:D8566; NID:9531238; PIDN:BA05913.1; PID:9531239

C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase  
E:58-546/Domain: cholinesterase homology <CH2>  
F:1227,459/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 561;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133  
DQ 120 EDCLYLNIY 128

RESULT 21

carboxylesterase (EC 3.1.1.1) egasyn - mouse  
N:Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 18-Jun-1999  
C:Accession: A55281  
R:Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Saumann, H.; Heintz, N.;  
Genomics 11, 956-967, 1991  
A>Title: Characterization and functional expression of a cDNA encoding egasyn (esterase-  
A:Reference number: A55281; MUID:92147141; PMID:1783403  
A:Accession: A55281  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-562 <OVN>

A:Cross-references: GB:S80191; NID:9244727; PIDN:AB82135.1; PID:9244728  
A>Note: sequence extracted from NCBI backbone (NCBI:80191, NCBI:80194)  
C:Superfamily: Cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum  
F:51-552/Domain: cholinesterase homology <CH5>  
F:122,467/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 562;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133  
DQ 115 EDCLYLNIY 123

RESULT 22

esterase precursor - Caenorhabditis briggsae  
C:Species: Caenorhabditis briggsae  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Jun-1999  
C:Accession: S27782  
R:Kennedy, B.P.; Aamodt, E.O.; Allen, F.L.; Chung, M.A.; Heschi, M.F.; McGhee, J.D.  
submitted to the EMBL Data Library, June 1992  
A:Description: The gut esterase gene (ges-1) from the nematode *Caenorhabditis elegans* a

A:Reference number: S27782  
A:Accession: S27782  
A:Molecule type: DNA  
A:Residues: 1-562 <XEN>  
A:Cross-references: EMBL:M96144; NID:9156311; PION:AAAB056.1; PID:9156312  
C:Genetics:  
A:Gene: ges-1  
A:Inserts: 54/3; 154/1; 325/-; 403/3; 448/1; 492/2  
C:Superfamily: cholinesterase; cholinesterase homology  
F:1-16/Domain: signal sequence #status predicted <ST3>  
F:17-562/Product: elastase #status predicted <MA>  
F:38-540/Domain: cholinesterase homology <CH5>

Query Match 1.1%; Score 9; DB 2; Length 562;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 PVVNTNYGK 35  
DQ 27 PVVNTNYGK 35

DQ 18 PVVNTNYGK 26

RESULT 23

hypothetical protein K11G9.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 31-Jan-2000  
C:Accession: T29718  
R:Greco, T.; Bradshaw, H.  
submitted to the EMBL Data Library, July 1996  
A:Description: The sequence of *C. elegans* cosmid K11G9.  
A:Reference number: Z20672  
A:Accession: T29718  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-565 <GRE>

A:Cross-references: EMBL:U64953; PIDN:AB04976.1; GSPDB:GN00023; CESP:K11G9.1  
A:Experimental source: strain Bristol N2; clone K11G9  
C:Genetics:  
A:Gene: CESP:K11G9.1  
A:Map position: 5  
A:Inserts: 31/3; 114/3; 144/2; 282/1; 352/1; 460/1  
C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.1%; Score 9; DB 2; Length 565;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 NYRLGILGF 211  
DQ 157 NYRLGILGF 165

RESULT 24

carboxylesterase (EC 3.1.1.1) precursor - pig  
N:Alternate names: proline-beta-naphthylamidase  
C:Species: *Sus scrofa domestica* (domestic pig)  
C>Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 18-Jun-1999  
C:Accession: S19307; S23607  
R:Matsumura, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miyi, K.; Kurokawa, K.; Takah  
FEBS Lett. 293, 37-41, 1991  
A>Title: The nucleotide and deduced amino acid sequences of porcine liver proline-bet

A:Reference number: S19307; MUID:92070571; PMID:1959668  
A:Accession: S19307  
A:Molecule type: mRNA  
A:Residues: 1-566 <MAT1>  
A:Cross-references: EMBL:X63323; NID:91930; PIDN:CAA44929.1; PID:91931  
A:Accession: S23607  
A:Molecule type: protein  
A:Residues: 19-40 <MAT2>  
A>Note: 28-lys and 33-leu were also found  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homocitrim  
F:1-18/Domain: signal sequence #status predicted <ST3>  
F:19-566/Product: carboxylesterase #status experimental <MA>  
F:51-552/Domain: cholinesterase homology <CH5>  
F:83/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:122,467/Active site: Ser, His #status predicted

Query Match 1.1%; Score 9; DB 2; Length 566;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133  
DQ 115 EDCLYLNIY 123

RESULT 25

carboxylesterase (EC 3.1.1.1) precursor, monocyte/macrophage [validated] - human  
A41010

N.Alterate names: carboxylesterase, hepatic; monocyte/macrophage serine esterase  
 C.Species: Homo sapiens (man)  
 C.Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 08-Dec-2000  
 A.Accession: A41010; J03037; A47376; A48816; PS0280; 161085; A48809; 157004  
 R.Abbreviation: J.S.; Sh., G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.  
 J. Biol. Chem. 266, 18832-18838, 1991  
 A.Title: A serine esterase released by human alveolar macrophages is closely related to  
 A.Reference number: A41010; MUID:9201649; PMID:1918003  
 A.Accession: A41010  
 A.Molecule type: mRNA  
 A.Residues: 1-567 <MCN>  
 A.Cross-references: GB:M73499; NID:9179927; PIDN:AAA35649.1; PID:9179928  
 A.Note: parts of this sequence, including the amino end of the mature protein, were conf  
 R.Zhong, R.M.; Calabrese, M.R.; Martin, E.M.; Fohl, L.R.  
 Life Sci. 48, PL43-PL49, 1991  
 A.Title: Cloning and sequencing of a human liver carboxylesterase isoenzyme.  
 A.Reference number: J03037; MUID:91148424; PMID:1997784  
 A.Accession: J03037  
 A.Molecule type: mRNA  
 A.Residues: 61-567 <JON>  
 A.Cross-references: GB:M55509; NID:9179929; PIDN:AAA35650.1; PID:9179930  
 R.Shibata, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.  
 Genomics 17, 76-82, 1993  
 A.Title: Molecular cloning and characterization of a human carboxylesterase gene.  
 A.Reference number: A47376; MUID:94010913; PMID:8406473  
 A.Accession: A47376  
 A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A.Molecule type: mRNA; DNA  
 A.Residues: 1-3; 'PALV', 8-11, 'A', 13-567 <SHI>  
 A.Cross-references: GB:D21088; NID:9455476; PIDN:BA04650.1; PID:9458470  
 A.Note: sequence extracted from NCBJ backbone (NCBI:176103) and corrected to correspond  
 R.Schunke, F.; Salmasi, A.; Kreipe, H.; Buck, F.; Faravassoli, M.R.; Radzun, H.J.  
 Blood 78, 506-512, 1991  
 A.Title: cDNA cloning and characterization of human monocyte/macrophage serine esterase-  
 A.Reference number: A49816; MUID:91300111; PMID:2075086  
 A.Accession: A49816  
 A.Molecule type: mRNA  
 A.Residues: 'G', 65-185, 'G', 187-361, 363-567 <ZSC>  
 A.Cross-references: GB:X52973; NID:936421; PIDN:CAA37147.1; PID:91335354  
 R.Ridles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.  
 Gene 108, 289-292, 1991  
 A.Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase.  
 A.Reference number: PS0280; MUID:92084550; PMID:748913  
 A.Accession: PS0280  
 A.Molecule type: mRNA  
 A.Residues: 114, 'H', 116-280, 'A', 282-300, 'GNSLYLTYRQREST', 318-336, 'R', 338-352, 'GSP', 3  
 A.Cross-references: GB:M65261; NID:9187028; PIDN:AAA83912.1; PID:9187029  
 A.Experimental source: liver  
 A.Note: differences between this sequence and other reports appear to be due to framesh  
 R.Kroetz, D.L.; McBride, O.W.; Gonzalez, F.J.  
 Biochemistry 32, 11606-11617, 1993  
 A.Title: Glycosyl-ation-dependent activity of baculovirus-expressed human liver carboxyl  
 A.Reference number: A48809; MUID:94032283; PMID:8218228  
 A.Accession: 161085  
 A.Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-55, 'G', 57-361, 363-535, 'G', 537-567 <KRO>  
 A.Cross-references: GB:L07765; NID:9180949; PIDN:AAA5711.1; PID:9180950  
 A.Accession: A48809  
 A.Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-17, 'A', 18-55, 'G', 57-535, 'G', 537-567 <KRO2>  
 A.Cross-references: GB:L07764; NID:9180947; PIDN:AAA16036.1; PID:9180948  
 A.Accession: 161085  
 A.Gene: GDB:CEB1; HNSE  
 A.Cross-references: GDB:128044; OMIM:114835  
 A.Map position: 16q13-16q22.1  
 C.Superfamily: cholinesterase, cholinesterase homology  
 C.Keyword: carboxylic ester hydrolase; endoplasmic reticulum; liver  
 F:1-16/Domain: signal sequence #status predicted <SIS>  
 F:119-145/Domain: propeptide #status predicted <PRO>  
 F:150-553/Domain: cholinesterase homology <CHE>  
 F:146-567/Product: carboxylesterase #status experimental <XAT>

F:564-567/Region: endoplasmic reticulum retention signal #status atypical  
 F:221,468/Active site: Ser, His #status predicted  
 Query Match 1.1%; Score 9; DB 1; Length 567;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Cy 125 EDCLYNLY 133  
 |||||  
 Db 114 EDCLYNLY 122  
 RESULT 26  
 A33668  
 sterol esterase (EC 3.1.1.13) precursor - bovine (fragment)  
 C.Species: Bos primigenius taurus (cattle)  
 C.Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 18-Jun-1999  
 A.Accession: A33668  
 R.Kyger, E.M.; Wiegand, R.C.; Lange, L.G.  
 Biochem. Biophys. Res. Commun. 164, 1302-1309, 1989  
 A.Title: Cloning of the bovine pancreatic cholesterol esterase/lysophospholipase.  
 A.Reference number: A33668; MUID:90073663; PMID:2590203  
 A.Accession: A33668  
 A.Status: preliminary; not compared with conceptual translation  
 A.Molecule type: mRNA  
 A.Residues: 1-597 <KYG>  
 A.Cross-references: GB:M28402; NID:9598081; PIDN:AAA56785.1; PID:9598082  
 C.Superfamily: cholinesterase; cholinesterase homology  
 C.Keyword: carboxylic ester hydrolase  
 F:48-583/Domain: cholinesterase homology <CHE>  
 Query Match 1.1%; Score 9; DB 2; Length 597;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Cy 124 NEDCLYNI 132  
 |||||  
 Db 95 NEDCLYNI 103  
 RESULT 27  
 A54413  
 acetylcholinesterase (EC 3.1.1.7) A precursor - Caenorhabditis elegans  
 C.Species: Caenorhabditis elegans  
 C.Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 21-Jul-2003  
 A.Accession: A54413; T29824  
 R.Aspaghus, M.; Fedon, Y.; Cousin, X.; Chatonnet, A.; Beryge, C.B.; Fournier, D.; Tottu  
 J. Biol. Chem. 269, 9957-9965, 1994  
 A.Title: cDNA sequence, gene structure, and in vitro expression of ace-1, the gene en  
 A.Reference number: A54413; MUID:94193691; PMID:8144590  
 A.Accession: A54413  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-620 <ARP>  
 A.Cross-references: GB:X75331; NID:9475060; PIDN:CAA53080.1; PID:9571831  
 3;Mu, X.; Le, T.T.  
 Submitted to the EMBL Data Library, May 1996  
 A.Description: The sequence of C. elegans cosmid W09B12.  
 A.Reference number: Z20693  
 A.Accession: Z29824  
 A.Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-620 <MUX>  
 A.Cross-references: EMBL:U58731; PIDN:AB00593.1; GSPDB:GN00028  
 A.Experimental source: strain Bristol N2; clone W09B12  
 C.Genetics:  
 A.Gene: CESP:ace-1  
 A.Map position: X  
 A.Intron: 13/3; 59/2; 154/2; 236/3; 296/2; 454/2; 509/2; 573/1; 606/2  
 C.Superfamily: cholinesterase; cholinesterase homology  
 C.Keyword: carboxylic ester hydrolase  
 F:45-567/Domain: cholinesterase homology <CHE>

Query Match 1.1%; Score 9; DB 2; Length 620;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 NFAKTADPN 537  
|||||  
504 NFAKTADPN 512

RESULT 28  
A:Accession: A56920  
A:Species: Drosophila melanogaster  
C:Date: 11-Aug-1995 #sequence\_revision: 11-Aug-1995 #text\_change 21-Jul-2000  
C:Accession: A56920  
R:All, V.J.; Patter, R.D.; Broadie, K.; Goodhan, C.S.  
Cell 81, 757-767, 1995  
A>Title: Gliotactin, a novel transmembrane protein on peripheral glia, is required to fd  
A:Reference number: A56920; MUID:955292343; PMID:7539719  
A:Accession: A56920  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-956 <AUL>  
A:Cross-references: GB:L39083; NID:9899061; PID:AA041579.1; PID:9899062  
C:Genetics:

A:Gene: FlyBase:G1  
A:Cross-references: FlyBase:FBgn0001987  
C:Superfamily: Cholinesterase homology  
C:Keywords: transmembrane protein  
F:178-701/Domain: cholinesterase homology <CHE>

Query Match 1.1%; Score 9; DB 2; Length 356;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PMWYIHG 176  
|||||  
253 PMWYIHG 261

RESULT 29  
A:Accession: T19267  
A:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T19267  
R:Harris, B.  
Submitted to the EMBL Data Library, September 1994  
A:Reference number: 219399  
A:Accession: T19267  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-231 <WLL>  
A:Cross-references: EMBL:Z37139; PID:CAA85488.1; GSPDB:GN00022; CESP:C14B1.8  
A:Experimental source: clone C14B1  
C:Genetics:

A:Gene: CESP:C14B1.8  
A:Map position: 3  
A:Introns: 25/1; 58/1; 117/2; 146/2; 181/2

Query Match 1.0%; Score 8; DB 2; Length 211;  
Best Local Similarity 100.0%; Pred. No. 7.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 RNKRYKEJ 327  
|||||  
176 RNKRYKEJ 183

RESULT 30  
T26999  
hypothetical protein Y48B6A.15 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
A:Accession: T26999  
R:Wall, M.  
Submitted to the EMBL Data Library, September 1999  
A:Reference number: Z20297  
A:Accession: T26999  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-281 <WLL>  
A:Cross-references: EMBL:AL110490; NID:e1542263; PID:CA854443.1; CESP:Y48B6A.15  
A:Experimental source: clone Y48B6A  
C:Genetics:

A:Gene: CESP:Y48B6A.15  
A:Introns: 29/3; 65/2; 139/2; 165/3

Query Match 1.0%; Score 8; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNI 132  
|||||  
125 EDCLYLNI 132

RESULT 31  
B75591  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 15-Sep-2000  
C:Accession: B75591  
R:White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.;  
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Ullrich, T.; Zalewski, C.  
Science 286, 1571-1577, 1999  
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: B75591  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-289 <WHL>  
A:Cross-references: GB:AE001863; GB:AE001825; NID:96460670; PID:AA12504.1; PID:96460670  
A:Experimental source: strain R1  
C:Genetics:

A:Gene: DRA0359  
A:Map position: 2  
C:Superfamily: Deinococcus radiodurans hypothetical protein DRA0359

Query Match 1.0%; Score 8; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 RGLRTPUP 44  
|||||  
78 RGLRTPUP 85

RESULT 32  
T40851  
Probable cysteine proteinase (EC 3.4.22.-) [similarity] - fission yeast (Schizosaccha  
N:Alternate names: probable GPI-anchor transamidase  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Jun-2000  
C:Accession: T40851  
R:Pamperger, U.; Pohl, T.; Wood, V.; Rajandream, N.A.; Barrell, B.G.  
Submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21952  
A:Accession: T40851  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-380 <RAM>  
A:Cross-references: EMBL:AL121783; PID:CA857844.1; GSPDB:GN00068; SPDB:SPCC11E10.02  
A:Experimental source: strain 972h-; cosmid c1E10  
C:Genetics:

A:Gene: SPDB:SPCCL1E13.02C  
A:Map position: 3  
C:Keywords: cysteine proteinase; hydrolase

Query Match 1.0%; Score 8; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 764 LRSPDDI 771  
Db 273 LRSPDDI 280

RESULT 33  
D30047  
hypothetical protein SA2240 (imported) - *Staphylococcus aureus* (strain N315);  
C:Species: *Staphylococcus aureus*  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
C:Accession: D90047  
R:Kurda, M.; Chla, T.; Uchiyama, T.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Gu, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shib, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A>Title: Whole genome sequencing of *reficci* list-resistant *Staphylococcus aureus*.  
A:Reference number: A89758; X013:2311952; PMID:11418146  
A:Accession: D90047  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-450 <R>  
A:Cross-references: GB:BA000018; PID:g13702401; P:DN:BA843542.1; GSPDB:GN00149  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA2240

Query Match 1.0%; Score 8; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ECCLYINI 132  
Db 80 ECCLYINI 87

RESULT 34  
S32561  
cysteine proteinase - *Plasmodium vinckei*  
C:Species: *Plasmodium vinckei*  
C:Date: 22-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 13-Sep-1995  
C:Accession: S32561  
R:Roenthal, P.U.  
Biochim. Biophys. Acta 1173, 91-93, 1993  
A>Title: A *Plasmodium vinckei* cysteine proteinase shares unique features with its plasmod  
A:Reference number: S32561; PMID:9325055; PMID:8485161  
A:Accession: S32561  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-506 <R>  
A:Cross-references: GB:L08500  
C:Superfamily: trophozoite cysteine proteinase

Query Match 1.0%; Score 8; DB 2; Length 506;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 VTAVGAS 684  
Db 391 VTAVGAS 398

RESULT 35  
G69804  
multidrug-efflux transporter homolog YfiU - *Bacillus subtilis*  
C:Species: *Bacillus subtilis*

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: G69804  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
C: Bro, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.Y.;  
A: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabbet, C.; Ferrari,  
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gal  
lech, C.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, K.; Kurita, K.; Lapidus, A.; Lardinc  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Poterete  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scan  
A:Authors: Schleich, S.; Schriener, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zunshtein, E.; Yoshikawa, H.; Danchin, A.  
A>Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*  
A:Reference number: A69580; PMID:9804033; PMID:9384377  
A:Accession: G69804  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-518 <R>  
A:Cross-references: GB:299108; GB:AL009126; NID:G2633055; PIDN:CAB12669.1; PID:G263311  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yfiU  
A:Superfamily: multidrug-efflux transporter  
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 1.0%; Score 8; DB 1; Length 518;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VEQYLVGP 58  
Db 303 VEQYLVGP 307

RESULT 36  
T3252  
hypothetical protein T28C12.5 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T32052  
R:Ledwith, C.; Wohlmann, P.; Graves, T.; Bredshaw, H.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of *C. elegans* csmid T28C12.  
A:Reference number: Z21117  
A:Accession: T32052  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-539 <LED>  
A:Cross-references: EMBL:AF016679; PIDN:AA66162.1; GSPDB:GN00023; CESP:T28C12.5  
A:Experimental source: strain Bristol N2; clone T28C12  
C:Genetics:  
A:Gene: CESP:T28C12.5  
A:Map position: 5  
A:Introns: 16/3; 57/3; 112/3; 262/2; 316/1; 373/3; 466/2  
C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.0%; Score 8; DB 2; Length 539;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 LGFJSTGD 216  
Db 135 LGFJSTGD 142

RESULT 37  
S51C43  
carboxylesterase (EC 3.1.1.1) precursor - Atlantic salmon (fragment)  
N:Alternate names: carboxylester lipase



C:Species: *Salmo salar* (Atlantic salmon)  
 C:Date: 01-Aug-1995 #sequence\_revision 23-Feb-1996 #text\_change 18-Jun-1999  
 C:Accession: S51043; S37074  
 R:Gjellevik, D.R.; Lorenz, J.B.; Male, R.  
 Eur. J. Biochem. 226, 603-612, 1994  
 A:Reference number: S51043; MIM:950848.9; PMID:8601575  
 A:Reference number: S51043  
 A:Accession: S51043  
 A:Molecule type: mRNA  
 A:Residues: 1-540 <GDE>  
 A:Cross-references: EMBL:Z25967; NID:9397952; PIDN:CAA81087.1; PID:9397953  
 C:Superfamily: Cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase  
 F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:14-540/Product: carboxylesterase #status predicted <NMT>  
 F:43-538/Domain: cholinesterase homology <CHE>

Query Match 1.0%; Score 8; DB 2; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 NEDCLYN 132  
 DB 91 EDCLYNI 98

RESULT 38  
 S41090  
 triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (*Geotrichum candidum*) (strain ATCC 34614)  
 C:Species: *Geotrichum candidum*  
 A:Variety: ATCC 34614  
 C:Date: 19-Mar-1997 #sequence\_revision 05-Feb-1999 #text\_change 18-Jun-1999  
 C:Accession: S41090  
 R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.  
 Eur. J. Biochem. 219, 119-125, 1994  
 A:Title: Polymorphism in the lipase genes of *Geotrichum candidum* strains.  
 A:Reference number: S41090; MIM:94139683; PMID:8306978  
 A:Accession: S41090  
 A:Molecule type: DNA  
 A:Residues: 1-544 <BER>  
 A:Cross-references: GB:U02622; NID:9409275; PIDN:AAA03435.1; PID:9409276  
 A:Experimental source: ATCC 34614  
 A:Note: only the translation of the mature protein is shown  
 C:Genetics:  
 A:Gene: lip1  
 C:Function:  
 A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid  
 F:24-541/Domain: cholinesterase homology <CHE>  
 F:215-219/Region: interfacial lipid recognition (GXSGX) motif  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
 F:61-105-276-288/Disulfide bonds: #status predicted  
 F:217/Active site: Ser #status predicted  
 F:283-364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYN 131  
 DB 102 NEDCLYN 109

RESULT 39  
 S41092  
 triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (*Geotrichum candidum*) (strain NRRL Y-552)  
 C:Species: *Geotrichum candidum*  
 A:Variety: NRRL Y-552  
 C:Date: 19-Mar-1997 #sequence\_revision 05-Feb-1999 #text\_change 18-Jun-1999  
 C:Accession: S41092  
 R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.  
 Eur. J. Biochem. 219, 119-125, 1994  
 A:Title: Polymorphism in the lipase genes of *Geotrichum candidum* strains.  
 A:Reference number: S41090; MIM:94139683; PMID:8306978  
 A:Accession: S41092  
 A:Molecule type: DNA  
 A:Residues: 1-544 <BER>  
 A:Cross-references: GB:U02524; NID:9408459; PIDN:AAA03428.1; PID:9408459  
 A:Experimental source: NRRL Y-552  
 A:Note: only the translation of the mature protein is shown  
 C:Genetics:  
 A:Gene: lip1  
 C:Function:  
 A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid  
 F:24-541/Domain: cholinesterase homology <CHE>  
 F:215-219/Region: interfacial lipid recognition (GXSGX) motif  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
 F:61-105-276-288/Disulfide bonds: #status predicted  
 F:217/Active site: Ser #status predicted  
 F:283-364/Binding site: carboxylate (Asn) (covalent) #status predicted

R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.  
 Eur. J. Biochem. 219, 119-125, 1994  
 A:Title: Polymorphism in the lipase genes of *Geotrichum candidum* strains.  
 A:Reference number: S41090; MIM:94139683; PMID:8306978  
 A:Accession: S41091  
 A:Molecule type: DNA  
 A:Residues: 1-544 <BER>  
 A:Cross-references: GB:U02525; NID:9408460; PIDN:AAA03429.1; PID:9408461  
 A:Experimental source: NRCC 205002  
 A:Note: only the translation of the mature protein is shown  
 C:Genetics:  
 A:Gene: lip1  
 C:Function:  
 A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid  
 F:24-541/Domain: cholinesterase homology <CHE>  
 F:215-219/Region: interfacial lipid recognition (GXSGX) motif  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
 F:61-105-276-288/Disulfide bonds: #status predicted  
 F:217/Active site: Ser #status predicted  
 F:283-364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYN 131  
 DB 102 NEDCLYN 109

RESULT 40  
 S41092  
 triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (*Geotrichum candidum*) (strain ATCC 34614)  
 C:Species: *Geotrichum candidum*  
 A:Variety: NRRL Y-552  
 C:Date: 19-Mar-1997 #sequence\_revision 05-Feb-1999 #text\_change 18-Jun-1999  
 C:Accession: S41092  
 R:Bertolini, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.  
 Eur. J. Biochem. 219, 119-125, 1994  
 A:Title: Polymorphism in the lipase genes of *Geotrichum candidum* strains.  
 A:Reference number: S41090; MIM:94139683; PMID:8306978  
 A:Accession: S41092  
 A:Molecule type: DNA  
 A:Residues: 1-544 <BER>  
 A:Cross-references: GB:U02524; NID:9408459; PIDN:AAA03428.1; PID:9408459  
 A:Experimental source: NRRL Y-552  
 A:Note: only the translation of the mature protein is shown  
 C:Genetics:  
 A:Gene: lip1  
 C:Function:  
 A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglutamic acid  
 F:24-541/Domain: cholinesterase homology <CHE>  
 F:215-219/Region: interfacial lipid recognition (GXSGX) motif  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
 F:61-105-276-288/Disulfide bonds: #status predicted  
 F:217/Active site: Ser #status predicted  
 F:283-364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYN 131  
 DB 102 NEDCLYN 109

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RESULT 41
S41093
C:Species: Geotrichum candidum
C:Accession: S41093
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Berthelin, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
E:J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41093
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02387; NID:9406507; PIDN:AAA03425.1; PID:9406508
A:Experimental source: NRRL Y-553
A:Note: only the translation of the mature protein is shown
C:Genetics:
A:Gene: lpd1
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglytamc ac
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:61-105,276-288/Disulfide bonds: #status predicted
F:217/Active site: Ser #status predicted
F:283,364/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 131
Db 102 NEDCLYN 109

RESULT 42
S41094
C:Species: Geotrichum candidum
C:Accession: S41094
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Berthelin, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
E:J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41094
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02541; NID:9408468; PIDN:AAA03430.1; PID:9408469
A:Experimental source: NRCC 205002
A:Note: only the translation of the mature protein is shown
C:Genetics:
A:Gene: lpd1
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglytamc ac
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:61-105,276-288/Disulfide bonds: #status predicted
F:217/Active site: Ser #status predicted
F:283,364/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 131
Db 102 NEDCLYN 109

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 131
Db 102 NEDCLYN 109

RESULT 43
S41095
C:Species: Geotrichum candidum
C:Accession: S41095
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Berthelin, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
E:J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41095
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02623; NID:9409277; PIDN:AAA03436.1; PID:9409278
A:Experimental source: NRRL Y-552
A:Note: only the translation of the mature protein is shown
C:Genetics:
A:Gene: lpd1
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglytamc ac
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:61-105,276-288/Disulfide bonds: #status predicted
F:217/Active site: Ser #status predicted
F:283,364/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 131
Db 102 NEDCLYN 109

RESULT 44
S41096
C:Species: Geotrichum candidum
C:Accession: S41096
C:Date: 19-Mar-1997 #sequence_revision 05-Feb-1999 #text_change 18-Jun-1999
R:Berthelin, M.C.; Laramee, L.; Thomas, D.Y.; Cygler, M.; Schrag, J.D.; Vernet, T.
E:J. Biochem. 219, 119-125, 1994
A:Title: Polymorphism in the lipase genes of Geotrichum candidum strains.
A:Reference number: S41090; MUID:94139683; PMID:8306978
A:Accession: S41096
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-544 <BER>
A:Cross-references: GB:U02625; NID:9409279; PIDN:AAA03437.1; PID:9409280
A:Experimental source: NRRL Y-553
A:Note: only the translation of the mature protein is shown
C:Genetics:
A:Gene: lpd1
A:Description: hydrolyzes triacylglycerols into fatty acids and glycerol
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid hydrolysis; pyroglytamc ac
F:24-541/Domain: cholinesterase homology <CHE>
F:215-219/Region: interfacial lipid recognition (GXSG) motif

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F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
 F:61-105,276-288/Disulfide bonds: #status predicted  
 F:217/Active site: Ser #status predicted  
 F:293,364/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 2; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYLN 131  
 DB 102 NEDCLYLN 109

RESULT 45  
 ACCUGC  
 C:Triacylglycerol lipase (EC 3.1.1.3) I precursor - yeast (Geotrichum candidum)  
 N:Alternate names: lipase  
 C:Species: Geotrichum candidum  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 31-Mar-2000  
 C:Accession: P04992; J00022  
 R:Vagstad, T.; Shimada, Y.; Sugihara, A.; Tomimaga, Y.  
 J. Biochem. 113, 776-780, 1993  
 A:Title: Cloning and sequencing of two chromosomal lipase genes from Geotrichum candidum  
 A:Reference number: P04992; X01D:93380967; PMID:8376874  
 A:Accession: P04992  
 A:Molecule type: DNA  
 A:Residues: 1-563 <NAG>  
 A:Note: the translation of residues 31-550 and the corresponding nucleotide sequence are  
 R:Shimada, Y.; Sugihara, A.; Tomimaga, Y.; Iizumi, T.; Tsunawasa, S.  
 J. Biochem. 106, 383-388, 1989  
 A:Title: cDNA molecular cloning of Geotrichum candidum lipase.  
 A:Reference number: J00022; X01D:90110016; PMID:2481574  
 A:Accession: J00022  
 A:Molecule type: mRNA  
 A:Residues: 1-563 <SH1>  
 A:Experimental source: strain ATCC 34614  
 A:Note: sequences of several small peptides were also determined  
 C:Comment: The extracellular lipase produced by Geotrichum candidum hydrolyzes all ester  
 C:Genetics:  
 A:Gene: lip1  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; pyroglutamic acid  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-563/Product: triacylglycerol lipase #status experimental <MAT>  
 F:234-238/Region: cholinesterase homology <CHE>  
 F:234-238/Region: interfacial lipid recognition (GXSG) motif  
 F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F:80-124,295-307/Disulfide bonds: #status predicted  
 F:236/Active site: Ser #status predicted  
 F:302,393/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 1; Length 563;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYLN 131  
 DB 121 NEDCLYLN 129

RESULT 46  
 P04993  
 C:Triacylglycerol lipase (EC 3.1.1.3) II precursor - yeast (Geotrichum candidum)  
 C:Species: Geotrichum candidum  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jun-2000  
 C:Accession: P04993; A46760  
 R:Vagstad, T.; Shimada, Y.; Sugihara, A.; Tomimaga, Y.  
 J. Biochem. 113, 776-780, 1993  
 A:Title: Cloning and sequencing of two chromosomal lipase genes from Geotrichum candidum  
 A:Reference number: P04993; X01D:93380967; PMID:8376874  
 A:Accession: P04993  
 A:Molecule type: DNA

A:Residues: 1-563 <NAG>  
 A:Note: the translation of residues 31-550 and the corresponding nucleotide sequence  
 R:Shimada, Y.; Sugihara, A.; Iizumi, T.; Tomimaga, Y.  
 J. Biochem. 107, 703-707, 1990  
 A:Title: cDNA cloning and characterization of Geotrichum candidum lipase II.  
 A:Reference number: A46760; X01D:90375435; PMID:2398037  
 A:Accession: A46760  
 A:Molecule type: mRNA  
 A:Residues: 1-563 <SH1>  
 A:Cross-references: GB:D00697; NID:g217926; PID:BA00603.1; PID:g217927  
 C:Comment: The extracellular lipase produced by Geotrichum candidum hydrolyzes all es  
 C:Genetics:  
 A:Gene: lip1  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; pyroglutamic acid  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-563/Product: triacylglycerol lipase II #status predicted <MAT>  
 F:234-238/Region: cholinesterase homology <CHE>  
 F:234-238/Region: interfacial lipid recognition (GXSG) motif  
 F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
 F:80-124,295-307/Disulfide bonds: #status predicted  
 F:236/Active site: Ser #status predicted  
 F:302,393/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.0%; Score 8; DB 1; Length 563;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYLN 131  
 DB 121 NEDCLYLN 128

RESULT 47  
 P89068  
 C:Protein T26C12.4b [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
 C:Accession: P89068  
 R:Anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio  
 A:Reference number: A75000; X01D:99069613; PMID:9851916  
 A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C  
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;  
 A:Accession: P89068  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-578 <STO>  
 A:Cross-references: GB:chr\_V; PID:ABR66160.1; PID:g215744; GSPDB:GN00023; CESP:T26C  
 C:Genetics:  
 A:Gene: T26C12.4b  
 A:Map position: 5  
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.0%; Score 8; DB 2; Length 578;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 UGFLSTGD 216  
 DB 159 UGFLSTGD 166

RESULT 48  
 S25062  
 C:Triacylglycerol lipase (EC 3.1.1.3) precursor - rabbit  
 N:Alternate names: cholesteryl esterase  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S25062; S29847  
 R:Collwell, N.; Aleman-Gomez, G.; Kumar, V.B.  
 submitted to the EMBL Data Library, May 1992

A:Description: Molecular cloning and expression of rabbit cholesterol esterase reveals  
 A:Reference number: S25062  
 A:Accession: S25062  
 A:Molecule type: mRNA  
 A:Residues: 1-593 <COL>  
 A:Cross-references: EMBL:X65944  
 R:Colwell, N.S.; Aleman-Gomez, J.A.; Vijaya Kumar, S.  
 Biochim. Biophys. Acta 1172, 175-183, 1993  
 A:Title: Molecular cloning and expression of rabbit pancreatic cholesterol esterase.  
 A:Reference number: S29847; MUID:93176805; PMID:8439587  
 A:Accession: S29847  
 A:Molecule type: mRNA  
 A:Residues: 1-44, 'Ac', 47-416, 'W', 418-457, 'Q', 460-485, 'W', 487-499, 'GSARKHMEPTLTENQSYLETN'  
 A:Cross-references: EMBL:X65944  
 A:Note: the difference near the carboxyl end is due to a frameshift error  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-593/Product: triacylglycerol lipase #status predicted <MAT>  
 F:51-543/Domain: cholinesterase homology <CHE>  
 F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:214,453/Active site: Ser, His #status predicted

Query Match 1.0% Score 8; DB 1; Length 593;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 209 LGFLSTCD 216  
 |||||  
 168 LGFLSTCD 175

RESULT 49  
 ACRYE  
 A:Description: acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric ray  
 N:Alternate names: acetylcholinesterase, asymmetric form  
 C:Species: Torpedo californica (Pacific electric ray)  
 C:Date: 17-Mar-1987 #sequence, revision 38-Nov-1996 #ext. change 15-Sep-2003  
 C:Accession: A00773; A60820; A1962; A23902; B4117; S15677  
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphée-Quigley, K.; Taylor, S.S.; F  
 Nature 319, 407-409, 1986  
 A:Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its  
 A:Reference number: A00773; MUID:86118676; PMID:3753747  
 A:Accession: A00773  
 A:Molecule type: mRNA  
 A:Residues: 'NS', 11-596 <SCH>  
 A:Cross-references: GB:X03439; NID:364389  
 A:Experimental source: electric organ  
 A:Note: parts of this sequence, including the amino and carboxyl ends of the mature prot  
 R:Schumacher, M.; Camp, S.; Maule, Y.; Newton, M.; Macphée-Quigley, K.; Taylor, S.S.; F  
 Fed. Proc. 45, 2976-2981, 1986  
 A:Title: Primary structure of acetylcholinesterase: implications for regulation and fund  
 A:Reference number: A60820; MUID:87054662; PMID:3536598  
 A:Accession: A60820  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 22-596 <SC2>  
 R:Schumacher, M.; Maule, Y.; Camp, S.; Taylor, P.  
 J. Biol. Chem. 263, 18979-18987, 1988  
 A:Title: Multiple messenger RNA species give rise to the structural diversity in acetylch  
 A:Reference number: A92701; MUID:89066695; PMID:3198606  
 A:Accession: A31962  
 A:Molecule type: mRNA  
 A:Residues: 1-23 <SC3>  
 A:Cross-references: EMBL:X03439; NID:364389  
 A:Experimental source: clones AChE-11 and AChE-18  
 A:Note: revision to sequence A00773  
 A:Accession: B31962  
 A:Molecule type: DNA, mRNA  
 A:Residues: 499-565 <SC4>  
 A:Cross-references: GB:X03439; NID:364389  
 A:Experimental source: clone AChE-1  
 R:Macphée-Quigley, K.; Taylor, P.; Taylor, S.

J. Biol. Chem. 260, 12185-12189, 1985  
 A:Title: Primary structures of the catalytic subunits from two molecular forms of acetyl  
 A:Reference number: A23902; MUID:86008285; PMID:3390071  
 A:Accession: A23902  
 A:Molecule type: protein  
 A:Residues: 22, 'B', 24-45, 214-237 <MAC>  
 A:Note: active site Ser identification  
 R:Kreienkamp, H.C.; Weise, C.; Raba, R.; Aaviksoar, A.; Huch, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A:Title: Aromatic substrates of the catalytic center of acetylcholinesterase from Torped  
 A:Reference number: A41117; MUID:91296772; PMID:2068091  
 A:Accession: A41117  
 A:Molecule type: protein  
 A:Residues: 130-108 <KR3>  
 A:Note: substrate binding site  
 R:Maule, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstrom, T.J.; Taylor, P.  
 Neuron 4, 289-301, 1990  
 A:Title: Single gene encodes glycoprophospholipid-anchored and asymmetric acetylcholine  
 A:Reference number: F50113; MUID:90166618; PMID:2306366  
 A:Accession: S15677  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 557-596 <XAU>  
 A:Cross-references: EMBL:X65616  
 R:Macphée-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.  
 J. Biol. Chem. 261, 13565-13570, 1986  
 A:Title: Profile of the disulfide bonds in acetylcholinesterase.  
 A:Reference number: A43099; MUID:87008586; PMID:3759980  
 A:Contents: annotation: disulfide bonds  
 R:Susman, J.L.; Harel, M.; Silman, I.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A:Reference number: A50061; PDB:1ACE  
 A:Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-55  
 R:Susman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman,  
 Science 253, 872-879, 1991  
 A:Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototyp  
 A:Reference number: A43098; MUID:91343928; PMID:1678899  
 A:Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-55  
 C:Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with  
 cholinesterase occurs on the outer surfaces of cell membranes, including those of erythro  
 C:Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer  
 C:Function:  
 A:Description: hydrolyzes acetylcholine to choline and acetate  
 A:Pathway: neurotransmitter degradation  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>  
 F:51-551/Domain: cholinesterase homology <CHE>  
 F:180,478,554/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:198-115,275-286,423-542/Disulfide bonds: #status experimental  
 F:105/Binding site: substrate (Tyr) #status experimental  
 F:121/Active site: Ser #status experimental  
 F:148,461/Active site: Glu, His #status predicted  
 F:437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:593/Disulfide bonds: interchain #status experimental

Query Match 1.0% Score 6; DB 1; Length 596;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 125 EDCYLTNI 132  
 |||||  
 113 EDCYLTNI 120

RESULT 50  
 A38866  
 A:Description: acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray  
 C:Species: Torpedo marmorata (marbled electric ray)  
 C:Date: 23-Apr-1993 #sequence, revision 15-Nov-1996 #ext. change 11-Jun-1999  
 C:Accession: A38866; A29682; S15696; A25650  
 R:Massoulié, C.; Bon, S.

submitted to the EMBL Data Library, June 1992

A:Reference number: A38868

A:Accession: A38868

A:Molecule type: mRNA

A:Residues: 1-599 <MAC>

A:Cross-references: EMBL:X65497; NID:g64424; PIDs:CAA29347.1; FID:g64415

R:Stokrov, J.L.; Krejci, E.; Massoulié, J.

EMBO J. 6, 1865-1873, 1987

A:Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of

A:Reference number: A29682; MUID:88004392; PMID:2820703

A:Accession: A29682

A:Molecule type: mRNA

A:Residues: 1-40, 'G', 'A', '2-226, 'G', '228-272, 'G', '274-284, 'E', '286-420, 'N', '422-599 <SIG>

A:Cross-references: EMBL:X65497

R:Stokrov, J.L.; Duval, N.; Anselmetti, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.

EMBO J. 7, 2983-2993, 1988

A:Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo e

A:Reference number: S01293; MUID:89030590; PMID:3161125

A:Accession: S15696

A:Molecule type: mRNA

A:Residues: 526-599 <SIG>

A:Cross-references: EMBL:X13172; NID:g64416; PIDs:CAA31570.1; PID:g64417

A:Experimental source: clone PAC22

R:Bon, S.; Chang, J.Y.; Strosberg, A.D.

FEBS Lett. 289, 206-212, 1986

A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-sol

A:Reference number: A9-370; MUID:8780761; PMID:3792544

A:Accession: A25650

A:Molecule type: protein

A:Residues: 25-40, 'G', 'A', '42-47 <RON>

C:Genetics:

A:Gene: AChE

C:Function:

A:Description: hydrolyzes acetylcholine to choline and acetate

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmi

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-599/Product: acetylcholinesterase #status predicted <MAC>

F:54-554/Domain: acetylcholinesterase homology <CHE>

F:83-440-481-557/Binding site: carbonyl site: (covalent) #status predicted

F:9-118-278-289-426-545/D:disulfide bonds: #status predicted

F:224-351-464/Active site: Ser, Glu, His #status predicted

F:596/Disulfide bonds: interchain #status predicted

Query Match 1.0%; Score 8; DB 2; Length 599;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNT 132

DB 116 EDCLYNT 123

RESULT 5:

A57701

sterol esterase (EC 3.1.1.13) precursor - mouse

N:Alternate names: bile salt-stimulated lipase; carboxy ester lipase; cholesterol ester

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 21-Jan-2000

C:Accession: A57701; J04384

R:Edmer, A.S.; Kamitani, K.; Jundberg, L.; Bjursell, G.; Nilsson, G.

Genomics 29, 115-122, 1995

A:Title: Molecular cloning and characterization of the mouse carboxyl ester lipase gene

A:Reference number: A57701; MUID:86079098; PMID:8530660

A:Accession: A57701

A:Molecule type: preliminary

A:Residues: 1-599 <LID>

A:Cross-references: GB:U37396; NID:g1049321; PIDs:AA625279.1; FID:g1049322

R:Mackay, K.; Lawn, R.M.

Gene 165, 255-259, 1995

A:Title: Characterization of the mouse pancreatic/mammary gland cholesterol esterase

A:Reference number: J04384; MUID:96096531; PMID:8522186

A:Accession: J04384

A:Molecule type: mRNA

A:Residues: 1-599 <MAC>

A:Cross-references: GB:U33169; NID:g1046362; PIDs:AAA20088.1; PID:g1046363

A:Experimental source: mammary gland

C:Comment: This enzyme is synthesized in the pancreas and is transported to the intest

cholesterol esters and fat-soluble vitamin esters, and acts synergistically with pan

ids.

C:Genetics:

A:Gene: CEase

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; cholesterol; heparin binding; mammary gland;

F:1-30/Domain: signal sequence #status predicted <SIG>

F:21-599/Product: sterol esterase #status predicted <MAC>

F:51-585/Domain: cholinesterase homology <CHE>

F:81-86/Region: heparin binding #status predicted

F:214-340-455/Active site: Ser, Asp, His #status predicted

Query Match 1.0%; Score 8; DB 2; Length 599;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNT 132

DB 98 EDCLYNT 105

RESULT 52

T37254

acetylcholinesterase (EC 3.1.1.7) 4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000

C:Accession: T37254

R:Grasso, M.; Culetto, E.; Combes, D.; Fedon, Y.; Tavant, J.P.; Arpagaus, M.

FEBS Lett. 424, 279-284, 1998

A:Title: Existence of four acetylcholinesterase genes in the nematodes Caenorhabdit

A:Reference number: 221648; MUID:98198570; PMID:9539167

A:Accession: T37254

A:Status: preliminary; translated from GB/EMBL/DDDU

A:Molecule type: mRNA

A:Residues: 1-602 <GRA>

A:Cross-references: EMBL:AF025379; NID:g5091493; PIDs:AA014017.1; PID:g5057126

A:Experimental source: strain N2

C:Genetics:

A:Gene: ace-4

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase

Query Match 1.0%; Score 8; DB 2; Length 602;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNT 132

DB 113 EDCLYNT 120

RESULT 53

A34967

sterol esterase (EC 3.1.1.13) precursor - rat

N:Alternate names: bile salt-stimulated lipase; carboxy ester lipase; cholesterol e

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Mar-1991 #sequence\_revision 22-Apr-1995 #text\_change 13-Aug-1999

C:Accession: A34967; A26603; A39595; S33476

R:Kissel, J.A.; Fontaine, R.N.; Turk, C.W.; Brockman, H.L.; Hu, D.Y.

Biochim. Biophys. Acta 1006, 227-236, 1989

A:Title: Molecular cloning and expression of cDNA for rat pancreatic cholesterol est

A:Reference number: A34967; MUID:90089378; PMID:2688744

A:Accession: A34967

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-512, 'T', 514-612 <KIS>  
 A:Cross-references: GB:X16054; NID:G955942; PIDN:CAA34169.1; PID:G955943  
 R:Han, J.H.; Stratowa, C.; Rulter, W.J.  
 C:Species: Aedes aegypti (yellow fever mosquito)  
 C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
 C:Accession: S66236  
 R:Anthony, N.; Rocheleau, T.; Mocelin, G.; See, H.C.; French-Constant, R.  
 FEBS Lett. 366, 461-465, 1995  
 A:Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene  
 A:Reference number: S66236; MUID:95361924; FXID:7655199  
 A:Accession: S66236  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-637 <ANT>  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-637/Product: acetylcholinesterase #status predicted <MAT>  
 F:57-594/Domain: cholinesterase homology <CH>

Query Match 1.0%; Score 8; DB 2; Length 612;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCJYINI 132  
 Db 98 EDCJYINI 105

RESULT 54  
 S66236  
 acetylcholinesterase (EC 3.1.1.7) precursor - yellow fever mosquito  
 C:Species: Aedes aegypti (yellow fever mosquito)  
 C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
 C:Accession: S66236  
 R:Anthony, N.; Rocheleau, T.; Mocelin, G.; See, H.C.; French-Constant, R.  
 FEBS Lett. 366, 461-465, 1995  
 A:Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene  
 A:Reference number: S66236; MUID:95361924; FXID:7655199  
 A:Accession: S66236  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-637 <ANT>  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-637/Product: acetylcholinesterase #status predicted <MAT>  
 F:57-594/Domain: cholinesterase homology <CH>

hypothetical protein T02B5.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
 C:Accession: T24344  
 R:McMurtry, A.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: 219878  
 A:Accession: T24344  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-656 <WIL>  
 A:Cross-references: EMBL:T81112; PIDN:CA903273.1; GSPDB:GN00023; CESP:T02B5.3  
 A:Experimental source: clone T02B5  
 A:Gene: CESP:T02B5.3  
 C:Genetics:  
 A:Map position: 5  
 A:Introns: 24/2; 90/2; 120/3; 188/1; 224/3; 283/3; 332/2; 412/2; 517/2; 622/1  
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.0%; Score 8; DB 2; Length 656;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 TNYEIGI 208  
 Db 162 TNYEIGI 169

RESULT 56  
 T32053  
 hypothetical protein T28C12.4a - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 01-Dec-2000  
 C:Accession: T32053; T32054  
 R:Edwith, J.; Wohldmann, P.; Graves, T.; Bradshaw, H.  
 submitted to the EMBL Data Library, July 1997  
 A:Description: The sequence of C. elegans cosmid T28C12.  
 A:Reference number: Z21117  
 A:Accession: T32053  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-658 <LED>  
 A:Cross-references: EMBL:AF036679; PIDN:AA66559.1; GSPDB:GN00023; CESP:T28C12.4a  
 A:Experimental source: strain Bristol K2; clone T28C12  
 A:Accession: T32054  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 61-658 <LED>  
 A:Cross-references: EMBL:AF036679; PIDN:AA66559.1; GSPDB:GN00023; CESP:T28C12.4b  
 A:Experimental source: strain Bristol N2; clone T28C12  
 C:Genetics:  
 A:Gene: CESP:T28C12.4a; CESP:T28C12.4b  
 A:Map position: 5  
 A:Introns: 70/1; 96/3; 137/3; 192/3; 366/2; 423/1; 480/3; 573/2  
 C:Superfamily: cholinesterase; cholinesterase homology

Query Match 1.0%; Score 8; DB 2; Length 658;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 LGFLSTGD 216  
 Db 239 LGFLSTGD 246

RESULT 57  
 T27394  
 hypothetical protein Y75B8A.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T27394  
 R:Barlow, K.  
 submitted to the EMBL Data Library, November 1998

A:Reference number: Z20361  
A:Accession: T77394  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-672 <WIL>  
A:Cross-references: EMBL:AL033514; NID:el343851; PDB:QMA2054.1; CESP:Y7538A.3  
A:Experimental source: clone Y7538A  
A:Genetics:  
A:Gene: CESP:Y7538A.3  
A:Introns: 52/1; 126/3; 243/1; 475/3; 525/1; 615/3

Query Match 1.0%; Score 8; DB 2; Length 672;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 124 NEDCLYN 121  
Db 114 NEDCLYN 121

RESULT 58  
T16455  
hypothetical protein F55D10.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T16455  
R:Leimbach, J.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid F55D10.  
A:Reference number: Z18516  
A:Accession: T16455  
A:Status: preliminary; translated from GE/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-730 <LEI>  
A:Cross-references: EMBL:U40948; NID:91072223; PID:91072224; PDB:AAA6127.1; CESP:F55D10.3  
A:Genetics:  
A:Gene: CESP:F55D10.3  
A:Introns: 48/3; 125/3; 181/3

Query Match 1.0%; Score 8; DB 2; Length 730;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 125 EDCLYLN 132  
Db 170 EDCLYLN 177

RESULT 59  
G64157  
probable organic solvent tolerance protein precursor H10730 - Haemophilus influenzae 'est  
C:Species: Haemophilus influenzae  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 28-Jul-2000  
C:Accession: G64157  
R:Fleischmann, R.C.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kesteven, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995  
A:Authors: Greth, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: M64000; MUID:95350630; PMID:7542800  
A:Accession: G64157  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-782 <TICR>  
A:Cross-references: GB:U3756; GB:42023; NID:51573729; PDB:AAQ2389.1; PID:G1573734;  
A:Superfamily: organic solvent tolerance protein  
C:Keywords: periplasmic space  
F:1-73/Domain: signal sequence #status predicted <SIG>  
F:24-782/Product: organic solvent tolerance protein #status predicted <MA>

Query Match 1.0%; Score 8; DB 1; Length 782;  
Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 50 PVEQYGV 57  
Db 705 PVEQYGV 712

RESULT 60  
A42112  
mucin-like peptide MLP 2677 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 10-Oct-1997  
C:Accession: A42112  
R:Xu, G.; Han, L.; Khatri, I.A.; Wang, D.; Bennick, A.; Fahim, R.E.; Forstner, G.; Biol. Chem. 267, 5401-5407, 1992  
A:Title: cDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide  
A:Reference number: A42112; MUID:92184794; PMID:1371999  
A:Accession: A42112  
A:Status: preliminary  
A:Molecule type: nucleic acid; protein  
A:Residues: 1-837 <XU>  
A:Experimental source: intestine  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBI:87420)  
C:Superfamily: von Willebrand factor type C repeat homology  
F:582-650/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 1.0%; Score 8; DB 2; Length 937;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 635 TTKRPAIT 642  
Db 329 TTKRPAIT 336

RESULT 61  
A53215  
protein kinase C (EC 2.7.1.1-) mu precursor - human  
N:Alternate names: protein kinase D  
C:Species: Homo sapiens (man)  
C:Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 11-Jun-1999  
C:Accession: A53215; S40279  
R:Johannes, F.J.; Prestle, J.; Eis, S.; Oberhagenann, P.; Pfleiderer, K.; J. Biol. Chem. 269, 6140-6146, 1994  
A:Title: PKCmu is a novel, atypical member of the protein kinase C family.  
A:Reference number: A53215; MUID:94164979; PMID:8119958  
A:Accession: A53215  
A:Molecule type: mRNA  
A:Residues: 1-912 <JOH>  
A:Cross-references: EMBL:X75756; NID:9438372; PDB:QMA53384.1; PID:9438373  
A:Genetics:  
A:Gene: GDB:FRKCM; HS:2891; PKCM  
A:Cross-references: GDB:330794  
A:Map position: 21pter-21qter  
C:Function:  
A:Description: catalyzes the formation of peptideL-serine-phosphate or peptideL-thre  
A:Note: expressed at low levels in a variety of tissues; phosphorylates a 30k protei  
ers  
C:Superfamily: protein kinase C mu; protein kinase C zinc-binding repeat homology; F  
C:Keywords: ATP; autophosphorylation; duplication; phospholipid binding; phosphoran  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:126-912/Product: protein kinase mu #status predicted <MAT>  
F:147-196/Domain: protein kinase C zinc-binding repeat homology <K21>  
F:171-320/Domain: protein kinase C zinc-binding repeat homology <K22>  
F:581-839/Domain: protein kinase homology <K1N>  
F:589-597/Region: protein kinase ATP-binding motif  
F:612,630,706,708/Active site: Lys, Glu, Asp, Tyr #status predicted

Query Match 1.0%; Score 8; DB 1; Length 912;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDEDIDHQ 163  
 DB 795 EDEDIDHQ 792

## RESULT 62

148719  
 protein kinase C (EC 2.7.1.1) mu precursor - mouse  
 N:Alternate names: protein kinase D  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jun-1999  
 C:Accession: 148719  
 R:Valverde, A.M.; Simmet-Smith, J.; Van Lint, C.; Rozengurt, E.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 8572-8576, 1994  
 A>Title: Molecular cloning and characterization of protein kinase D: a target for diacyl  
 A:Reference number: 148719; MIM:14359973; PMID:8078925  
 A:Accession: 148719  
 A>Status: translated from GE/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-918 <RES>  
 A:Cross-references: EMBL:Z34524; NID:9520877; PID:CAA84283.1; PID:9520878

## C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
 sely related human enzyme, this protein is reported to bind phorbol esters  
 C:Superfamily: protein kinase C mu; protein kinase C zinc-binding repeat homology; prote  
 C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid  
 F:1-25/Domains: signal sequence #status predicted <SIG>  
 F:126-918/Product: protein kinase mu #status predicted <MAT>  
 F:145-194/Domains: protein kinase C zinc-binding repeat homology <KZ1>  
 F:227-326/Domains: protein kinase C zinc-binding repeat homology <KZ2>  
 F:587-845/Domains: protein kinase homology <KLN>  
 F:595-603/Region: protein kinase ATP-binding motif  
 F:618,636,712,714/Active site: Cys, Glu, Asp, Lys #status predicted

## Query Match

Best Local Similarity 100.0%; Score 6; DB 1; Length 918;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDEDIDHQ 163  
 DB 791 EDEDIDHQ 798

## RESULT 63

561041  
 glutamate synthase (NADH2) (EC 1.4.1.14) glt- precursor [similarity] - yeast (Saccharomy  
 N:Alternate names: protein D:448; protein YCD171c  
 C:Species: Saccharomyces cerevisiae  
 C>Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 03-Jun-2002  
 C:Accession: 561041; S67723  
 R:Polh, T.M.  
 submitted to the EMBL Data Library, November 1995  
 A:Reference number: S61041  
 A:Accession: S61041  
 A:Molecule type: DNA  
 A:Residues: 1-2145 <POH>  
 A:Cross-references: EMBL:Z67750; NID:9161256; PID:CAA91574.1; PID:9161267  
 R:Polh, T.M.  
 submitted to the Protein Sequence Database, July 1996  
 A:Reference number: S67708  
 A:Accession: S67723  
 A:Molecule type: DNA  
 A:Residues: 1-2145 <POW>  
 A:Cross-references: EMBL:Z74219; NID:91431273; PID:CAA98745.1; PID:91431274; MIPS:YDL17  
 A:Experimental source: strain S289C  
 C:Genetics:  
 A:Gene: SGD:GLT1  
 A:Cross-references: SGD:S0002330; MIPS:YDL171c  
 A:Map position: 4L  
 C:Superfamily: glutamate synthase (NADH)  
 C:Keywords: 3Fe-4S; metalloprotein; oxidoreductase; transmembrane protein  
 F:1-53/Domains: propeptide #status predicted <PRO>

F:54-2145/Product: glutamate synthase #status predicted <YLT>  
 F:1077-1093/Domains: transmembrane #status predicted <TM1>  
 F:1172-1188/Domains: transmembrane #status predicted <TM2>  
 F:54/Active site: Cys #status predicted  
 F:1185,1191,1196/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 100%; Score 8; DB 2; Length 2145;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 KRREHTR 709  
 DB 1648 KRREHTR 1655

## RESULT 64

534739  
 trans-cinnamate 4-monooxygenase (EC 1.14.13.11) - kidney bean (fragment)  
 N:Alternate names: trans-cinnamic acid hydroxylase  
 C:Species: Phaseolus vulgaris (kidney bean)  
 C>Date: 19-Mar-1997 #sequence\_revision 07-Nov-1997 #text\_change 05-Mar-1999  
 C:Accession: 534739  
 R:Rodgers, M.W.; Zimmerlin, A.; Merck-Reichardt, D.; Bolwell, G.P.  
 Arch. Biochem. Biophys. 304, 74-80, 1993  
 A>Title: Microsomal associated heme proteins from French bean: characterization of  
 A:Reference number: 534739; MIM:93312024; PMID:8323300  
 A:Molecule type: protein  
 A:Residues: 1-23 <ROD>  
 C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
 C:Keywords: heme; oxidoreductase

Query Match 0.9%; Score 7; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 439 KTIWALF 445  
 DB 8 KTIWALF 14

## RESULT 65

A38296  
 sterol esterase (EC 3.1.1.13) - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 14-Nov-1997  
 C:Accession: A38296  
 R:D'Persio, L.P.; Fontaine, R.N.; Hui, D.Y.  
 J. Biol. Chem. 265, 16801-16806, 1990  
 A>Title: Identification of the active site serine in pancreatic cholesteryl esterase  
 A:Reference number: A38296; MIM:91009095; PMID:2211595  
 A:Accession: A38296  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-29 <DIP>  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein

Query Match 0.9%; Score 7; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 AFGGDPK 247  
 DB 11 AFGGDPK 17

## RESULT 66

742967  
 hypothetical protein 53 - ateline herpesvirus 3 (strain 73)  
 C:Species: ateline herpesvirus 3  
 A:Variety: strain 73  
 C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 19-May-2000



C/Accession: T42967  
R:Albrecht, C.C.; Fleckenstein, B.  
Submitted to the EMBL Data Library, August 1998  
A:Description: Primary structure of the herpesvirus acies genome.  
A:Reference number: 222274  
A:Accession: T42967  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-89 <ALB>  
A:Cross-references: EMBL:AF063424; PIDN:AAC95579.1  
A:Experimental source: strain 73  
C:Superfamily: cytomagalovirus UL73 protein

Query Match 0.9%; Score 7; DB 2; Length 89;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 GASTLFL 688  
|||||  
DB 63 GASTLFL 75

RESULT 67  
F70511  
Probable PE protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 03-Nov-2000  
C/Accession: F70511  
R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: F70511  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-98 <COL>  
A:Cross-references: GB:Z97559; GB:AL123456; NID:G3361820; PIDN:GAB10700.1; PID:ej29638;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: PE  
C:Superfamily: Mycobacterium leprae hypothetical protein B1620\_C2\_218

Query Match 0.9%; Score 7; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 TTKVPP 616  
|||||  
DB 36 TTKVPP 42

RESULT 66  
A73155  
Hypothetical protein PAB2083 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
C/Accession: A73155  
R:anonymous; Genoscope  
Submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
A:Reference number: A73001  
A:Accession: A73155  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-103 <KAM>  
A:Cross-references: GB:AJ248284; GB:AJ096836; NID:G5457730; PIDN:GAB49320.1; PID:e51522  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB2083

Query Match 0.9%; Score 7; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 YGRRSP 629  
|||||  
DB 74 YGRRSP 80

RESULT 69  
AG1814  
Ribosome binding factor A (imported) - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C/Accession: AG1814  
R:Karako, T.; Nakamura, Y.; WolK, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriig  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takakawa, N.; Yamada, M.; Yasuda, M.; Tabata  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG1814  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-113 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA877587.1; PID:G17135041; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: rbfA  
C:Superfamily: Escherichia coli protein P15B

Query Match 0.9%; Score 7; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 RSPDIP 772  
|||||  
DB 118 RSPDIP 124

RESULT 70  
G39768  
Cholinesterase (EC 3.1.1.8) - rhesus macaque (fragment)  
C:Species: Macaca mulatta (rhesus macaque)  
C>Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 18-Jun-1999  
C/Accession: G39768  
R:Arpaian, M.; Chaconnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.;  
C: Biol. Chem. 266, 6966-6974, 1991  
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinase  
A:Reference number: A39768; MUID:91201348; PMID:2016308  
A:Accession: G39768  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-141 <ARP>  
A:Cross-references: GB:M62777; NID:G342078; PIDN:AAA16836.1; PID:G342079  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; glycoprotein  
F.1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match 0.9%; Score 7; DB 2; Length 141;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYN 131  
|||||  
DB 23 EDCLYN 29

RESULT 71  
B39768  
Cholinesterase (EC 3.1.1.8) - sheep (fragment)  
C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)  
C>Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 18-Jun-1999

C:Accession: E39768  
 R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Barreils, C.F.; Nog  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester  
 A:Reference number: A39768; MUID:91201348; PMID:2016306  
 A:Accession: E39768  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-141 <ARP>  
 A:Cross-references: GB:M62780; NID:G165830; PIDN:AAA1509.1; PID:G165831  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match 0.9%; Score 7; DB 2; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 EDCLYLN 131  
 Db 23 EDCLYLN 29

RESULT 72  
 E39768  
 Cholinesterase (EC 3.1.1.8) - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 18-Jun-1999  
 A:Accession: E39768  
 R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Barreils, C.F.; Nog  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester  
 A:Reference number: A39768; MUID:91201348; PMID:2016306  
 A:Accession: E39768  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-141 <ARP>  
 A:Cross-references: GB:M62410; NID:G162738; PIDN:AAA51412.1; PID:G162739  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match 0.9%; Score 7; DB 2; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 EDCLYLN 131  
 Db 23 EDCLYLN 29

RESULT 73  
 E39768  
 Cholinesterase (EC 3.1.1.8) - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 16-Jun-1999  
 A:Accession: E39768  
 R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Barreils, C.F.; Nog  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester  
 A:Reference number: A39768; MUID:91201348; PMID:2016306  
 A:Accession: E39768  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-141 <ARP>  
 A:Cross-references: GB:M62778; NID:G164387; PIDN:AAA1005.1; PID:G164388  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match 0.9%; Score 7; DB 2; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131  
 Db 23 EDCLYLN 29

RESULT 74  
 E39768  
 Cholinesterase (EC 3.1.1.8) - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 18-Jun-1999  
 A:Accession: E39768  
 R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Barreils, C.F.;  
 J. Biol. Chem. 266, 6966-6974, 1991  
 A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholine  
 A:Reference number: A39768; MUID:91201348; PMID:2016306  
 A:Accession: E39768  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-141 <ARP>  
 A:Cross-references: GB:M62411; NID:G163910; PIDN:AAA51451.1; PID:G163911  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:1-141/Domain: cholinesterase homology (fragment) <CHE>

Query Match 0.9%; Score 7; DB 2; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

125 EDCLYLN 131  
 Db 23 EDCLYLN 29

RESULT 75  
 A41503  
 AF/R1 pilus chain A precursor - Escherichia coli (strain RDEC-1)  
 C:Species: Escherichia coli  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Oct-1999  
 R:Wolff, M.K.; Bodeker, E.C.  
 Infect. Immun. 58, 1124-1128, 1990  
 A:Title: Cloning of the genes for AF/R1 pilin from rabbit enteroadherent Escherichia  
 A:Reference number: A41503; MUID:90202141; PMID:2969392  
 A:Accession: A41503  
 A:Molecule type: DNA  
 A:Residues: 1-162 <MOJ>  
 A:Cross-references: GB:M32083; NID:G145209; PIDN:AAA23422.1; PID:G145210  
 C:Comment: An 86-megadalton plasmid mediates production of the AF/R1 pilus for attac  
 the AF/R1 pilus.  
 C:Genetics:  
 A:Gene: atpA  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-162/Product: AF/R1 pilus A chain #status predicted <VAR>

Query Match 0.9%; Score 7; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 VIVITIN 203  
 Db 9 VIVITIN 15

Search completed: November 5, 2003, 15:26:16  
 Job time : 24 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 5, 2003, 15:25:49 ; Search time 35 Seconds

(without alignments)  
4004.212 Million cell updates/sec

Title: US-09-978-423a-375

Perfect score: 816

Sequence: 1 WNSNVLMKTALAIKRTLI.....TFSGGQNTLPHGHSTTRY 816

Scoring table: CLUSTAL W, Gapcost 60.0

Searched: 644079 seqs, 171749292 residues

Word size: 0

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: Published Applications AA:  
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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95	7	0.9	103	11	US-09-764-872-254	Sequence 254, App
96	7	0.9	109	15	US-10-083-357-775	Sequence 775, App
97	7	0.9	117	8	US-08-976-063C-12	Sequence 12, Appl
98	7	0.9	134	15	US-10-156-761-15049	Sequence 15049, A
99	7	0.9	147	11	US-09-984-271-209	Sequence 209, App
100	7	0.9	172	12	US-10-029-386-32562	Sequence 32562, A

## ALIGNMENTS

RESULT 1  
US-09-978-295A-375Sequence 375, Application US/09978295A  
Patent No. US20020156006A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

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APPLICANT: Hillan, Kenneth J

APPLICANT: Kijavits, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Kuper, Mary A.

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic

FILE REFERENCE: P26302C11

CURRENT APPLICATION NUMBER: US/09/978, 295A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 10; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SPTGRRRPPPPPSWSWGIKNTTFAAFCCHLDERSLSDMKPIWTFALDLMTV 120  
CY 121 QDNEFCYLNIVFTEGANTKXADITSDRGEDEDIHQNSKKPMVYIHGGSYME 180  
DB 121 QDNEFCYLNIVFTEGANTKXADITSDRGEDEDIHQNSKKPMVYIHGGSYME 180  
CY 181 GTGNMIDGSLASGVNVTITNYRGLIGLGLSLGDAQAKKYGILLDOIALRMIEENV 240  
DB 181 GTGNMIDGSLASGVNVTITNYRGLIGLGLSLGDAQAKKYGILLDOIALRMIEENV 240  
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RESULT 2  
US-09-978-697-375  
Sequence 375, Application US/03978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen  
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APPLICANT: Kijavitt, Yaw J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Kapley, Yany A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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RESULT 3  
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Sequence 375, Application US/09978192A  
Patent No. US20020177553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Harpeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillier, Kenneth J.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William J.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FID REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978, 192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30

[illegible]





PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
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PRIOR APPLICATION NUMBER: 60/083322

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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 816; DB 10; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 61 SPTGRGRRFPQPPSPSWTSGIRNTQFAVCPGHLDESLHDMPIWFTNLTJLMTYV 120

Db 61 SPTGERRFPPEPPSSMTGIRNTQFANVCQHLDERSLHEKXLMITFANTLDTMTV 120  
QY 121 OQONEDCLYNIVYPTEDGANTKKNADJITSNDGEDEDIHQNSKKPVMVYHGGSYME 180  
Db 122 OQONEDCLYNIVYPTEDGANTKKNADJITSNDGEDEDIHQNSKKPVMVYHGGSYME 180  
QY 181 GTGNMIGSILASTGNYVITINRGLDLPSTGDAKANGGLDDOIALMIEENNG 240  
Db 181 GTGNMIGSILASTGNYVITINRGLDLPSTGDAKANGGLDDOIALMIEENNG 240  
QY 241 AFGDPKRVTFSSGAGASCUSLTLSSHSEGLFOKATIDSGTASASMANVQPAKYTE 300  
Db 241 AFGDPKRVTFSSGAGASCUSLTLSSHSEGLFOKATIDSGTASASMANVQPAKYTE 300  
QY 301 LADKVCNMDLTTDMVECLRRKRYKELDQITPATYHIAFGPVIDGVPIDPQJLMEQ 360  
Db 301 LADKVCNMDLTTDMVECLRRKRYKELDQITPATYHIAFGPVIDGVPIDPQJLMEQ 360  
QY 361 GEFINDIMLVNQGBGLKFEVDGVNKEDEVNEDPFSVSNVENVYGFBSKCTLAE 420  
Db 361 GEFINDIMLVNQGBGLKFEVDGVNKEDEVNEDPFSVSNVENVYGFBSKCTLAE 420  
QY 421 IKPMYTCMAKXENETBRKCTVALFTCHQVAVAVAADHAQYSPTYFAFYHGOSEM 480  
Db 421 IKPMYTCMAKXENETBRKCTVALFTCHQVAVAVAADHAQYSPTYFAFYHGOSEM 480  
QY 481 KPSWADSHGDEVPYVFGIPMIGPTELFSCNFSKNDVYSATVYVYTWTFKAGDPKQV 540  
Db 481 KPSWADSHGDEVPYVFGIPMIGPTELFSCNFSKNDVYSATVYVYTWTFKAGDPKQV 540  
QY 541 POCFELHTKXNRFEEVAMSKNPKDLYHIGLKPVRSHYBATAKVAFLVPSJHML 600  
Db 541 POCFELHTKXNRFEEVAMSKNPKDLYHIGLKPVRSHYBATAKVAFLVPSJHML 600  
QY 601 NEFOYVSTTKVPPDMTSFPYTRRSPAKMTPTSRPAITPAANPKSKCKHKTGPD 660  
Db 601 NEFOYVSTTKVPPDMTSFPYTRRSPAKMTPTSRPAITPAANPKSKCKHKTGPD 660  
QY 661 TTVLETKDYSELSTVIAVGASJLFLNLAFAPALYKCKKRRHETRRSPQRNTND 720  
Db 661 TTVLETKDYSELSTVIAVGASJLFLNLAFAPALYKCKKRRHETRRSPQRNTND 720  
QY 721 IAHQNEIMSLQKQLEHDBECSCAHQTLTGPDDYTLTFRSPDIPXTNNTT 780  
Db 721 IAHQNEIMSLQKQLEHDBECSCAHQTLTGPDDYTLTFRSPDIPXTNNTT 780  
QY 781 MIPNLTGMQPLHTFNTFSSGQNSTLPHSHSTRV 816  
Db 781 MIPNLTGMQPLHTFNTFSSGQNSTLPHSHSTRV 816

RESULT 5  
US-09-978-189-375  
Sequence 375, Application US/C9978189  
Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul C.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavrin, Ivar C.

APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William J.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978.189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/066250  
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PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match: 100.0%; Score 816; DB 1; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 916; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MNSVLLMTALAIKFTLDSQAYPVWNTYKIRGLRPLFNEILGPECYLGPPYA 60  
61 SEPTGERPQPEPPSSWTGIRNTTQFANVCPQHLDBSLHMLPLWFTNLDTMTYV 120  
61 SEPTGERPQPEPPSSWTGIRNTTQFANVCPQHLDBSLHMLPLWFTNLDTMTYV 120  
121 QDNEDCLYNIYVTEEGANTKRAODITSDRGEDECIHDQSKKPVWYTHGGSYME 180  
121 QDNEDCLYNIYVTEEGANTKRAODITSDRGEDECIHDQSKKPVWYTHGGSYME 180  
181 GTGNMIDSLASYNVIVITINRGLGEFSTGQAAKQNYGLLDQIALRWIEENVG 240  
181 GTGNMIDSLASYNVIVITINRGLGEFSTGQAAKQNYGLLDQIALRWIEENVG 240  
241 AFGSDPKAVITFGSAGASCVSLLTSHYSSGLCKALIOGCTALSSAANVCPAKYTRI 300  
241 AFGSDPKAVITFGSAGASCVSLLTSHYSSGLCKALIOGCTALSSAANVCPAKYTRI 300  
301 LADKVGCMMLDTTDWVECLRNKYNKEIQOTITPATYHAFGPVIDGVIPDDPOLKLEQ 360  
301 LADKVGCMMLDTTDWVECLRNKYNKEIQOTITPATYHAFGPVIDGVIPDDPOLKLEQ 360  
361 GEFLLYNDIMLGYNQEGELKFDVGIVDNEDGVTPNDPDSVSNFVDNLGYEGEKDTERET 420  
361 GEFLLYNDIMLGYNQEGELKFDVGIVDNEDGVTPNDPDSVSNFVDNLGYEGEKDTERET 420  
421 IKFMYTDADKENPEPTRKKTVALFTTEQWMAFAAALHQAQYGSPTFFYAFYHHCQSEM 480  
421 IKFMYTDADKENPEPTRKKTVALFTTEQWMAFAAALHQAQYGSPTFFYAFYHHCQSEM 480  
481 KPSWADSAHGDEVVPFGIPMIQPTLPSCNFSKNDVLSAVVMTYKTNFAKTGDPNPV 540  
481 KPSWADSAHGDEVVPFGIPMIQPTLPSCNFSKNDVLSAVVMTYKTNFAKTGDPNPV 540

Db 491 KPSWADSHAGCEVPYVVGCIEMIGSTELFSCNFSKNDVYLSAVMTYTNFAKTGDENGEV 540  
Qy 541 POCSTFIHKPNEEEVAVMSKYNPKDQLYHIGLKRPRVDHYRATKVAFWLELVBPHLNL 600  
Db 541 PODTKFIHKPNEEEVAVMSKYNPKDQLYHIGLKRPRVDHYRATKVAFWLELVBPHLNL 600  
Qy 601 NEIFQVSTTTKVPPEPMTSPFYGTRSPAKIWPTRKPAITPANNPKSKDHPKGTGED 660  
Db 601 NEIFQVSTTTKVPPEPMTSPFYGTRSPAKIWPTRKPAITPANNPKSKDHPKGTGED 660  
Qy 661 TTVLIERKDYSTELSTIIVAGASLFLFNILAFALYKKKXKRNHETRRSPQRTTND 720  
Db 661 TTVLIERKDYSTELSTIIVAGASLFLFNILAFALYKKKXKRNHETRRSPQRTTND 720  
Qy 721 IAHQNEIWSLQMKQLEHDEHCESLQAHDTLRITCPRDYTLTLRRSFDIPLMTPTNTT 780  
Db 721 IAHQNEIWSLQMKQLEHDEHCESLQAHDTLRITCPRDYTLTLRRSFDIPLMTPTNTT 780  
Qy 781 MIPNTLTGMQPLHTFNFTSGGQNSTNLPHGSHSTRV 816  
Db 781 MIPNTLTGMQPLHTFNFTSGGQNSTNLPHGSHSTRV 816

## RESULT 6

US-09-978-608A-375  
Sequence 375, Application US/09978608A  
Publication No. US20030045462A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijaviri, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Acids Encoding the Same  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P26302P22  
CURRENT APPLICATION NUMBER: US/09/978,608A  
CURRENT FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 375  
LENGTH: 816  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-608A-375

## Query Match

Best Local Similarity 100.0%; Score 816; DB 11; Length 816;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNSNVLLMTALAIKFTLLDSQAQYEVVNTWYKQKIGLRTPLFNEILGPVQYLVGPVA 60

Db 1 MNSNVLLMTALAIKFTLLDSQAQYEVVNTWYKQKIGLRTPLFNEILGPVQYLVGPVA 60  
Qy 61 SPTGERRFPPEPSSWTGIRNTOTFAVCFQHLDBRSLLHDMPLMTANLDTLMTYV 120  
Db 61 SPTGERRFPPEPSSWTGIRNTOTFAVCFQHLDBRSLLHDMPLMTANLDTLMTYV 120  
Qy 121 QDNEEDCLYNIYVTEDEGANTKXNADDITSNDRGEDEHDONSKKPVWYIHGGSYME 180  
Db 121 QDNEEDCLYNIYVTEDEGANTKXNADDITSNDRGEDEHDONSKKPVWYIHGGSYME 180  
Qy 181 GTGNMIDGSIILASGNVITITNRYRLGLISLSTGQDAKKNVGLLOIQALRMIEENVG 240  
Db 181 GTGNMIDGSIILASGNVITITNRYRLGLISLSTGQDAKKNVGLLOIQALRMIEENVG 240  
Qy 241 AFQGPDKRVTIFGSGAGASCVSLLTSHYSSGLFOKAICSGTALSSNAVYCPAKYRI 300  
Db 241 AFQGPDKRVTIFGSGAGASCVSLLTSHYSSGLFOKAICSGTALSSNAVYCPAKYRI 300  
Qy 301 LADKVGCMMDTDMVECLRNKXKELIOCTTPTATYHAFGVICGQVIFDDQOILMEQ 360  
Db 301 LADKVGCMMDTDMVECLRNKXKELIOCTTPTATYHAFGVICGQVIFDDQOILMEQ 360  
Qy 361 GEFLLNYDIMLGNVCGEGLKFDVGIQDNEDGVTPNDPDSVSNFYDNLYGYEGCKTLRET 420  
Db 361 GEFLLNYDIMLGNVCGEGLKFDVGIQDNEDGVTPNDPDSVSNFYDNLYGYEGCKTLRET 420  
Qy 421 IKFMYTDADKENPETRRKTLVALFTDQWAPAAADLHAQYGSPTYFYAFHHCQSEM 480  
Db 421 IKFMYTDADKENPETRRKTLVALFTDQWAPAAADLHAQYGSPTYFYAFHHCQSEM 480  
Qy 481 KPSWADSHAGCEVPYVVGCIEMIGSTELFSCNFSKNDVYLSAVMTYTNFAKTGDENGEV 540  
Db 481 KPSWADSHAGCEVPYVVGCIEMIGSTELFSCNFSKNDVYLSAVMTYTNFAKTGDENGEV 540  
Qy 541 PODTKFIHKPNEEEVAVMSKYNPKDQLYHIGLKRPRVDHYRATKVAFWLELVBPHLNL 600  
Db 541 PODTKFIHKPNEEEVAVMSKYNPKDQLYHIGLKRPRVDHYRATKVAFWLELVBPHLNL 600  
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Qy 661 TTVLIERKDYSTELSTIIVAGASLFLFNILAFALYKKKXKRNHETRRSPQRTTND 720  
Db 661 TTVLIERKDYSTELSTIIVAGASLFLFNILAFALYKKKXKRNHETRRSPQRTTND 720  
Qy 721 IAHQNEIWSLQMKQLEHDEHCESLQAHDTLRITCPRDYTLTLRRSFDIPLMTPTNTT 780  
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Qy 781 MIPNTLTGMQPLHTFNFTSGGQNSTNLPHGSHSTRV 816  
Db 781 MIPNTLTGMQPLHTFNFTSGGQNSTNLPHGSHSTRV 816

## RESULT 7

US-09-978-585A-375  
Sequence 375, Application US/0978585A  
Publication No. US20030049633A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey

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? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kijavita, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James.
? APPLICANT: Paol, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? TITLE OF INVENTION: Acids Encoding the Same
? FILE REFERENCE: P2630P14
? CURRENT APPLICATION NUMBER: US/09/978,385A
? CURRENT FILING DATE: 2001-10-16
? NUMBER OF SEQ ID NOS: 624
? Prior Application removed - See File Wrapper or Palm
? SEQ ID NO 375
? LENGTH: 816
? TYPE: PR
? ORGANISM: Homo sapiens
? US-09-978-585A-375

Query Match      100.0% Score 816; DB 11; Length 816;
Best local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 QDNEEDCLYNTYVTFEDGANTKNADITSNREDESDIDHOKSKPVVYIGGSYE 180
DB 121 QDNEEDCLYNTYVTFEDGANTKNADITSNREDESDIDHOKSKPVVYIGGSYE 180
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QY 181 GTCNMIDGSLASGVYVITITNFGSLGFGSTDOAAKNGYGLDQICLPRITEENVG 240
DB 181 GTCNMIDGSLASGVYVITITNFGSLGFGSTDOAAKNGYGLDQICLPRITEENVG 240
QY 241 AFGSDPKRYTTFSGSGAGASCVALTLTSHYSEGLFQKALIQSGTALSSAAVYCPAXYTRI 300
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DB 361 GEFVYNDIMLVNCGSGKLFVYDIDNEGVPPTNFCSSVNFVNCUUYGEKQILSEET 420
QY 421 IKFVYTDMAKDEKPETRKRTVALCTDHOQAPAVAAADJHAGYCSFTYFAVYHRCSEW 480
DB 421 IKFVYTDMAKDEKPETRKRTVALCTDHOQAPAVAAADJHAGYCSFTYFAVYHRCSEW 480
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DB 481 KPSMADSAHGDVPPYFGLPMIGPELPSGNSKQDVVSAVYCTWTKFKITDPPQPV 540
QY 541 POSTKEIHTKPRFEEVASKYNPXQDLYLHIGLPRRDRBYRATKVAFMELVPHJNL 600
DB 541 POSTKEIHTKPRFEEVASKYNPXQDLYLHIGLPRRDRBYRATKVAFMELVPHJNL 600
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DB 601 NEIFQVSTTTKVPPEPDMTSFPYGRSPAKIMPTTKPALTPANNPQSGKDPKHTGPE 660
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DB 721 TAAHNETIMSLQKOLEHDEGSLQAHDTLRUCPPDYTLTLRRSPDDIPLMTPTIT 780
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DB 781 MIPNTLQOPLHTFNTFSGGQNSTLPHGSHTRV 816

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? Publication No. US20030050239A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Flivarov, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Geider, Hanspeter
? APPLICANT: Gerlt, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kijavita, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Napier, Mary A.
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? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2630P14
? CURRENT APPLICATION NUMBER: US/09/978,191A
? CURRENT FILING DATE: 2001-10-15
? PRIOR APPLICATION NUMBER: 09/918565
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/06225C
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/064249
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? PRIOR APPLICATION NUMBER: 60/077791
? PRIOR FILING DATE: 1998-03-12
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PRIOR	APPLICATION NUMBER:	60/085704
PRIOR	FILING DATE:	1998-05-15
PRIOR	APPLICATION NUMBER:	60/085697

Query Match 100.0%; Score 816; DB 11; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 1 MNSNVLMK:TALEIKFTLIDSOQYPPVNTNKGKINGLETPLPNEILGPEVEYLGVPVA 60
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Cy 191 GTGNMIDGSIASGNVITITNRLIGFLSGDQAAKNGCGLDQIALPMIENNG 240
Db 191 GTGNMIDGSIASGNVITITNRLIGFLSGDQAAKNGCGLDQIALPMIENNG 240
Cy 241 AFGDPRKVTIFSGAGASCVSLLTSHYSEGLFOKA:IGSGTALSSMANVYPAKYFI 300
Db 241 AFGDPRKVTIFSGAGASCVSLLTSHYSEGLFOKA:IGSGTALSSMANVYPAKYFI 300
Cy 301 LADKVGCM:DTTMEWECLEKRNKKELIQCTTPATYHAFGVYIGDVPDPDPCILMEQ 360
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Cy 481 KPSNADSAHDEGVYVYVGIPIWIGTELPSCNFSNDYMSAVMTYVNTAKTGDEPQVY 540
Db 481 KPSNADSAHDEGVYVYVGIPIWIGTELPSCNFSNDYMSAVMTYVNTAKTGDEPQVY 540
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Db 541 FQTRKF:HTKFNREEEVAMSKVNPXKOLYLH:GKPRVCRHYATKAYAFMELEVPJLHNI 600
Cy 601 NEIFQVSTTRKVPFPDMGSPFPGSRSPAKTAPFTTRPA:TTANPKRSEKCHXKGPED 660
Db 601 NEIFQVSTTRKVPFPDMGSPFPGSRSPAKTAPFTTRPA:TTANPKRSEKCHXKGPED 660
Cy 661 TTVLETRKDYSTELSVT:AVGASLLF:NLIAFALYKKKOKSRHETHRRPSPQRYNTND 720
Db 661 TTVLETRKDYSTELSVT:AVGASLLF:NLIAFALYKKKOKSRHETHRRPSPQRYNTND 720
Cy 721 LAHIONEIYSLQMKQ:EHHECECSIAHCTLR:TCPPDYLTL:RASEDPDIP:MTNKNT 780
Db 721 LAHIONEIYSLQMKQ:EHHECECSIAHCTLR:TCPPDYLTL:RASEDPDIP:MTNKNT 780
Cy 781 MIPNTLTGMCP:HTFNTFSGGQNSCNLPHGSHSTRV 816
Db 781 MIPNTLTGMCP:HTFNTFSGGQNSCNLPHGSHSTRV 816

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RESULT 3  
 US-09-978-403A-375  
 ; Sequence 375, Application US/09978403A  
 ; Publication No. US2003005024CAT  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerlitsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurey, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kilavni, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Kapler, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630PIC7  
 CURRENT APPLICATION NUMBER: US/09/978,403A  
 CURRENT FILING DATE: 2002-03-19  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/085697

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121 CGONEPCLYNIYVPTDGAATKKMADDEITSDRGDEDDHONSXKPMVYIHGSVYE 180  
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121 CGONEPCLYNIYVPTDGAATKKMADDEITSDRGDEDDHONSXKPMVYIHGSVYE 180  
181 GTGNMIDGSLASGVNIYVITINRGLIGFJSTGQAAKNGVGLDDOTQALRWIEENVG 240  
181 GTGNMIDGSLASGVNIYVITINRGLIGFJSTGQAAKNGVGLDDOTQALRWIEENVG 240  
181 GTGNMIDGSLASGVNIYVITINRGLIGFJSTGQAAKNGVGLDDOTQALRWIEENVG 240  
241 AFGGDPKRVITIFSGGASGVSIITLTSVSEGLFOKATIOSGTALSSMANVOPAKYTRI 300  
241 AFGGDPKRVITIFSGGASGVSIITLTSVSEGLFOKATIOSGTALSSMANVOPAKYTRI 300  
301 LADYVGCNMLDTTDMVECLRNKXKELICOTTITPATYHIAFGFVIDGVIPDDPQILMEQ 360  
301 LADYVGCNMLDTTDMVECLRNKXKELICOTTITPATYHIAFGFVIDGVIPDDPQILMEQ 360



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Query Match 100.0% Score 816; DB 11; Length 816;  
Best Local Similarity 100.0%; Pct. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 SPTGERFPPEPPSSWTG:RNTTQPAVCPQLDERSL:HMPLMFTANLDTLTYY 120  
121 GQONEDCYLNIYVPTGKATKXKADITSDNGEDSDIDQSKKPVVYHSGSYME 183  
121 GQONEDCYLNIYVPTGKATKXKADITSDNGEDSDIDQSKKPVVYHSGSYME 180  
181 GTGNMIDGSLAS:GNV:VITINRYLGLF:STGDOAAKNGYL:QOIQALWIEENVG 240  
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241 AFGDPRKVTTFSGSAGSVCVSLTSHSYSGLFQKAI:CGSTLSSNANVYQPAKTR 300  
241 AFGDPRKVTTFSGSAGSVCVSLTSHSYSGLFQKAI:CGSTLSSNANVYQPAKTR 300  
301 LADKVCNMLDITTMVECLRNKNYKE:TCGTTPATYHIAFGPVIDGVI:PDDEQIIMEQ 360  
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361 GEFVNYDMLGVNOGEGIKFVDGIVDNEGVTENDPFPVS:NFPVDN:YGPBEGDOLRET 420  
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661 TVVLETRDYSTELSVTIAVGASLLFNIAFPALYYKKDKRHEHTRRPS:PORNTTND 720  
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721 IALIONERISLOXKOLEHDECESLQADTLRLTCPEPDYLLTRBSDDQJPLMTPTIT 780  
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Publication No. US20030054405A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desrochers, Juc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleo  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Ford, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C65  
CURRENT APPLICATION NUMBER: US/09/999.833a  
CURRENT FILING DATE: 200-10-24  
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Db 1 MUNSVMILMTALAIKFTLIDSCAOPYVWNTNGKIRGRTPLPNEILGVEOYLGVPYA 60
Cy 61 SPTGERFOPPEPSSWTGIRNTTFFAAVGCGLDERSLILKVLPIKFWANLDTLNTY 120
Db 61 SPTGERFOPPEPSSWTGIRNTTFFAAVGCGLDERSLILKVLPIKFWANLDTLNTY 120
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Cy 181 GTGNMIDGSIILASGVNIYVITINYPJLIGLPLSTGDOAKAGNYGLDQICALFIEENVG 240
Db 181 GTGNMIDGSIILASGVNIYVITINYPJLIGLPLSTGDOAKAGNYGLDQICALFIEENVG 240
Cy 241 AFGDDPKRVTFSSGAGASCVSLLTSHYSEGLFQKAIISGTRALSSMANVYQKATRI 300
Db 241 AFGDDPKRVTFSSGAGASCVSLLTSHYSEGLFQKAIISGTRALSSMANVYQKATRI 300
Cy 301 LADYVGCNMLDTTMEVCELRNKYKELIQOTITPATYHIAFGVIDGVIIPDDPOLIMEQ 360
Db 301 LADYVGCNMLDTTMEVCELRNKYKELIQOTITPATYHIAFGVIDGVIIPDDPOLIMEQ 360
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Cy 421 IKFWYTDWADKENETBRKTLVALFTDHCWAPAAADLHAQVGSPTYFYAFYHHCSEY 480
Db 421 IKFWYTDWADKENETBRKTLVALFTDHCWAPAAADLHAQVGSPTYFYAFYHHCSEY 480
Cy 481 KPSMADSAGDEVEYVVGIMIGTELFSQNFSSNDVMJSAVMTYTNTNPAKIGDPQPV 540
Db 481 KPSMADSAGDEVEYVVGIMIGTELFSQNFSSNDVMJSAVMTYTNTNPAKIGDPQPV 540
Cy 541 PDKTFITKXNREBEVAMSKYNKCDLYLHIGLXPRVHYATKAFLMLVPHLNL 600
Db 541 PDKTFITKXNREBEVAMSKYNKCDLYLHIGLXPRVHYATKAFLMLVPHLNL 600
Cy 601 NEIFQVSTTKVPDPMTSPFVGTTRSPAKIMETTKRPAITPANPKSKDPKTKGPE 660
Db 601 NEIFQVSTTKVPDPMTSPFVGTTRSPAKIMETTKRPAITPANPKSKDPKTKGPE 660
Cy 661 TTVLIERKRDVSTLSTIIVAGASLFLNIAFALYXDKRPHETRRPSQRNTND 720
Db 661 TTVLIERKRDVSTLSTIIVAGASLFLNIAFALYXDKRPHETRRPSQRNTND 720
Cy 721 IAHQNEEIMSLQKQLEHDECELSLOAHDTLRITCPDDYTLTLRRSPDIPJMTPTIT 780
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/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Boeststein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geisler, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul C.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavira, Ivar J.
/ APPLICANT: Kuo, Sophia S.
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APPLICANT: Kapler, Mary A.  
APPLICANT: Pat, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David J.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Wood, William I.  
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C12  
CURRENT APPLICATION NUMBER: US/09/981,915A  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: 09/91,8585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/0662250  
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PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328

PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
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PRIOR APPLICATION NUMBER: 60/080334  
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PRIOR APPLICATION NUMBER: 60/081070  
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PRIOR APPLICATION NUMBER: 60/084414  
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PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07

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PRIOR APPLICATION NUMBER: 60/084639
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PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

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Query Match      100.0%; Score 816; DB 11; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MANSVLLMLTALAIAKTLDQAQVYVNTNGKRGRLTPJENILGPEYQYGVFA 60
DB 1 MANSVLLMLTALAIAKTLDQAQVYVNTNGKRGRLTPJENILGPEYQYGVFA 60
QY 61 SPPTGERRFPQPPPPSKWTGIRNTQCPAAVCPOGJDRSRJCHMLTINFANLCTNTV 120
DB 61 SPPTGERRFPQPPPPSKWTGIRNTQCPAAVCPOGJDRSRJCHMLTINFANLCTNTV 120
QY 121 ODQNECLYNTIYVPEEDGANTKNADITSNRGEDEIDHONSKKPVVYIHGSYME 190
DB 121 ODQNECLYNTIYVPEEDGANTKNADITSNRGEDEIDHONSKKPVVYIHGSYME 190
QY 191 GTGMWIGSILASGVNIVITNIRGLGFLSTGQAAGNVGLDQICARMEENVG 240
DB 191 GTGMWIGSILASGVNIVITNIRGLGFLSTGQAAGNVGLDQICARMEENVG 240
QY 241 AFGDPRKVTIFSGAGASCVSLLTSHYSEGLFOKAIIDSGTALSSMANVQPAKYTI 300
DB 241 AFGDPRKVTIFSGAGASCVSLLTSHYSEGLFOKAIIDSGTALSSMANVQPAKYTI 300
QY 301 LADRVGCMALDITDMVCLRNKVKELIQCTIIPATYHIFGVJIGDVIIPDDPOLMEQ 360
DB 301 LADRVGCMALDITDMVCLRNKVKELIQCTIIPATYHIFGVJIGDVIIPDDPOLMEQ 360
QY 361 GEFANDIMLVNNGEGLKFEVDGIVNEDGVTENDPFSVSNVJNLYGPECKTLRET 420
DB 361 GEFANDIMLVNNGEGLKFEVDGIVNEDGVTENDPFSVSNVJNLYGPECKTLRET 420
QY 421 IKFMYTMAKKEKNEDETRKTLVALFTDHQVAVPAVAADLHAGVSGFTYFAVYHCCSM 480
DB 421 IKFMYTMAKKEKNEDETRKTLVALFTDHQVAVPAVAADLHAGVSGFTYFAVYHCCSM 480
QY 481 KPSVADSAGGEVYVVGIPMIGTELFSCNPSKNVMSAVMTVNTPAKTDGDNQV 540
DB 481 KPSVADSAGGEVYVVGIPMIGTELFSCNPSKNVMSAVMTVNTPAKTDGDNQV 540

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QY 541 POSTKITHKPNRFEVANSKYVKKDLYLHGLKXRVDRHYRATVAFMLEVPHLNT 600
DB 541 POSTKITHKPNRFEVANSKYVKKDLYLHGLKXRVDRHYRATVAFMLEVPHLNT 600
QY 601 NEIFQVSTTTKVPDDMTSPFYGRSPAKIWPITKRPATIPANNPKSKDPKTKGED 660
DB 601 NEIFQVSTTTKVPDDMTSPFYGRSPAKIWPITKRPATIPANNPKSKDPKTKGED 660
QY 661 TVULIEFKRYSSTLSVTLAVGASLLFELNLAALYYKKDKRREHTRRSPQNTND 720
DB 661 TVULIEFKRYSSTLSVTLAVGASLLFELNLAALYYKKDKRREHTRRSPQNTND 720
QY 721 IAHQNEIWSLQKLEHDECESLQADTLRLTCCPDYTLIRSPDIPLMPTNTIT 780
DB 721 IAHQNEIWSLQKLEHDECESLQADTLRLTCCPDYTLIRSPDIPLMPTNTIT 780
QY 781 MIPNTLGMPPLHTFNTFSGQNSTVLPHGSHSTRV 816
DB 781 MIPNTLGMPPLHTFNTFSGQNSTVLPHGSHSTRV 816

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RESULT 13
US-09-978-824-375
Sequence 375, Application US/09978824
Publication No. US20030055216A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Mei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grima-di, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavrin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C14
CURRENT APPLICATION NUMBER: US/09/978, 824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11

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PRIOR APPLICATION NUMBER: 60/385573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 1; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MINSNVLMWLTALNIFETLLDSOQYPVVNTNNGKRGKRTPLNPIILGQVQYGVYR 63  
DB 1 XLSNVLMWLTALNIFETLLDSOQYPVVNTNNGKRGKRTPLNPIILGQVQYGVYR 60  
QY 61 SPTGERFPQPPSPSSMTGIRNTQPAVCPQHLDESSCLNDMIPWFTALNLTMTYV 120  
DB 61 SPTGERFPQPPSPSSMTGIRNTQPAVCPQHLDESSCLNDMIPWFTALNLTMTYV 120  
QY 122 QDNEDECLYNIYVFTEDGANTKKADITSNDRGFEIDHONSKEKPVVYTHGGSYVE 180  
DB 121 QDNEDECLYNIYVFTEDGANTKKADITSNDRGFEIDHONSKEKPVVYTHGGSYVE 180  
QY 181 GTGNMIDGSLASGVNIVTTINRGLIPLSTQDAKXGVGLDQIALRMEYV 240  
DB 181 GTGNMIDGSLASGVNIVTTINRGLIPLSTQDAKXGVGLDQIALRMEYV 240  
QY 241 AFGQDPKRVTFPGSGAGASVSLTLNHSVEGLFQKALIQSGTASNNANXQPKYTR 300  
DB 241 AFGQDPKRVTFPGSGAGASVSLTLNHSVEGLFQKALIQSGTASNNANXQPKYTR 300  
QY 301 LAKVGNMJDITDVECLNKNYKEJQGTITRATYAFQPVLDGQTECDQILMEQ 350  
DB 301 LAKVGNMJDITDVECLNKNYKEJQGTITRATYAFQPVLDGQTECDQILMEQ 350  
QY 361 GEFINDIMLVNQGEGKXVDGIVNEDGVTPNDFPVSVPVENVLYVPEKCLTERT 420  
DB 361 GEFINDIMLVNQGEGKXVDGIVNEDGVTPNDFPVSVPVENVLYVPEKCLTERT 420  
QY 421 IKENYTMADKENPFRRTKTLVLFTHQVVAFAVADLHMQGSTYVATVYHHCQSEM 480  
DB 421 IKENYTMADKENPFRRTKTLVLFTHQVVAFAVADLHMQGSTYVATVYHHCQSEM 480  
QY 481 KPSWADSAHGDEVYVYGIFPMIGPTLFGSNFSKQDVLAVVYVMTWTFKAGCPNCPV 540  
DB 481 KPSWADSAHGDEVYVYGIFPMIGPTLFGSNFSKQDVLAVVYVMTWTFKAGCPNCPV 540  
QY 541 PCKTKEHTKPNRFEERAMSKYVPCDLYLHGLAKRYVDHFRATVAAWELVPHLNL 600  
DB 541 PCKTKEHTKPNRFEERAMSKYVPCDLYLHGLAKRYVDHFRATVAAWELVPHLNL 600  
QY 601 NEIFQVYSTTKVPPDNTSFPYGTSSPAKIPWTKRPAITFPANPKSKDPKGTGPE 660  
DB 601 NEIFQVYSTTKVPPDNTSFPYGTSSPAKIPWTKRPAITFPANPKSKDPKGTGPE 660  
QY 661 TVULIEFRDYSTEJLVTAIVGASLLFLNLAPALYKKDKRHEHTRSPQNTTND 720  
DB 661 TVULIEFRDYSTEJLVTAIVGASLLFLNLAPALYKKDKRHEHTRSPQNTTND 720  
QY 721 IAHQNEIWSLCKQLEHDESESLQAHCTCLTCTPPYTLTLRSPDILKMNIT 780  
DB 721 IAHQNEIWSLCKQLEHDESESLQAHCTCLTCTPPYTLTLRSPDILKMNIT 780  
QY 781 MIPYLTGQOPLTFTNTFSSQGNSTNLPHGSHTRV 816  
DB 781 MIPYLTGQOPLTFTNTFSSQGNSTNLPHGSHTRV 816

## RESULT 14

US-09-978-585A-375  
Sequence 375, Application US/09318585A  
Publication No. US2003060406A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desrochers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Oiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, V. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P101  
CURRENT APPLICATION NUMBER: US/09/978,585A  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR FILING DATE: 1998-03-27

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PRIOR	APPLICATION NUMBER:	60/084441
PRIOR	FILING DATE:	1998-05-06
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PRIOR	FILING DATE:	1998-05-07
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PRIOR	FILING DATE:	1998-05-07
PRIOR	APPLICATION NUMBER:	60/084600
PRIOR	FILING DATE:	1998-05-07
PRIOR	APPLICATION NUMBER:	60/084627
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PRIOR	APPLICATION NUMBER:	60/084643
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PRIOR	APPLICATION NUMBER:	60/085339
PRIOR	FILING DATE:	1998-05-13
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PRIOR	FILING DATE:	1998-05-13
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PRIOR	FILING DATE:	1998-05-15
PRIOR	APPLICATION NUMBER:	60/085573
PRIOR	FILING DATE:	1998-05-15
PRIOR	APPLICATION NUMBER:	60/085704
PRIOR	FILING DATE:	1998-05-15
PRIOR	APPLICATION NUMBER:	60/085697
PRIOR	FILING DATE:	1998-05-15
PRIOR	APPLICATION NUMBER:	60/086233

Query Match	100.0%	Score 816	DB 11	Length 816
Best Local Similarity	100.0%	Pred. No. 0		
Matches 816	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY MENSNTLMLTALAKETLIDSCAQCYVVMNNYKIGRLRFLPNEIIGPEQCYGVGVYA 60  
 DB 1 MANSNTLMLTALAKETLIDSCAQCYVVMNNYKIGRLRFLPNEIIGPEQCYGVGVYA 60  
 QY 61 SPTPTGERFPQPEPPSSMTGIRNTTQPAAYCPQGLDERSLLHMLPMTFNTANLDTMTYV 120  
 DB 61 SPTPTGERFPQPEPPSSMTGIRNTTQPAAYCPQGLDERSLLHMLPMTFNTANLDTMTYV 120  
 QY 121 QQONEDCLYNIYVPTEDGANTKQNAEDITSNDGEDEDIDQNSKKPVVYIHGSGYME 180  
 DB 121 QQONEDCLYNIYVPTEDGANTKQNAEDITSNDGEDEDIDQNSKKPVVYIHGSGYME 180  
 QY 161 GTGMYGIGSLIASGNYVITINRGLIGLSLFGDQAKKNGYGLDQIALRWIENYVG 240  
 DB 161 GTGMYGIGSLIASGNYVITINRGLIGLSLFGDQAKKNGYGLDQIALRWIENYVG 240  
 QY 241 AFGGDPRVYTIPOSGAGASCVSLLTISHYSEGLFOKAIIOGSLASSMNVNYQPAKYTRI 300

Db 241 AFGGDPKRVITIFSGGAGACVSLILLSHSESLFQAIITQSGTASSMWVNYQPKYTRI 300  
QY 301 LADKVGCMMLDTDMWECLELRNKKYKEJJCQITTPATYHAFGPVTDGVTCPDQPILEQ 360  
Db 301 LADKVGCMMLDTDMWECLELRNKKYKEJJCQITTPATYHAFGPVTDGVTCPDQPILEQ 360  
QY 361 GEFNLVDIMLVNQGQGLKFPVDSIVNEDGVTPNDFSVSNFVNLXOYPRCKQLTET 420  
Db 361 GEFNLVDIMLVNQGQGLKFPVDSIVNEDGVTPNDFSVSNFVNLXOYPRCKQLTET 420  
QY 421 IKFNTDMADKKEPFRKKTVAJFTDQWAFAPAAALDAOYGSEPTTYATYHHCQSEM 480  
Db 421 IKFNTDMADKKEPFRKKTVAJFTDQWAFAPAAALDAOYGSEPTTYATYHHCQSEM 480  
QY 481 KPSMADSACDSEVPYFGIPIKIGTECFSCNFSKNDVMSAVMTYNTWTFATGPNQPV 540  
Db 481 KPSMADSACDSEVPYFGIPIKIGTECFSCNFSKNDVMSAVMTYNTWTFATGPNQPV 540  
QY 541 PQTPIHTKPNRFEVAVSKNPKQQLYHIGLKPRVDHYRATKVAFWLELVHLNR 600  
Db 541 PQTPIHTKPNRFEVAVSKNPKQQLYHIGLKPRVDHYRATKVAFWLELVHLNR 600  
QY 601 NEFFQVSTTKVPPEDMTSPYGTGRSPAKIMPTTKRPAFPANPKSKPKKTSQED 660  
Db 601 NEFFQVSTTKVPPEDMTSPYGTGRSPAKIMPTTKRPAFPANPKSKPKKTSQED 660  
QY 661 TTVLIEFKADYS-ELSVITVAAGASJLFNIIAPAAVYKCKRRHSHRRSPQNTND 720  
Db 661 TTVLIEFKADYS-ELSVITVAAGASJLFNIIAPAAVYKCKRRHSHRRSPQNTND 720  
QY 721 IATIQNEELMSLQKLESDHCESESQAADTLCRTCPDPTITLRSPQCLPLN-FNIT 780  
Db 721 IATIQNEELMSLQKLESDHCESESQAADTLCRTCPDPTITLRSPQCLPLN-FNIT 780  
QY 781 MIENTLTCNPLHTFNTFSGGQRTSLPRCHSTTRV 846  
Db 781 MIENTLTCNPLHTFNTFSGGQRTSLPRCHSTTRV 846

RESULT 15  
US-09-978-423a-375  
Sequence 375, Application JS/03978423A  
Publication No. US20030369176A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flaxaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerbert, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, V. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: K-Javin, Ivar J.  
APPLICANT: Kuc, Sophia S.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Tomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630PIC21  
CURRENT APPLICATION NUMBER: US/09/978,423A  
CURRENT FILING DATE: 2002-05-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 816, DB 11, Length 816:

Best Local Similarity 100.0%: Pred. No. 0: Matches 816: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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 1 MUNSVMULTALAIKFTLIDSOAQPVNTNYGKIRGLRPLNEILGPVEQYAGPYA 60  
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 61 SPTGERFOPPEPSSWGTGIRNTQFAVCPQHLDRSLHDMPTWFTANLDTMTYV 120  
 121 QONEDCLYNIYVTEGANTKKNADITSDNDEGEZJHDCSKXPVWYIHGGSYME 180  
 121 QONEDCLYNIYVTEGANTKKNADITSDNDEGEZJHDCSKXPVWYIHGGSYME 180  
 181 GTGNMIDGSIASGVNVTINNYRLGILGISTGDOAKKNYGLDIOALRMTEENVG 240  
 181 GTGNMIDGSIASGVNVTINNYRLGILGISTGDOAKKNYGLDIOALRMTEENVG 240  
 181 GTGNMIDGSIASGVNVTINNYRLGILGISTGDOAKKNYGLDIOALRMTEENVG 240  
 241 AFGDPKXVITFGSGAGASCUSLTLSYSEGLFOKAIQSGTALSSAANYQPAKTRI 300  
 241 AFGDPKXVITFGSGAGASCUSLTLSYSEGLFOKAIQSGTALSSAANYQPAKTRI 300  
 301 LADKVCNMLDTTDEVECLRNKNYKELQOTITPATYHIAFGPIJCGDVPDDPQILMEQ 360  
 301 LADKVCNMLDTTDEVECLRNKNYKELQOTITPATYHIAFGPIJCGDVPDDPQILMEQ 360  
 361 GEFNLVIMLVNOCSEGLKPYDGVNEDGVTPNDFDSVSNFYDNLVYGEJGKOLRET 420  
 361 GEFNLVIMLVNOCSEGLKPYDGVNEDGVTPNDFDSVSNFYDNLVYGEJGKOLRET 420  
 421 IKEMYTADKNEPTEPRKTLVALFTHQWAPAAALHXYSPPTFYAFYHCOSEX 480  
 421 IKEMYTADKNEPTEPRKTLVALFTHQWAPAAALHXYSPPTFYAFYHCOSEX 480  
 481 KPSMADSAHGDVEVPYFGIPMIGTELFSCFSSXNDVLSAVVYTWNTFAKTGDPPOV 540  
 481 KPSMADSAHGDVEVPYFGIPMIGTELFSCFSSXNDVLSAVVYTWNTFAKTGDPPOV 540  
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 601 NEIFQVSTTKVPPEDKTSFPYGRSRPAKIMPTTKAPATPANNGHSCDPRKTCGE 660  
 661 TIVLETKADYSTELSVTIAVGASLLFNILAFALVYKKDRRHETRRPSFORNTND 720



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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 816 DB 1: Length 816;  
 Best Local Similarity 100.0% Pred. No. 0;  
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 MNSNVLLMTALAIKFTLIDSOAQYPTWNTYKIRGLRTPFLPRETLGPVECYLGVPA 60

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 QY 61 SEPTGERFOPPEPSSWTG:RNTTQFAACPGHJCSRLHMLPMTNLTMTTV 120  
 DB 61 SEPTGERFOPPEPSSWTG:RNTTQFAACPGHJCSRLHMLPMTNLTMTTV 120  
 QY 121 ODQNECDLYNIYVTEDEGANTKQADITNSDGEDEHDQSKKRVWYIIGGSYME 180  
 DB 121 ODQNECDLYNIYVTEDEGANTKQADITNSDGEDEHDQSKKRVWYIIGGSYME 180  
 QY 181 GTGKMDGSIILASYNVVTITNRLGLGLSTGCOAKKNYGLDIOALRMIEENVG 240  
 DB 181 GTGKMDGSIILASYNVVTITNRLGLGLSTGCOAKKNYGLDIOALRMIEENVG 240  
 QY 241 AFGSDPKAVTIFGSGAGASCVSLTLTSHYSEGLFCOKAIQSGTALSSAAVYQPAKYTRI 300  
 DB 241 AFGSDPKAVTIFGSGAGASCVSLTLTSHYSEGLFCOKAIQSGTALSSAAVYQPAKYTRI 300  
 QY 301 LADKVCNMLTETDWECLRNKRYKELCQITTPATYHIAFGVIGDVI:EDDQILMEQ 360  
 DB 301 LADKVCNMLTETDWECLRNKRYKELCQITTPATYHIAFGVIGDVI:EDDQILMEQ 360  
 QY 361 GEFINVDMLGVNCGES:KFDGIVUNEDGVTPNDFESVSNFYDNLGVGEQCTJRET 420  
 DB 361 GEFINVDMLGVNCGES:KFDGIVUNEDGVTPNDFESVSNFYDNLGVGEQCTJRET 420  
 QY 421 IKFYTDMAKXENPETERKTLVALFTJHQAFAVAADJHAQYGSFTYFVAFYHHCQSEM 480  
 DB 421 IKFYTDMAKXENPETERKTLVALFTJHQAFAVAADJHAQYGSFTYFVAFYHHCQSEM 480  
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 QY 661 TTVLETRKDYSTEISVITAVGASLIPNIIAFAALYKCKRREHETRRSPONTEND 720  
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RESULT 17  
 US-09-999-830A-375

Sequence 375, Application US/09999830A  
 Publication No. US2003007700A1

GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Juc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleo  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Forg, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gertlisen, Mary E.  
 APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaidi, G. Christopher  
APPLICANT: Guiney, Austin L.  
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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CURRENT APPLICATION NUMBER: US/09/999,83CA  
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PRIOR APPLICATION NUMBER:	60/083558
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PRIOR APPLICATION NUMBER:	60/085339
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085388
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085322
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700
PRIOR FILING DATE:	1998-05-15

PRIOR APPLICATION NUMBER: 60/085669  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0% Score 216; DB 11; Length 816;  
 Best Local Similarity 100.0% Pred No. 3;  
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MUNSVMMLTALAIKFTTDSQAQYPPVNNYNGKRGSRPLPNEILSPVYIGVPA 60  
 1 MUNSVMMLTALAIKFTLIDSOAFVNTNNGKIRGRPLPNEILSPVYIGVPA 60  
 61 SPTGERRPPSPSSMTGIRNTTGFANVCECHLERSLHDMPIFTALDITMTV 120  
 61 SPTGERRPPSPSSMTGIRNTTGFANVCECHLERSLHDMPIFTALDITMTV 120  
 121 QDNECCYUNIVYPTEDGANTTKNADITSDRGDEEDHONSKKPVYVTHGSSVME 180  
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 181 GTGNMIDGSLASGVYVTTINRGLGLSTGDAAGNGLDQLOALEEENNG 240  
 181 GTGNMIDGSLASGVYVTTINRGLGLSTGDAAGNGLDQLOALEEENNG 240  
 241 AFGDPRKVTIFSGAGACVSLTSHYSSGFOXAIGSSATLSMAVNPAYVTEI 300  
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 301 LADRVGCMMLDTTDMVECLRNKNKELIQTTTPATYHAFGPVIGDVIPODPCILMEQ 360  
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 361 GEFLNYDLMGVNGBELKFDVGVNEDGVTENDPFSNSNVNMLXGPEKCTLAET 420  
 361 GEFLNYDLMGVNGBELKFDVGVNEDGVTENDPFSNSNVNMLXGPEKCTLAET 420  
 421 IKFMYTDMADKENETRRKTLVALFTDHQWAPAVADLHAQGSPTVEYAFYHGOSEM 480  
 421 IKFMYTDMADKENETRRKTLVALFTDHQWAPAVADLHAQGSPTVEYAFYHGOSEM 480  
 481 KPSWADSAHGDVEVYVGGIPYIGTELFSCNFSKNDVLSAVNTVTNTNPAKGDENOPV 540  
 481 KPSWADSAHGDVEVYVGGIPYIGTELFSCNFSKNDVLSAVNTVTNTNPAKGDENOPV 540  
 541 PODRKFIHTKREEREVAVMSKYNPKDCYLHISLKPAPVHPATKAFMLEVPHLHNL 600  
 541 PODRKFIHTKREEREVAVMSKYNPKDCYLHISLKPAPVHPATKAFMLEVPHLHNL 600  
 601 NEIFQYVSTTKVPPDVTSPFYSTRSSPAKIMPTTSPATTPANFKSKPHKGPED 660  
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 661 TTVLIETKPDVSTSLTIAVAGASLLEINLAFALAYKKKXKREHREHRSPOKNTTN 720  
 661 TTVLIETKPDVSTSLTIAVAGASLLEINLAFALAYKKKXKREHREHRSPOKNTTN 720  
 721 IAHQNEEINSLQKOLEHCEHCESLQAHDTLRJTCFDEVTILTRSSPDIPVXTPTT 780  
 721 IAHQNEEINSLQKOLEHCEHCESLQAHDTLRJTCFDEVTILTRSSPDIPVXTPTT 780  
 781 MIPNTLTGMPLEHTFNTSSGONSINLPHGSTRV 816  
 781 MIPNTLTGMPLEHTFNTSSGONSINLPHGSTRV 816

## RESULT 19

us-09-978-187b-375

Sequence 375, Application US/099781878  
 Publication No. US20030096744A1

## GENERAL INFORMATION:

APPLICANT: Askenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Flivaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gertsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillar, Kenneth J.  
 APPLICANT: K.Javan, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630PICS  
 CURRENT APPLICATION NUMBER: US/09/978,187B  
 PRIOR FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
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Best Local Similarity 100.0%; Pred. No. 0;  
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1 MNSNVLMWLTALAKFTLIDSOAYVWNTNGKIRGJRTPLPNEILGVEQYLGVPYA 60  
61 SPPTGERRPQPEPPSSWTGIRNTTQPAAYVCPQHLDRSLJLHMLPIWFTANLDTLMTYV 120  
61 SPPTGERRPQPEPPSSWTGIRNTTQPAAYVCPQHLDRSLJLHMLPIWFTANLDTLMTYV 120  
121 QDQVEDCLYNIYPTEDGANTKXNADITSNPGDEDCJHDQNSKXPPWVYIHGGSYME 180  
121 QDQVEDCLYNIYPTEDGANTKXNADITSNPGDEDCJHDQNSKXPPWVYIHGGSYME 180  
121 QDQVEDCLYNIYPTEDGANTKXNADITSNPGDEDCJHDQNSKXPPWVYIHGGSYME 180

QY 161 GTGNNIDGSIILASGNVIVITINRBLGSLGSLSTGCGAANKVGLLDQIALDWIBENNG 240  
DB 181 GTGNNIDGSIILASGNVIVITINRBLGSLGSLSTGCGAANKVGLLDQIALDWIBENNG 240  
QY 241 AFGGDPKRVITIFGSGAGASCVSLTLSSHSEGLFOKAIIOGDTLSSMAVNYOPAKYTRI 300  
DB 241 AFGGDPKRVITIFGSGAGASCVSLTLSSHSEGLFOKAIIOGDTLSSMAVNYOPAKYTRI 300  
QY 301 LADKVGCMMLDITDMVECLRNKNKYEKLIQOTITPATYHIAFGVIDGVIIPDDQILMEQ 360  
DB 301 LADKVGCMMLDITDMVECLRNKNKYEKLIQOTITPATYHIAFGVIDGVIIPDDQILMEQ 360  
QY 361 GEFNLNDIMLGAVNQGEGIKFVDGIVNDEGVTNDFPDSNSFNDNLYGPEGKOTLRET 420  
DB 361 GEFNLNDIMLGAVNQGEGIKFVDGIVNDEGVTNDFPDSNSFNDNLYGPEGKOTLRET 420  
QY 421 IKFMYTMAADKENPETRRKTLVALFTDHQWVAFAVAADLIAOVGSPFYFAFYHHCQSEM 480  
DB 421 IKFMYTMAADKENPETRRKTLVALFTDHQWVAFAVAADLIAOVGSPFYFAFYHHCQSEM 480  
QY 481 KPSWADSAHGDDEVYVFGIPMIGPTELFSCNFSKNDVMSAVMTITWTFANKTDPYQV 540  
DB 481 KPSWADSAHGDDEVYVFGIPMIGPTELFSCNFSKNDVMSAVMTITWTFANKTDPYQV 540  
QY 541 FODTKFIHTKPRREPEEVAWSKYNPKDQLYHIGLKPVRDCHVRATKVAFAVCELVPHLHNT 600  
DB 541 FODTKFIHTKPRREPEEVAWSKYNPKDQLYHIGLKPVRDCHVRATKVAFAVCELVPHLHNT 600  
QY 601 NEIFQVSTTTKVPVPPMTSPFYGTRSRPAKIMPTTKRPAITPANPKHCKDHKGPPE 660  
DB 601 NEIFQVSTTTKVPVPPMTSPFYGTRSRPAKIMPTTKRPAITPANPKHCKDHKGPPE 660  
QY 661 TTVLETRKDYSTELSVTIAVAGASLFLNLTAFALAYKKKREHETRRSPQPTTND 720  
DB 661 TTVLETRKDYSTELSVTIAVAGASLFLNLTAFALAYKKKREHETRRSPQPTTND 720  
QY 721 TTVLETRKDYSTELSVTIAVAGASLFLNLTAFALAYKKKREHETRRSPQPTTND 720  
DB 721 TTVLETRKDYSTELSVTIAVAGASLFLNLTAFALAYKKKREHETRRSPQPTTND 720  
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DB 781 KIPNTLTGKOPLHTEPFSGCONSTNLPHGSTRV 816  
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DB 781 KIPNTLTGKOPLHTEPFSGCONSTNLPHGSTRV 816

RESULT 2C  
US-09-978-643A-375  
Sequence 375, Application US/0978643A  
Publication No. US20030104998A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Borstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleo  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Feng, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geisler, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaud, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavita, Ivar J.  
APPLICANT: Kujo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Pann, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C16  
CURRENT APPLICATION NUMBER: US/09/978,643A  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 375  
LENGTH: 816  
TYPE: RPT  
ORGANISM: Homo sapiens  
US-09-978-643A-375

Query Match 100.0%; Score 816; DB 11; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YLNSVTLMLTALAIAKTTLDQAVPVNNTNGKIRGLTFLPRLILGVEQYLGVPYA 60  
2 MUNSNTLMLTALAIAKTTLDQAVPVNNTNGKIRGLTFLPRLILGVEQYLGVPYA 60  
61 SPTGERARFQPEPSSWTGIRNTTQFAAFCQHDERSLHDKYLPIMFALDITMTYV 120  
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121 QDNEDECLYNIYFEDGANTKKNADITSNORGEDEDHONSRRPMVYHGGSIYE 180  
121 QDNEDECLYNIYFEDGANTKKNADITSNORGEDEDHONSRRPMVYHGGSIYE 180  
121 QDNEDECLYNIYFEDGANTKKNADITSNORGEDEDHONSRRPMVYHGGSIYE 180  
121 QDNEDECLYNIYFEDGANTKKNADITSNORGEDEDHONSRRPMVYHGGSIYE 180  
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181 GTGNNIDGSIILASGNVIVITINRBLGSLGSLSTGCGAANKVGLLDQIALDWIBENNG 240  
241 AFGGDPKRVITIFGSGAGASCVSLTLSSHSEGLFOKAIIOGDTLSSMAVNYOPAKYTRI 300  
241 AFGGDPKRVITIFGSGAGASCVSLTLSSHSEGLFOKAIIOGDTLSSMAVNYOPAKYTRI 300  
301 LADKVGCMMLDITDMVECLRNKNKYEKLIQOTITPATYHIAFGVIDGVIIPDDQILMEQ 360  
301 LADKVGCMMLDITDMVECLRNKNKYEKLIQOTITPATYHIAFGVIDGVIIPDDQILMEQ 360  
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361 GEFNLNDIMLGAVNQGEGIKFVDGIVNDEGVTNDFPDSNSFNDNLYGPEGKOTLRET 420  
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RESULT 21  
US-09-978-375a-375  
Sequence 375, Application US/09978375A  
Publication No. US20030130181A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C24  
CURRENT APPLICATION NUMBER: US/09/978,375A  
CURRENT FILING DATE: 2002-04-19  
Prior Application removed - See File Wrapper or Paim  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 375  
LENGTH: 816  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-978-375a-375

Query Match 100.0%; Score 816; DB 12; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MINSNVLTWLTALAKFTETJCSOAGYPPVNTYKIRGRTLPETLIGPVGYGYVYA 60  
DB 1 MINSNVLTWLTALAKFTETJCSOAGYPPVNTYKIRGRTLPETLIGPVGYGYVYA 60

QY 61 SPTGERRFOPEPESSWTGIRNTTQFAAVCPQJDERSLDHMLPIWFTANLDTLMTYV 120  
DB 61 SPTGERRFOPEPESSWTGIRNTTQFAAVCPQJDERSLDHMLPIWFTANLDTLMTYV 120

QY 121 QONRECLYLTNYVPEDCANTRKACADCTJSDRGEDETHQNSKKRPVNTYHGGSTME 180  
DB 121 QONRECLYLTNYVPEDCANTRKACADCTJSDRGEDETHQNSKKRPVNTYHGGSTME 180

QY 181 GTANMIDGSLASGVAVYTTINVRGLIGFTSGOAKKGVGLDQIQALRNTEENVG 240  
DB 181 GTANMIDGSLASGVAVYTTINVRGLIGFTSGOAKKGVGLDQIQALRNTEENVG 240

QY 241 AFGDPEKRVITFGSGAGACVSLTLTSHVSEGLFGKXATIQSGTALSSAANVQPAKYTRI 300  
DB 241 AFGDPEKRVITFGSGAGACVSLTLTSHVSEGLFGKXATIQSGTALSSAANVQPAKYTRI 300

QY 301 LADKVGCMMLDTTDEWECGRNKNYKELLIOQTTPATYHIAFGSVIDGVI PDDPQILMEQ 360  
DB 301 LADKVGCMMLDTTDEWECGRNKNYKELLIOQTTPATYHIAFGSVIDGVI PDDPQILMEQ 360

QY 361 GEFLLNDIMLGNQVGGGLKAFVDGIVNEGVCTPNDPDSVSNVNDLXGYPSKOTLRZT 420  
DB 361 GEFLLNDIMLGNQVGGGLKAFVDGIVNEGVCTPNDPDSVSNVNDLXGYPSKOTLRZT 420

QY 421 IKFMVYDMADKENPEFRKRTLVLFTHQWAAVAADJLAQVGSSTYFAFHHQOSEM 480  
DB 421 IKFMVYDMADKENPEFRKRTLVLFTHQWAAVAADJLAQVGSSTYFAFHHQOSEM 480

QY 481 KPSWADSAGDEVPYVFGIPIMGPTLFCSCNFSKNDVMSAVVMYTWTFEAKTGDPNQPV 540  
DB 481 KPSWADSAGDEVPYVFGIPIMGPTLFCSCNFSKNDVMSAVVMYTWTFEAKTGDPNQPV 540

QY 541 PQTKEFHTKPNFEEVAMSKNPKQOLYHIGLKRVRDHYATKAFVLELVPHLNL 600  
DB 541 PQTKEFHTKPNFEEVAMSKNPKQOLYHIGLKRVRDHYATKAFVLELVPHLNL 600

QY 601 NEIFQVSTTKVPPTMTSPYGRSRPAKIPTTKRPAITPANNPKSKDPKTKGPD 660  
DB 601 NEIFQVSTTKVPPTMTSPYGRSRPAKIPTTKRPAITPANNPKSKDKPKTKGPD 660

QY 661 TVVLETKRDYSTELSVTTAVGASLLPLNLAFAAAYKKDKRRHETRRPSPQRTTND 720  
DB 661 TVVLETKRDYSTELSVTTAVGASLLPLNLAFAAAYKKDKRRHETRRPSPQRTTND 720

QY 721 IAHNQEIMSLQMKOLEHDECESEIQAHTLALCTCPDPTLTLRSPDDIPIMTPTWIT 780  
DB 721 IAHNQEIMSLQMKOLEHDECESEIQAHTLALCTCPDPTLTLRSPDDIPIMTPTWIT 780

QY 781 MIPNLTGQPLHFTNTFSGGQSTNLPHGSHSTRV 816  
DB 781 MIPNLTGQPLHFTNTFSGGQSTNLPHGSHSTRV 816

RESULT 22  
US-09-978-188a-375  
Sequence 375, Application US/09978188A  
Publication No. US20030139328A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C8

[illegible]

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? PRIOR APPLICATION NUMBER: 60/085339
? PRIOR FILING DATE: 1998-05-13
? PRIOR APPLICATION NUMBER: 60/085338
? PRIOR FILING DATE: 1998-05-13
? PRIOR APPLICATION NUMBER: 60/085323
? PRIOR FILING DATE: 1998-05-13
? PRIOR APPLICATION NUMBER: 60/085582
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085703
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085669
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085579
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085580
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085573
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085704
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085697
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Query Match 100.0% Score 816; DB 12; Length 816;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSNVLLWLTALAIKFTLIDSOAYPVNTNYKIRGLRTELPEE:AGPEQYLGAVYA 60
DB : MNSNVLLWLTALAIKFTLIDSOAYPVNTNYKIRGLRTELPEE:AGPEQYLGAVYA 60
QY 61 SEPTGERRFQPEPPSSNIGINTTOFAVVCQHLDERLHDLPIETANLCLMRYV 120
DB 61 SEPTGERRFQPEPPSSNIGINTTOFAVVCQHLDERLHDLPIETANLCLMRYV 120
QY 121 QONEDCXYLNIVYFPECDGATCKNADCTSNRDEDEHONSKRPYVYHGGSTYE 180
DB 121 QONEDCXYLNIVYFPECDGATCKNADCTSNRDEDEHONSKRPYVYHGGSTYE 180
QY 191 STANXVDSGLASVGNVYITINRYGLIGLSTGCAAKNGVJLDOQLMTEENVG 240
DB 191 STANXVDSGLASVGNVYITINRYGLIGLSTGCAAKNGVJLDOQLMTEENVG 240
QY 241 AFGGDPKRYTIFSSGAGSCVSLTSHVSEGLFGAALQSGTALSSAANYCPAKYRRI 300
DB 241 AFGGDPKRYTIFSSGAGSCVSLTSHVSEGLFGAALQSGTALSSAANYCPAKYRRI 300
QY 301 LADKVCNMLDTTDEYECLEKRNKVKELICQTTTPATYH:AFGQVTDGQVTPPPQTLMEQ 360
DB 301 LADKVCNMLDTTDEYECLEKRNKVKELICQTTTPATYH:AFGQVTDGQVTPPPQTLMEQ 360
QY 361 3EFLNDYKVGVOGSGKLFVNGVDNENGVPRNEDSEVSNFVNLGYPERKTLSET 420
DB 361 3EFLNDYKVGVOGSGKLFVNGVDNENGVPRNEDSEVSNFVNLGYPERKTLSET 420
QY 421 IKEMYTDMACKENPERRRTLVLFCTDHOVAPAVACDHAAGSEYFVAHYHCOSEN 480
DB 421 IKEMYTDMACKENPERRRTLVLFCTDHOVAPAVACDHAAGSEYFVAHYHCOSEN 480
QY 481 KFSWADSAHGDVEYVFG:PMIGPTELFSCNFKODVLSAVMTMTWTFAKTGDPNCPV 540
DB 481 KFSWADSAHGDVEYVFG:PMIGPTELFSCNFKODVLSAVMTMTWTFAKTGDPNCPV 540
QY 541 PCOTKFIHKRNFEEVAVSKYNPKDQYLHGLKRPVDEHRAKVAFWLWELVHNL 600
DB 541 PCOTKFIHKRNFEEVAVSKYNPKDQYLHGLKRPVDEHRAKVAFWLWELVHNL 600
QY 601 NEIFQYVSTTTKPPEDMTSPYGTGRSPAKIMPTTKRPAITPANNPKSKDPHTGSED 660
DB 601 NEIFQYVSTTTKPPEDMTSPYGTGRSPAKIMPTTKRPAITPANNPKSKDPHTGSED 660
QY 661 TTVLJETKRDYSTELSVTLAVGASLLFLNLFAALYKKDKRKHETHRSPQNTTND 720
DB 661 TTVLJETKRDYSTELSVTLAVGASLLFLNLFAALYKKDKRKHETHRSPQNTTND 720
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QY 721 IAHIONEIMSLQKLEHDECS:QAHDTLRITCPDPYTLTJRRSPDIPLXTPNTIT 780
DB 721 IAHIONEIMSLQKLEHDECS:QAHDTLRITCPDPYTLTJRRSPDIPLXTPNTIT 780
QY 781 MIPNTLTGMQPLHTEMTFSGGQNSTLPHGSHSTRV 816
DB 781 MIPNTLTGMQPLHTEMTFSGGQNSTLPHGSHSTRV 816
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## RESULT 21

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US-09-978-298A-375
? Sequence 375, Application US/09978298A
? Publication No. US20030134785A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gertlisen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Guiney, Austin B.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kijavich, Ivar O.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David B.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tamas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? TITLE OF INVENTION: Acids Encoding the Same
? FILE REFERENCE: P630PIC2
? CURRENT APPLICATION NUMBER: US/09/978,298A
? CURRENT FILING DATE: 2001-10-15
? PRIOR APPLICATION NUMBER: 09/918585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
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? PRIOR APPLICATION NUMBER: 60/078936
? PRIOR FILING DATE: 1998-03-20
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PROR APPLICATION NUMBER: 60/075910  
PROR FILING DATE: 1998-03-20  
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PROR FILING DATE: 1998-03-27  
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PROR FILING DATE: 1998-04-23  
PROR APPLICATION NUMBER: 60/083336  
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PROR APPLICATION NUMBER: 60/083322  
PROR FILING DATE: 1998-04-28  
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PROR FILING DATE: 1998-05-15  
PROR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; EB 12; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 8.6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 XNNSVULMLTFLAKFTLIDSCQYPPVNTNGKIRGRTPLPNEILGPVEQYLGYPYA 60  
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Db      1 MNSNVLMTLTALAIFKFTLIDSOAQYVNVNTNGKRGLETPELNEILGVEGYLGVPYA 60
Qy      61 SPTGERRRFPPEPPSSMTGIRNTTQFAAVCPCHLDBERSLHMLPMTFANLDTLMTYV 120
Db      62 SPTGERRRFPPEPPSSMTGIRNTTQFAAVCPCHLDBERSLHMLPMTFANLDTLMTYV 120
Qy      121 QDQNEDECLYNTIYPTEDGANTKKNAADITSNDRGEDEDHDCNSKKPVMVYTHGGSYME 180
Db      121 QDQNEDECLYNTIYPTEDGANTKKNAADITSNDRGEDEDHDCNSKKPVMVYTHGGSYME 180
Qy      161 GTGNMIDGSIILASVGNVITITNFRGLGFLSTGDDAAGNGLDQIALRWIEENVG 240
Db      181 GTGNMIDGSIILASVGNVITITNFRGLGFLSTGDDAAGNGLDQIALRWIEENVG 240
Qy      241 AFGSDPKRVITIFSGGAGASCVSLLTSHYSEGLFQKALIOSGTALSSMAVNYOPAKYTRI 300
Db      241 AFGSDPKRVITIFSGGAGASCVSLLTSHYSEGLFQKALIOSGTALSSMAVNYOPAKYTRI 300
Qy      301 LADYVGCMMLDTTDMVECLRNKVKELIQCTTTPATYHAFGVIDGDVTPDDPQILMEQ 360
Db      301 LADYVGCMMLDTTDMVECLRNKVKELIQCTTTPATYHAFGVIDGDVTPDDPQILMEQ 360
Qy      361 GEFPLNDYLGAVYQGEGLKFPVGIIVNEDGVTEHCEPFSVSNVNDLYGYPESKTLRET 420
Db      361 GEFPLNDYLGAVYQGEGLKFPVGIIVNEDGVTEHCEPFSVSNVNDLYGYPESKTLRET 420
Qy      421 IKFMYTDMADKENPETRKTVALFTDHCYVAPAVAADLHAQYGSPTFYAFYHQCSEM 480
Db      421 IKFMYTDMADKENPETRKTVALFTDHCYVAPAVAADLHAQYGSPTFYAFYHQCSEM 480
Qy      481 KPSMAASAHDEVPYVFGIIMIGTPELFCSCNFSKNDVMASAVMTYVTFATKGDENOV 540
Db      481 KPSMAASAHDEVPYVFGIIMIGTPELFCSCNFSKNDVMASAVMTYVTFATKGDENOV 540
Qy      541 PCTKFIHTKPNRFEVYASKYNPKDOLYHIGLKRPRVDHYZATVAFMLEVPHLETL 600
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Qy      601 NEIFQYVSTTKYVPPPOVTSFPGYTRRSAPAKIWTTPKPAITFANPKSKKEFRKTPSD 660
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Qy      661 TTVLIEFKRQYSTELASTYVAGSLFLNLAFAAYKCKXBRSETHRRPSGCRNTMD 720
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Qy      721 IAHIONEELMSLQKLEHDEHCESELQADTLRLTGPEDYTJTLRSPDIPXTPNIT 780
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Qy      781 MIPVLTGQPLHTNTFSGGONSTVPHGSHSTRV 816
Db      781 MIPVLTGQPLHTNTFSGGONSTVPHGSHSTRV 816

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RESULT 24  
US-10-143-331a-375  
Sequence 375, Application US-10-143331a  
Publication No. US20030138439A1  
GENERAL INFORMATION:

APPLICANT: Askerazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Betstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geiber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.

```

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar U.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniele.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P26301C39
CURRENT APPLICATION NUMBER: US/10/143,031A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
REMARKING PRIOR Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORIGIN: Homo sapiens
US-10-143-331a-375
Query Match : 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity: 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 331 LADKVSNNLCTTDMVECLRNKNYKELIQITTPATYHIAFGVLDGVAIPDDPQILMEQ 360  
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Prior Application Number: 60/062250  
Prior Filing Date: 1997-10-17  
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Db 361 GEPLNYDMLGVNGGEGKFPVDSIVENEDGCTPNDFPFSNFPDNLKSPRGKDLREI 420  
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Prior Application Number: 60/065311  
Prior Filing Date: 1997-11-13  
Prior Application Number: 60/066364  
Qy 421 IKFMYTMAADKENPEPTRKTLVALFTDCHQWAPAVAADLHAQVSPFYFAFYHCCSEM 480  
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Prior Filing Date: 1998-03-10  
Prior Application Number: 60/077632  
Db 421 IKFMYTMAADKENPEPTRKTLVALFTDCHQWAPAVAADLHAQVSPFYFAFYHCCSEM 480  
Prior Filing Date: 1998-03-11  
Prior Application Number: 60/077641  
Qy 481 KPSWADSAHSGDEVVPGIEMIISPELESCNFSNDVMSAVONTWYTNFAKTQDPVQV 540  
Prior Filing Date: 1998-03-11  
Prior Application Number: 60/077649  
Db 481 KPSWADSAHSGDEVVPGIEMIISPELESCNFSNDVMSAVONTWYTNFAKTQDPVQV 540  
Prior Filing Date: 1998-03-11  
Prior Application Number: 60/077791  
Qy 541 PODTFEITKPNRFEVWMSKYNPNPCOYLHIGLKPVRGVRKTKVAFWELVPRHNL 600  
Prior Filing Date: 1998-03-12  
Prior Application Number: 60/078004  
Db 541 PODTFEITKPNRFEVWMSKYNPNPCOYLHIGLKPVRGVRKTKVAFWELVPRHNL 600  
Prior Filing Date: 1998-03-13  
Prior Application Number: 60/078886  
Qy 601 NEIFQVYSTTKVPDPNTSFPYGTIRSGPANKIMFTTKRPAITPANPKHSGKDPKGTED 660  
Prior Filing Date: 1998-03-20  
Prior Application Number: 60/078910  
Db 601 NEIFQVYSTTKVPDPNTSFPYGTIRSGPANKIMFTTKRPAITPANPKHSGKDPKGTED 660  
Prior Filing Date: 1998-03-20  
Prior Application Number: 60/078936  
Qy 661 TTVLETRKRVSTELSTVTAAGSLLENLAPALYKKDKRHEHREESQRTNTR 720  
Prior Filing Date: 1998-03-25  
Prior Application Number: 60/079656  
Db 661 TTVLETRKRVSTELSTVTAAGSLLENLAPALYKKDKRHEHREESQRTNTR 720  
Prior Filing Date: 1998-03-26  
Prior Application Number: 60/079664  
Qy 721 IAHONEEIVSLQWQCEHDECESLQAHDTLRLTCCPEYTLTTRSSPDIPLXTPYIT 780  
Prior Filing Date: 1998-03-27  
Prior Application Number: 60/079294  
Db 721 IAHONEEIVSLQWQCEHDECESLQAHDTLRLTCCPEYTLTTRSSPDIPLXTPYIT 780  
Prior Filing Date: 1998-03-27  
Prior Application Number: 60/079699  
Qy 781 MIPNTLTQMOPUHTNNTSGGQNSNIPGCHSTRV 816  
Prior Filing Date: 1998-03-27  
Prior Application Number: 60/079663  
Db 781 MIPNTLTQMOPUHTNNTSGGQNSNIPGCHSTRV 816  
Prior Filing Date: 1998-03-27  
Prior Application Number: 60/079728  
Prior Filing Date: 1998-03-27  
Prior Application Number: 60/079786  
Prior Filing Date: 1998-03-27  
Prior Application Number: 60/079920  
Prior Filing Date: 1998-03-30  
Prior Application Number: 60/079923  
Prior Filing Date: 1998-03-30  
Prior Application Number: 60/080105  
Prior Filing Date: 1998-03-31  
Prior Application Number: 60/080107  
Prior Filing Date: 1998-03-31  
Prior Application Number: 60/080165  
Prior Filing Date: 1998-03-31  
Prior Application Number: 60/080194  
Prior Filing Date: 1998-03-31  
Prior Application Number: 60/080327  
Prior Filing Date: 1998-04-01  
Prior Application Number: 60/080328  
Prior Filing Date: 1998-04-01  
Prior Application Number: 60/080333  
Prior Filing Date: 1998-04-01  
Prior Application Number: 60/080334  
Prior Filing Date: 1998-04-01  
Prior Application Number: 60/081070  
Prior Filing Date: 1998-04-08  
Prior Application Number: 60/081049  
Prior Filing Date: 1998-04-08  
Prior Application Number: 60/081071  
Prior Filing Date: 1998-04-08  
Prior Application Number: 60/081195  
Prior Filing Date: 1998-04-08  
Prior Application Number: 60/081203  
Prior Filing Date: 1998-04-09

RESULT 25  
US-10-002-967A-375  
Sequence 375, Application US/10002967A  
Publication No. US20030148373A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kiliavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Pecht, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C72  
CURRENT APPLICATION NUMBER: US/10002,967A  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585

PRIO APPLICATION NUMBER: 60/081229  
PRIO FILING DATE: 1998-04-09  
PRIO APPLICATION NUMBER: 60/081955  
PRIO FILING DATE: 1998-04-15  
PRIO APPLICATION NUMBER: 60/081817  
PRIO FILING DATE: 1998-04-15  
PRIO APPLICATION NUMBER: 60/081919  
PRIO FILING DATE: 1998-04-15  
PRIO APPLICATION NUMBER: 60/081952  
PRIO FILING DATE: 1998-04-15  
PRIO APPLICATION NUMBER: 60/081918  
PRIO FILING DATE: 1998-04-15  
PRIO APPLICATION NUMBER: 60/082368  
PRIO FILING DATE: 1998-04-21  
PRIO APPLICATION NUMBER: 60/082569  
PRIO FILING DATE: 1998-04-21  
PRIO APPLICATION NUMBER: 60/082704  
PRIO FILING DATE: 1998-04-22  
PRIO APPLICATION NUMBER: 60/082854  
PRIO FILING DATE: 1998-04-22  
PRIO APPLICATION NUMBER: 60/082703  
PRIO FILING DATE: 1998-04-22  
PRIO APPLICATION NUMBER: 60/082797  
PRIO FILING DATE: 1998-04-22  
PRIO APPLICATION NUMBER: 60/082796  
PRIO FILING DATE: 1998-04-23  
PRIO APPLICATION NUMBER: 60/083356  
PRIO FILING DATE: 1998-04-27  
PRIO APPLICATION NUMBER: 60/083322  
PRIO FILING DATE: 1998-04-28  
PRIO APPLICATION NUMBER: 60/083392  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083495  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083496  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083499  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083545  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083554  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083558  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083559  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083550  
PRIO FILING DATE: 1998-04-29  
PRIO APPLICATION NUMBER: 60/083742  
PRIO FILING DATE: 1998-04-30  
PRIO APPLICATION NUMBER: 60/084366  
PRIO FILING DATE: 1998-05-05  
PRIO APPLICATION NUMBER: 60/084414  
PRIO FILING DATE: 1998-05-06  
PRIO APPLICATION NUMBER: 60/084441  
PRIO FILING DATE: 1998-05-06  
PRIO APPLICATION NUMBER: 60/084637  
PRIO FILING DATE: 1998-05-07  
PRIO APPLICATION NUMBER: 60/084639  
PRIO FILING DATE: 1998-05-07  
PRIO APPLICATION NUMBER: 60/084640  
PRIO FILING DATE: 1998-05-07  
PRIO APPLICATION NUMBER: 60/084638  
PRIO FILING DATE: 1998-05-07  
PRIO APPLICATION NUMBER: 60/084600  
PRIO FILING DATE: 1998-05-07  
PRIO APPLICATION NUMBER: 60/084627  
PRIO FILING DATE: 1998-05-07  
PRIO APPLICATION NUMBER: 60/084643  
PRIO FILING DATE: 1998-05-07  
PRIO APPLICATION NUMBER: 60/085339  
PRIO FILING DATE: 1998-05-13  
PRIO APPLICATION NUMBER: 60/085336

PRIO FILING DATE: 1998-05-13  
PRIO APPLICATION NUMBER: 60/085323  
PRIO FILING DATE: 1998-05-13  
PRIO APPLICATION NUMBER: 60/085582  
PRIO FILING DATE: 1998-05-15  
PRIO APPLICATION NUMBER: 60/085700  
PRIO FILING DATE: 1998-05-15  
PRIO APPLICATION NUMBER: 60/085689  
PRIO FILING DATE: 1998-05-15  
PRIO APPLICATION NUMBER: 60/085579  
PRIO FILING DATE: 1998-05-15  
PRIO APPLICATION NUMBER: 60/085560  
PRIO FILING DATE: 1998-05-15  
PRIO APPLICATION NUMBER: 60/085573  
PRIO FILING DATE: 1998-05-15  
PRIO APPLICATION NUMBER: 60/085704  
PRIO FILING DATE: 1998-05-15  
PRIO APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 12; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MUNSVMMLTALAIFKTLDSQAQVYNTNTNGKIRGRTPLPNETIGFVQYLVPA 60  
1 MUNSVMMLTALAIFKTLDSQAQVYNTNTNGKIRGRTPLPNETIGFVQYLVPA 60  
61 SPPTGERFQPPPEPSSMTGIRNTTQFAVCPHOLDBRSILHMLPWFANLDTLTYV 120  
61 SPPTGERFQPPPEPSSMTGIRNTTQFAVCPHOLDBRSILHMLPWFANLDTLTYV 120  
121 QDNEDCLYNTIYPTEDGANTKMAADITSNDGEDEDIDONSKKPMVNTIHGSSYNE 180  
121 QDNEDCLYNTIYPTEDGANTKMAADITSNDGEDEDIDONSKKPMVNTIHGSSYNE 180  
181 GTGMMDGSLASGVNTIYKPLGILGFLSTGQAAKANGSLDQICQAKRFEENVG 240  
181 GTGMMDGSLASGVNTIYKPLGILGFLSTGQAAKANGSLDQICQAKRFEENVG 240  
241 AFGSDPRKVTIFSGGASCVSLTSHSYEGLFQKAIIGSTALSSMAVNYQPARYTR 300  
241 AFGSDPRKVTIFSGGASCVSLTSHSYEGLFQKAIIGSTALSSMAVNYQPARYTR 300  
301 LADYVGCNMLDITDMECLRNKVKELIQCTIPATYHAFGVIGDVIYPPDQILMEQ 360  
301 LADYVGCNMLDITDMECLRNKVKELIQCTIPATYHAFGVIGDVIYPPDQILMEQ 360  
361 GEFNYDIMGVNOGEGELKFVDEIVNEDGVTEPNDPFSVSNFVDN.YGYPSGKTLLRAT 420  
361 GEFNYDIMGVNOGEGELKFVDEIVNEDGVTEPNDPFSVSNFVDN.YGYPSGKTLLRAT 420  
421 IKENYTDMAKXENPEIRKTLVALFTDHQVAVAVADLHAQVGSFTTYAFYHHCQSEM 480  
421 IKENYTDMAKXENPEIRKTLVALFTDHQVAVAVADLHAQVGSFTTYAFYHHCQSEM 480  
481 KPSWADSAHGCCEVPYVVG.FPIGPTELSNFKSNVMSAAVNTYWTNPAKAGDNOQY 540  
481 KPSWADSAHGCCEVPYVVG.FPIGPTELSNFKSNVMSAAVNTYWTNPAKAGDNOQY 540  
541 FQDTKFTHTKPNREEVAVSKYNPKQULYHIGLKRVRDHYATATYAFWLELVPHLNL 600  
541 FQDTKFTHTKPNREEVAVSKYNPKQULYHIGLKRVRDHYATATYAFWLELVPHLNL 600  
601 NEIFQVSTTKVPPPMTSFPGTRSPAKIPPTTKRAITANNPKSKDPKHXGCPED 660  
601 NEIFQVSTTKVPPPMTSFPGTRSPAKIPPTTKRAITANNPKSKDPKHXGCPED 660  
661 TTVLIEFKRQVSTELSTIYVAGSLPLNLIAFAALYKKDKRHRHETRRSPQRRTTND 720  
661 TTVLIEFKRQVSTELSTIYVAGSLPLNLIAFAALYKKDKRHRHETRRSPQRRTTND 720  
721 IAHIONEIWSLOMKOLEHDEGESIQADHTLRLCPDVTYTLRSPDIPLMYNTTIT 780  
721 IAHIONEIWSLOMKOLEHDEGESIQADHTLRLCPDVTYTLRSPDIPLMYNTTIT 780

Db 721 IAH1QNEIWSLQWKQLEHCESESLQAHDTLRCLTCLPPDYTLTLRRSPDDIP-MTENTIT 780  
QY 781 MIPTLTGKQPLHTFNTFSSGQNSCNLPHGSHSTRV 816  
Db 781 MIPTLTGKQPLHTFNTFSSGQNSCNLPHGSHSTRV 816

RESULT 26  
US-10-017-083A-375

Sequence 375 Application US/1017083A  
Publication No. US20030148376A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dar  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlesen, Mary E.  
APPLICANT: Goddard, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuc, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pat, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P167  
CURRENT APPLICATION NUMBER: US/10/017,083A  
CURRENT FILING DATE: 2001-10-24  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 375  
LENGTH: 816  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-017-083A-375

Query Match 100.0% Score 816, DB 12, Length 816,  
Best Local Similarity 100.0% Pred. No. 0,  
Matches 816, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 MINSNVLMALAKETLIDSOQYPVNTNYSKIGTLPPLNELLGVEGYLPPVA 60  
Db 1 MINSNVLMALAKETLIDSOQYPVNTNYSKIGTLPPLNELLGVEGYLPPVA 60  
QY 61 SPTTGERRFPQEPPEPSSWTGIRNTTQFAAVCPCHLDERSLHDXLPTMTFANLDTMTYV 120  
Db 61 SPTTGERRFPQEPPEPSSWTGIRNTTQFAAVCPCHLDERSLHDXLPTMTFANLDTMTYV 120  
QY 121 GQONEDCLYNIYVTEGANTKKAADITSDNGCEPDEHDQSKKPKPVYVHGGSYVE 180  
Db 121 GQONEDCLYNIYVTEGANTKKAADITSDNGCEPDEHDQSKKPKPVYVHGGSYVE 180  
QY 181 GTGNVLDGSLASGVNVYITINRFLGLGLSTGDAKGVNGLDQIQALKEIENWG 240  
Db 181 GTGNVLDGSLASGVNVYITINRFLGLGLSTGDAKGVNGLDQIQALKEIENWG 240  
QY 241 AFGGPKKRVITFGSGAGASCVSLLTSHSEGLFCXA-IGSGTALSSKAVNYQAKYTRI 300

Db 241 AFGGPKKRVITFGSGAGASCVSLLTSHSEGLFCXA-IGSGTALSSKAVNYQAKYTRI 300  
QY 301 LADKVGCMMLDITDMVECLRNKRYKELIQOTITPATYHIAFGVVIDGVIPDDPQILMEQ 360  
Db 301 LADKVGCMMLDITDMVECLRNKRYKELIQOTITPATYHIAFGVVIDGVIPDDPQILMEQ 360  
QY 361 GEPILNYDMLGVNGBGLKFDVGIUNDEGVTNDDDFVSNSKVDNLVGFPEKDTLRET 420  
Db 361 GEPILNYDMLGVNGBGLKFDVGIUNDEGVTNDDDFVSNSKVDNLVGFPEKDTLRET 420  
QY 421 IKPMYTMADKNEPCEKRTLVALLFDHCWAVAPVADLHAQYGSPTYFYAFYHHCQSEY 480  
Db 421 IKPMYTMADKNEPCEKRTLVALLFDHCWAVAPVADLHAQYGSPTYFYAFYHHCQSEY 480  
QY 481 KPSMADSHGDEVYVYVIGIMIGTLEFSCNFEKNDVMLSAVVMTWTWTFAKGIDENOV 540  
Db 481 KPSMADSHGDEVYVYVIGIMIGTLEFSCNFEKNDVMLSAVVMTWTWTFAKGIDENOV 540  
QY 541 PDDTKFIHTKPNRFEVAVMSKYNPKDLYLHIGLKPRVDRHYRATVAFWLELVPLHLN 600  
Db 541 PDDTKFIHTKPNRFEVAVMSKYNPKDLYLHIGLKPRVDRHYRATVAFWLELVPLHLN 600  
QY 601 NEIFQYVSTTKVPPPYTSPPYGTSSPAKIWPITKRPAITPANNPKSKDPKGTGPE 660  
Db 601 NEIFQYVSTTKVPPPYTSPPYGTSSPAKIWPITKRPAITPANNPKSKDPKGTGPE 660  
QY 661 TTVLIEKRDVSTSLTIIVAGASLFLNITLAFNAAYKKOKRREHETRRSPQRCTTND 720  
Db 661 TTVLIEKRDVSTSLTIIVAGASLFLNITLAFNAAYKKOKRREHETRRSPQRCTTND 720  
QY 721 IAH1QNEIWSLQWKQLEHCESESLQAHDTLRCLTCLPPDYTLTLRRSPDDIP-MTENTIT 780  
Db 721 IAH1QNEIWSLQWKQLEHCESESLQAHDTLRCLTCLPPDYTLTLRRSPDDIP-MTENTIT 780  
QY 781 MIPTLTGKQPLHTFNTFSSGQNSCNLPHGSHSTRV 816  
Db 781 MIPTLTGKQPLHTFNTFSSGQNSCNLPHGSHSTRV 816

## RESULT 27

US-10-143-030A-375  
Sequence 375 Application US/10143030A  
Publication No. US20030147901A1  
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dar  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlesen, Mary E.  
APPLICANT: Goddard, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuc, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pat, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C33  
CURRENT APPLICATION NUMBER: US/10/143,010A  
CURRENT FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 375  
LENGTH: 816  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-143-030A-375  
Query Match 100.0%; Score 816; DS 12; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MUNSVMWCTALAIKFTLDSQAOYVNTVNGKIRGKRTPLNELLGVEQYGVPA 60  
DB 1 MUNSVMWCTALAIKFTLDSQAOYVNTVNGKIRGKRTPLNELLGVEQYGVPA 60  
QY 61 SPTGERRFPQPPPPSWTGTIRNTQFAVCPQJLERSLJHMDLZAFITANLDTXVY 120  
DB 61 SPTGERRFPQPPPPSWTGTIRNTQFAVCPQJLERSLJHMDLZAFITANLDTXVY 120  
QY 121 QDQDECCLYNIYVPEDEGANKKMDLISNDRGSDCDHONSKKPPVYVCHGSSYE 180  
DB 121 QDQDECCLYNIYVPEDEGANKKMDLISNDRGSDCDHONSKKPPVYVCHGSSYE 180  
QY 181 GTNKLDSGLIASYGNVYVITINVRDLGLISTGDAQAKNGYGLDQIQALRWTEENVG 240  
DB 181 GTNKLDSGLIASYGNVYVITINVRDLGLISTGDAQAKNGYGLDQIQALRWTEENVG 240  
QY 241 AFGGDPKRVITFGSGAAGACVSLTISHVSEGLFCFAIIOSGALSSWAVNYQFAKTYRI 300  
DB 241 AFGGDPKRVITFGSGAAGACVSLTISHVSEGLFCFAIIOSGALSSWAVNYQFAKTYRI 300  
QY 301 LADVAGCNMLDTDMVECLANKYKELIQTTIPATYHAFGVYDGVYEPDPPQIMEQ 360  
DB 301 LADVAGCNMLDTDMVECLANKYKELIQTTIPATYHAFGVYDGVYEPDPPQIMEQ 360  
QY 361 GEFANVYDMLGVNCGEGLKFCVCGIVNEEDCVTPNDPDSVSNVDMLYGVPEGKDTLRET 420  
DB 361 GEFANVYDMLGVNCGEGLKFCVCGIVNEEDCVTPNDPDSVSNVDMLYGVPEGKDTLRET 420  
QY 421 IKPNVTEMADEXNEPEPRKTLVALFTDHCVAFAVAADLAHVGSPSTYVAFHHQOSM 480  
DB 421 IKPNVTEMADEXNEPEPRKTLVALFTDHCVAFAVAADLAHVGSPSTYVAFHHQOSM 480  
QY 481 KPSWASAHGDEVYVFGIPMIPTTELFSCNFSKRDVYMSAVMTMTWTFATGDENGPV 540  
DB 481 KPSWASAHGDEVYVFGIPMIPTTELFSCNFSKRDVYMSAVMTMTWTFATGDENGPV 540  
QY 541 PQTKEFHTKPNRFEVAVMSKNPKOOLYHIGLKRVRVDRHATKVAALVLEVPRLNL 600

QY 541 PQTKEFHTKPNRFEVAVMSKNPKOOLYHIGLKRVRVDRHATKVAALVLEVPRLNL 600  
DB 541 PQTKEFHTKPNRFEVAVMSKNPKOOLYHIGLKRVRVDRHATKVAALVLEVPRLNL 600  
QY 601 NEIFQVSTTKVPDPDMTSFPGYGRSRSPAKTWPTRKPAITPANNPKXS KDPHKTGPD 660  
DB 601 NEIFQVSTTKVPDPDMTSFPGYGRSRSPAKTWPTRKPAITPANNPKXS KDPHKTGPD 660  
QY 661 TTVLETRKDYSTELSVITAVGASLLEFNILAEALYKKEKRHEHRRPSPORXTND 720  
DB 661 TTVLETRKDYSTELSVITAVGASLLEFNILAEALYKKEKRHEHRRPSPORXTND 720  
QY 721 IAHQNEFMSLQKOLEBHDHCEESIQADHILRLTGPPTVTJURSPDDILMTPTT 780  
DB 721 IAHQNEFMSLQKOLEBHDHCEESIQADHILRLTGPPTVTJURSPDDILMTPTT 780  
QY 781 MIRPILTMQPLHTFNTFSGQNSTLPHSHSTRV 816  
DB 781 MIRPILTMQPLHTFNTFSGQNSTLPHSHSTRV 816  
RESULT 28  
US-10-145-128A-375  
Sequence 375, Application US/10145128A  
Publication No. US2003015761S1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flivaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutrey, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavyn, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C46  
CURRENT APPLICATION NUMBER: US/10/145,128A  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
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PRIOR FILING DATE: 1998-03-11



PRIOR APPLICATION NUMBER: 60/079669  
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 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 12; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSNVJLMLTALIKFTLDSQOQYVNVNTNYGKIRGLTLPJNETLGPVEOYLGPVYA 60  
 DB 1 MNSNVJLMLTALIKFTLDSQOQYVNVNTNYGKIRGLTLPJNETLGPVEOYLGPVYA 60  
 QY 61 SPTGERFOPPEPPSSWTG:RNTTGFPAVCPOHLDERSLHDX:PIWFTANLDTLNTYV 120  
 DB 61 SPTGERFOPPEPPSSWTG:RNTTGFPAVCPOHLDERSLHDX:PIWFTANLDTLNTYV 120  
 QY 121 ODQWEDCCLYLIVYPTDEGANTKCNADSDISNDGCEDEIHDOXSKXWVYIHGSSYME 180  
 DB 121 ODQWEDCCLYLIVYPTDEGANTKCNADSDISNDGCEDEIHDOXSKXWVYIHGSSYME 180

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QY 181 GTGMMIDGSIILASGVNTVITINRILGILSLSTGDDAAGKNGVLLDQIOLAKMIEENVG 240
DB 181 GTGMMIDGSIILASGVNTVITINRILGILSLSTGDDAAGKNGVLLDQIOLAKMIEENVG 240
QY 241 AFGGDPKRVITIFGSGAGASCVSLLTSLHSYGLFOKAIIOGSTRALSSMANVQPAKTRT 300
DB 241 AFGGDPKRVITIFGSGAGASCVSLLTSLHSYGLFOKAIIOGSTRALSSMANVQPAKTRT 300
QY 301 LADKVGCMNLDITDMVECLRNKNYKEIIQOTITPATVHIAFGPVIDGCVIPDDPOIIMBQ 360
DB 301 LADKVGCMNLDITDMVECLRNKNYKEIIQOTITPATVHIAFGPVIDGCVIPDDPOIIMBQ 360
QY 361 GEFLLNYDMLGNGOEGSKFVDSGVNEDGVTNDFPDSVSNFVDNLYGPEGKDTLRET 420
DB 361 GEFLLNYDMLGNGOEGSKFVDSGVNEDGVTNDFPDSVSNFVDNLYGPEGKDTLRET 420
QY 421 IKFVYTDWADKENETRRKTLVALFTDQWVAPVAADJLHAQYGSPTFYFAFYHHCOSM 480
DB 421 IKFVYTDWADKENETRRKTLVALFTDQWVAPVAADJLHAQYGSPTFYFAFYHHCOSM 480
QY 481 KPSWADSAHGDVFPVFCIPKIGPTELFSCNFSKXDVYLSVWTVYTNPAKTODEVQPV 540
DB 481 KPSWADSAHGDVFPVFCIPKIGPTELFSCNFSKXDVYLSVWTVYTNPAKTODEVQPV 540
QY 541 PQTFRITKXENRFEVAVMSKYNPKCOYLHIGSKPRVPCBPYTKAFLECYPHLHNL 600
DB 541 PQTFRITKXENRFEVAVMSKYNPKCOYLHIGSKPRVPCBPYTKAFLECYPHLHNL 600
QY 601 NEIFQVASTTKRPPDXTSPYGRASPAKIMPTKSPA-TTPANPQSKDCHKTGPED 660
DB 601 NEIFQVASTTKRPPDXTSPYGRASPAKIMPTKSPA-TTPANPQSKDCHKTGPED 660
QY 661 TTVLLETKRDYSTEISVITANGASJLFENILAFALYKKDKRHEHTRRSPQKNTND 720
DB 661 TTVLLETKRDYSTEISVITANGASJLFENILAFALYKKDKRHEHTRRSPQKNTND 720
QY 721 IAHIONEISLOMKOLEHRECEESLOHRTLRITCPEDYLLRASPDPILPYTANIT 780
DB 721 IAHIONEISLOMKOLEHRECEESLOHRTLRITCPEDYLLRASPDPILPYTANIT 780
QY 781 MIPNTLTGMQPLHFNTEFGGQNSTNLPHGSHTRV 816
DB 781 MIPNTLTGMQPLHFNTEFGGQNSTNLPHGSHTRV 816

RESULT 30
US-10-143-028A-375
/ Sequence 375, Application US/10143028A
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Boistein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geber, Hanspeter
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin J.
/ APPLICANT: Hillan, Kenneth C.
/ APPLICANT: Kijavits, Ivar J.
/ APPLICANT: Kuc, Sophia S.
/ APPLICANT: Kuper, Mary A.
/ APPLICANT: Pan, James.
/ APPLICANT: Pao, Nicholas P.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
```

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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C37
CURRENT APPLICATION NUMBER: US/10143.028A
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/066255
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077647
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-143-028A-375

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNSNVLLMTALAIKFTLIDSDAQYVNVNTYKIRGLRTPAPNEILGVEQYLGVPVA 60

QY 61 SPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDBRSJLHDLPTMFTANLDTMTYV 120
DB 61 SPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDBRSJLHDLPTMFTANLDTMTYV 120

QY 121 QDQNEDCLYINIVYPTEDGANTKKXNADDTISNDRGEDEDIHDQSKKPVVYIHGGSYME 180
DB 121 QDQNEDCLYINIVYPTEDGANTKKXNADDTISNDRGEDEDIHDQSKKPVVYIHGGSYME 180

QY 181 GTGMMIDGSIILASGVNTVITINRILGILSLSTGDDAAGKNGVLLDQIOLAKMIEENVG 240
DB 181 GTGMMIDGSIILASGVNTVITINRILGILSLSTGDDAAGKNGVLLDQIOLAKMIEENVG 240

QY 241 AFGGDPKRVITIFGSGAGASCVSLLTSLHSYGLFOKAIIOGSTRALSSMANVQPAKTRT 300
DB 241 AFGGDPKRVITIFGSGAGASCVSLLTSLHSYGLFOKAIIOGSTRALSSMANVQPAKTRT 300

QY 301 LADKVGCMNLDITDMVECLRNKNYKEIIQOTITPATVHIAFGPVIDGCVIPDDPOIIMBQ 360
DB 301 LADKVGCMNLDITDMVECLRNKNYKEIIQOTITPATVHIAFGPVIDGCVIPDDPOIIMBQ 360

QY 361 GEFLLNYDMLGNGOEGSKFVDSGVNEDGVTNDFPDSVSNFVDNLYGPEGKDTLRET 420
DB 361 GEFLLNYDMLGNGOEGSKFVDSGVNEDGVTNDFPDSVSNFVDNLYGPEGKDTLRET 420

QY 421 IKFVYTDWADKENETRRKTLVALFTDQWVAPVAADJLHAQYGSPTFYFAFYHHCOSM 480
DB 421 IKFVYTDWADKENETRRKTLVALFTDQWVAPVAADJLHAQYGSPTFYFAFYHHCOSM 480
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CY 481 KPSWADSAHDEUYVYVGVGIPTELFSCNFSKNDYKSAVVTWYNFANCGDNCQV 540  
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CY 541 POCDFHTKPNRFEENAKYKPKDLYIHIGKERYNHYATYCAWLEVPILNL 600  
DB 541 POCDFHTKPNRFEENAKYKPKDLYIHIGKERYNHYATYCAWLEVPILNL 600  
CY 601 NEIFQVSTTKVPPDPTSPFYCTRSPAKIMPTTRPAITFANNPKSKDCHKGPD 660  
DB 601 NEIFQVSTTKVPPDPTSPFYCTRSPAKIMPTTRPAITFANNPKSKDCHKGPD 660  
CY 661 TTULSTKRDVSTLSTLTVAGSALFLNLILAPALYKCKGRHETRRPSPQNTND 720  
DB 661 TTULSTKRDVSTLSTLTVAGSALFLNLILAPALYKCKGRHETRRPSPQNTND 720  
CY 721 IAHQNEEISLCKQKEHCECELOAHDTLTLCPDPTLTLRSPDILMPTNTT 780  
DB 721 IAHQNEEISLCKQKEHCECELOAHDTLTLCPDPTLTLRSPDILMPTNTT 780  
CY 781 MIPNTLTGMOPLMTFNTFSGQNSYMLFCHSTTRV 816  
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RESULT 31  
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Sequence 375, Application US/10143029A  
Publication No. US20030180311A1  
GENERAL INFORMATION:  
APPLICANT: Asakenzaki, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botschein, David  
APPLICANT: Bozcoyets, Luc  
APPLICANT: Ealon, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul C.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hilan, Kenneth J.  
APPLICANT: Kiyavan, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Ray, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Acids Encoding and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 22630PIC4  
CURRENT FILING DATE: US/10/143,029A  
PRIOR APPLICATION NUMBER: 2001-07-19  
PRIOR FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-04-15

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4 PRIOR APPLICATION NUMBER: 60/085573
5 PRIOR FILING DATE: 1998-05-15
6 PRIOR APPLICATION NUMBER: 60/085704
7 PRIOR FILING DATE: 1998-05-15
8 PRIOR APPLICATION NUMBER: 60/085697
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10 Query March 100.0% Score 816; DB 12; Length 816;
11 Best Local Similarity 100.0%; Pred. No. 3;
12 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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15 DE 1 MNSNVNLMTALAIKFLIDSOAQYPVWNTYNGKIRGLTLPENIIGPVEGYGVPA 60
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17 CY 61 SPPTGRRRQPEPPSSMTGIRNTTOPAAVPCGLRERSLHMLIKWTANLDTMTYV 120
18 CH 61 SPPTGRRRQPEPPSSMTGIRNTTOPAAVPCGLRERSLHMLIKWTANLDTMTYV 120
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21 DB 121 QDQNEDELYLVYVTEDEQANTKKNADDTISNDEGEDCHDKSKRPWVYIHGGSYNE 180
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23 CY 181 GTGSMIDGSLASVGNVIVITINRGLGLFTSGDQAAKNGYGLDQIOLRMIENNG 240
24 DB 181 GTGSMIDGSLASVGNVIVITINRGLGLFTSGDQAAKNGYGLDQIOLRMIENNG 240
25
26 CY 241 AFGGDPKAVTIFGSSAGACSVSLTSHYSEGLFOKAIIGSGTALSSMAVNYQPAKXTI 300
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29 CY 301 LARVQCNKLTTEVECCRKAKYKELIQOTITPATYHAFGVYIGDVPCDQILMEC 360
30 DB 301 LARVQCNKLTTEVECCRKAKYKELIQOTITPATYHAFGVYIGDVPCDQILMEC 360
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32 CY 361 GEFLLNDYVLGNVQSEGKLFVDGIYVNDGYTNDGPFSSVSNVYNDYVYGPSCQTLRET 420
33 DB 361 GEFLLNDYVLGNVQSEGKLFVDGIYVNDGYTNDGPFSSVSNVYNDYVYGPSCQTLRET 420
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35 CY 421 IKFMYTDMADKENPCTRRKTLVALFTHQWAPAVNADLHAQYGFYVAFYHNGQSEM 480
36 DB 421 IKFMYTDMADKENPCTRRKTLVALFTHQWAPAVNADLHAQYGFYVAFYHNGQSEM 480
37
38 CY 481 KPSWADSAAGDEVYVFGIPIGPELFSCNFSKNDYMSAVYMTYVTFNPAKTGDNQCV 540
39 DB 481 KPSWADSAAGDEVYVFGIPIGPELFSCNFSKNDYMSAVYMTYVTFNPAKTGDNQCV 540
40
41 CY 541 POOTKRIHKPRFEFVAMSKYNPEDQYVLHIGKPRVDRHYPATKVAEFLVPLHNL 600
42 DB 541 POOTKRIHKPRFEFVAMSKYNPEDQYVLHIGKPRVDRHYPATKVAEFLVPLHNL 600
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44 CY 601 NEIFQVYVSTTKVPPDMTSPFYGTGRSPAKIMTTRRALITPAANPKSKDPRKTPED 660
45 DB 601 NEIFQVYVSTTKVPPDMTSPFYGTGRSPAKIMTTRRALITPAANPKSKDPRKTPED 660
46
47 CY 661 TVLVLETKDYSYTELAVIAGVALLFLNIAFAALYKKDKRHRHTHRSPQRTTND 720
48 DB 661 TVLVLETKDYSYTELAVIAGVALLFLNIAFAALYKKDKRHRHTHRSPQRTTND 720
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50 CY 721 IAHQNEBELMSLOMQLHEDHCEBLOAHDLRLTCPPDVTLLRSPDDIPLKTPNTIT 780
51 DB 721 IAHQNEBELMSLOMQLHEDHCEBLOAHDLRLTCPPDVTLLRSPDDIPLKTPNTIT 780
52
53 CY 781 MIPNLTGQPLHTFNTFSGGQNSNLPHGHSTTRV 816
54 DB 781 MIPNLTGQPLHTFNTFSGGQNSNLPHGHSTTRV 816
55
56 RESULT 32
57 US-10-145-089A-375
58 Sequence 375, Application US/10145089A

```

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Publication No.: J820030C:80867A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin, P.
APPLICANT: Bastein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Fivazolf, Ellen
APPLICANT: Fonzy, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaud, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth C.
APPLICANT: Kilevin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James I.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Willats, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC31
CURRENT APPLICATION NUMBER: US/10/145,389A
CURRENT FILING DATE: 2002-09-04
PRIORITY APPLICATION NUMBER: 09/918585
PRIORITY FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: 60/062253
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/064249
PRIORITY FILING DATE: 1997-11-03
PRIORITY APPLICATION NUMBER: 60/065111
PRIORITY FILING DATE: 1997-11-13
PRIORITY APPLICATION NUMBER: 60/066364
PRIORITY FILING DATE: 1997-11-21
PRIORITY APPLICATION NUMBER: 60/077450
PRIORITY FILING DATE: 1998-03-10
PRIORITY APPLICATION NUMBER: 60/077632
PRIORITY FILING DATE: 1998-03-11
PRIORITY APPLICATION NUMBER: 60/077641
PRIORITY FILING DATE: 1998-03-11
PRIORITY APPLICATION NUMBER: 60/077649
PRIORITY FILING DATE: 1998-03-11
PRIORITY APPLICATION NUMBER: 60/077791
PRIORITY FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 916
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-089A-375
Query Match 100.0%, Score 816, DB 12, Length 816,
Best Local Similarity 100.0%, Pred. No. 0,
Matches 816, Conservative 0, Mismatches 0, Indels 0, Gaps 0
1 MNSNVTLMTLAIKIFLIDSCAQYPTVNTNYGKIGLRTPLENEILGFEVQYLVGPPA 60
1 MNSNVTLMTLAIKIFLIDSCAQYPTVNTNYGKIGLRTPLENEILGFEVQYLVGPPA 60
61 SPTGSRRRQPPPPSPSGVGINNTGPPAVCPDH:DESSLHDMCFWFLANLDTLNTYV 120
61 SPTGSRRRQPPPPSPSGVGINNTGPPAVCPDH:DESSLHDMCFWFLANLDTLNTYV 120

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0Y      QODNECGLVNTIYVPREGGANTKKCAADITSNSEGEEDJHDQSKRPWWYHGSYSYE 180
Db      121 CQDNECCULNTIYPTDEGANTRKKAADITNENGBEDDHQDSKRPAWVIHHGSYSYE 180
CY      181 GTGNMIDSGSLASGVNIYITINVELGILSLSGDQAANKNYOLDDICQLRMIEBNG 240
De      181 GTGNMIDSSSLASGVNIYITINVELSIGLISGDQAANKNYGLDDIQCALSWIEBNVG 240
CY      241 AFGDPDRPVITIGSGAGASCVSLTLLSHVSGLRQKAIIOSTGLSSMANVOXAKYTR 300
Cb      241 AFSGDKRVITIGSGAGASCVSLTLLSHVSGLRQKAIIOSTGLSSMANVOXAKYTR 300
CY      301 LADKVGCNMJLTTEMECELRNKXYAELHQOITATAYHAIFGPVIDSDVIPDDFOLIIMEQ 360
Cb      301 LADKVGCNMJLTDDEVBCLRKNKYAELLQOITATAYHAIFGPVIDSDVIPDDFOLIIMEQ 360
CY      361 GEFLENDIMLVNQVCGEGLKEVDGIIDNEDGVTPDFCSVENFEVDNLVYGSPEGKDILTET 420
Cb      361 GEFLENDIMLVNQVCGEGLKEVDGIIDNEDGVTPDFCSVENFEVDNLVYGSPEGKDILTET 420
CY      421 IKEMVTDMADKENPEPRRKTLVALFTDHQMAPAVAADLHAQVGSPTYFAFYHHQSEM 480
Cb      421 IKEMVTDMADKENPEPRRKTLVALFTDHQMAPAVAADLHAQVGSPTYFAFYHHQSEM 480
CY      481 KESWAASSAGDEVPIYFPGIMPGRPELSCNFSKNDIMLSAVMTTYTNNAKTGDZPOV 540
Cb      481 KPMAOASAHQDEVPYFGIPMGTELPSCNFSKNDVLSAVMTTYTNNAKTGDZPOV 540
CY      541 POOTKEIHTRKPNRFEEVAMSKNPDOUYLHGKPRRDHYRAKYAFMLEVPHLAN 600
Cb      541 POTKEIHTRKPNRFEEVAMSKNPDOUYLHGKPRRDHYRAKYAFMLEVPHLAN 600
CY      601 NEIFOVYSTTKVPPPDMSFPFYGRSRPAKIWTYKRAPATPANNPKSKCPHXTPED 660
Cb      601 NEIFOVYSTTKVPPPDMSFPFYGRSRPAKIWTYKRAPATPANNPKSKCPHXTPED 660
CY      661 TYVLITFKDCYSTELSVTAIVCASLFFNILAPALYYKCKRHEHHRSPSPORANTND 720
Cb      661 TYVLITFKDYSELSVTAIVCASLFFNILAPALYYKCKRHEHHRSPSPORANTND 720
CY      721 IAHIONEELMSQMKOLEHDECESLOAHDTLRLTCPEDTYTIRSPDPLMTENT 780
Cb      721 IAHIQUESIELMSQMKOLEHDECESLOAHDTLRLTCPEDTYTILRRSPDPIPLMTENT 780
CY      781 MIPNLTGMOPHTENTFSGGONSINLPHGSTTR 816
Cb      781 MIPNLTGMOPHTENTFSGGONSINLPHGSTTR 816

RESULT 33
US-10-013-926A-375
Sequence 375, Application US/001992EA
Publication No. US20090187241A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar D.
APPLICANT: Kuo, Sophia S.

```

```

? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James.
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
?
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2630P1C80
? CURRENT APPLICATION NUMBER: US/10/013,926A
? PRIOR FILING DATE: 2002-09-13
? PRIOR APPLICATION NUMBER: 09/918585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/064249
? PRIOR FILING DATE: 1997-11-03
? PRIOR APPLICATION NUMBER: 60/065311
? PRIOR FILING DATE: 1997-11-13
? PRIOR APPLICATION NUMBER: 60/066364
? PRIOR FILING DATE: 1997-11-21
? PRIOR APPLICATION NUMBER: 60/077450
? PRIOR FILING DATE: 1998-03-10
? PRIOR APPLICATION NUMBER: 60/077632
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/077641
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/077649
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/077791
? PRIOR FILING DATE: 1998-03-12
? Remaining Prior Application data removed - See file wrapper or PAM.
? NUMBER OF SEQ ID NOS: 624
? SEQ ID NO: 375
? LENGTH: 816
? TYPE: PRT
? ORGANISM: Homo sapiens
?
? US-10-013-926A-375
?
? Query Match 100.0%; Score 816; DB 12; Length 816;
? Best Local Similarity 100.0%; Pred. No. 0;
? Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
?
? QY 1 MINSVLLMLTALAKFTLIDSOAQYPVVNTNYSKRGRLPLNELIGVEQYLGYPVA 60
? DB 1 MINSVLLMLTALAKFTLIDSOAQYPVVNTNYSKRGRLPLNELIGVEQYLGYPVA 60
?
? QY 61 SEPTGERRCPEPSSWTGIRNTTOFAAVCPQHLDESLHMLPWFNANDTLXTYV 120
? DB 61 SEPTGERRCPEPSSWTGIRNTTOFAAVCPQHLDESLHMLPWFNANDTLXTYV 120
?
? QY 121 COQNEDELYLVIVTEDEGANTKKNADITSDRGEDEDIDQSKRPVYVYIHGSYVE 180
? DB 121 COQNEDELYLVIVTEDEGANTKKNADITSDRGEDEDIDQSKRPVYVYIHGSYVE 180
?
? QY 181 GTGNMIDGSLASVGNVIVITINHLGLSLSTGCKAKNRGLDQICDLKRENNVG 240
? DB 181 GTGNMIDGSLASVGNVIVITINHLGLSLSTGCKAKNRGLDQICDLKRENNVG 240
?
? QY 241 AFGDPKRVTFIIGSGAGASCVALTLTSHYSGDFGKATIGSGTALSMANVYCPAKYTRI 300
? DB 241 AFGDPKRVTFIIGSGAGASCVALTLTSHYSGDFGKATIGSGTALSMANVYCPAKYTRI 300
?
? QY 301 LADKVGCMMDTDMVECLRNKRYKELIQCTITPAATYHIAFGVYIDGVTFDDPQILMEG 360
? DB 301 LADKVGCMMDTDMVECLRNKRYKELIQCTITPAATYHIAFGVYIDGVTFDDPQILMEG 360
?
? QY 361 GEFLNYDMLGYNCGEGSKFYDGTVDNEDGCTPDPDFSVNPFYDN: XGYPEGGCTLRRT 420
? DB 361 GEFLNYDMLGYNCGEGSKFYDGTVDNEDGCTPDPDFSVNPFYDN: XGYPEGGCTLRRT 420

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? QY 421 IKFMYTMDADKENETRKTLVALFTDQWVAPVADLHFAOYGSPTYFYAHHCQSEM 480
? DB 421 IKFMYTMDADKENETRKTLVALFTDQWVAPVADLHFAOYGSPTYFYAHHCQSEM 480
?
? QY 481 KPSVADSAGCEVYVVGIPMIGSTELFSCNFSKNDVMSANVTWTNNAKGC2NCPV 540
? DB 481 KPSVADSAGCEVYVVGIPMIGSTELFSCNFSKNDVMSANVTWTNNAKGC2NCPV 540
?
? QY 541 PDCIFHTKPNREEVAMSKYNKCDQYLHIGKPRVRCCHYATKAFMLLEVPHLNL 600
? DB 541 PDCIFHTKPNREEVAMSKYNKCDQYLHIGKPRVRCCHYATKAFMLLEVPHLNL 600
?
? QY 601 NEIPOYVSTTKVPPDMTSPFYTRSPAKIMYTTKPAITPANNPQSKDEHYKGPED 660
? DB 601 NEIPOYVSTTKVPPDMTSPFYTRSPAKIMYTTKPAITPANNPQSKDEHYKGPED 660
?
? QY 661 TVVLETRKDYSTELTIAVGASLELNLIAFAALYKKDKSRHETRRPSPQRTTND 720
? DB 661 TVVLETRKDYSTELTIAVGASLELNLIAFAALYKKDKSRHETRRPSPQRTTND 720
?
? QY 721 IAHIONEIMLQYKOLEHDECSLOAHDTLRLCTCPDYTLTLRSGPDIPATNTNTIT 780
? DB 721 IAHIONEIMLQYKOLEHDECSLOAHDTLRLCTCPDYTLTLRSGPDIPATNTNTIT 780
?
? QY 781 MIPMTLGMQPLATFNTFPGGQNSTNLPKHSSTRV 816
? DB 781 MIPMTLGMQPLATFNTFPGGQNSTNLPKHSSTRV 816
?
? RESULT 34
? US-10-145-017A-375
? Sequence 375, Application US/10145017A
? Publication No. US20030196365A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dar
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Giang
? APPLICANT: Geber, Hanspeter
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gunney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kijavini, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James.
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
?
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2630P1C80
? CURRENT APPLICATION NUMBER: US/10/145,017A
? PRIOR FILING DATE: 2001-10-19
? PRIOR APPLICATION NUMBER: 09/918585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/064249
? PRIOR FILING DATE: 1997-11-03

```

```

PRIOR APPLICATION NUMBER: 60/065312
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077453
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PAM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-017A-375

```

Query Match Best Local Similarity 100.0% Score 816; DB 12; Length 816;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 1 MENSVLMTALAIKELLIDSOACPVNTNYGKIRGRTPLNEILCPVEQYGVPA 60
DB 1 MENSVLMTALAIKELLIDSOACPVNTNYGKIRGRTPLNEILCPVEQYGVPA 60
CY 61 SPPTGERRPPPEPSSWTGIRNTTQFAVCPQRLDERLHDMPIRMTALDITNTYV 120
DB 61 SPPTGERRPPPEPSSWTGIRNTTQFAVCPQRLDERLHDMPIRMTALDITNTYV 120
CY 121 QDCNECLVNIYVPTEDGANTKNADDTSDRGEDEIHQNSKRPVYVTHGSGYK 180
DB 121 QDCNECLVNIYVPTEDGANTKNADDTSDRGEDEIHQNSKRPVYVTHGSGYK 180
CY 181 GTGNTDGSILASGVNVTITTYRLGICFLSTPCQAKNGYGLDQIALRWLENYG 240
DB 181 GTGNTDGSILASGVNVTITTYRLGICFLSTPCQAKNGYGLDQIALRWLENYG 240
CY 241 AFGSDPKRVTIFSGAGASCVSLLTSHVSEGLFOYATIGSTALSSKAWYQPKYTR 300
DB 241 AFGSDPKRVTIFSGAGASCVSLLTSHVSEGLFOYATIGSTALSSKAWYQPKYTR 300
CY 301 LADKVGCMJDTTDMVECLRNKYNKELIQITTPACTYHIAFGVITGVYIPDPQILMEQ 360
DB 301 LADKVGCMJDTTDMVECLRNKYNKELIQITTPACTYHIAFGVITGVYIPDPQILMEQ 360
CY 361 GEFUNYDMLGVNKGELKFDGIVNEGCVTNDPDESVSNVCKLVGPEGKTLRET 420
DB 361 GEFUNYDMLGVNKGELKFDGIVNEGCVTNDPDESVSNVCKLVGPEGKTLRET 420
CY 421 IKRYWTMADEKNEPEPRKTVALFTDQWVAVAADAHACYSPTFYAFYHHCSEY 480
DB 421 IKRYWTMADEKNEPEPRKTVALFTDQWVAVAADAHACYSPTFYAFYHHCSEY 480
CY 481 KPSWADSAAGDEVPYVIGIPIGTELFSCFKNVYKSAVYVYTWTFATCGDNGYV 540
DB 481 KPSWADSAAGDEVPYVIGIPIGTELFSCFKNVYKSAVYVYTWTFATCGDNGYV 540
CY 541 PCOTKFIHTKPNFEEFAVSKYKPCOLYHICLKPVRCHVAACTVAAPMLEVPELNT 600
DB 541 PCOTKFIHTKPNFEEFAVSKYKPCOLYHICLKPVRCHVAACTVAAPMLEVPELNT 600
CY 601 NEFFQVSTTKVPPDPVTSFPYGRSSPAKIWPCTKAPATPAHPKSKCPKCTGPEQ 660
DB 601 NEFFQVSTTKVPPDPVTSFPYGRSSPAKIWPCTKAPATPAHPKSKCPKCTGPEQ 660
CY 661 TTVLIEFKRDTSLSTLAVGASLLFLNLAFAAYKKDKRKHETHRPSPQNTND 720
DB 661 TTVLIEFKRDTSLSTLAVGASLLFLNLAFAAYKKDKRKHETHRPSPQNTND 720

```

RESULT 35  
US-10-164-728A-375  
Sequence 375; Application US/10164728A  
Publication No. US20030186368A1

GENERAL INFORMATION:

```

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Yary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavrin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acid Reference: P630P043
CURRENT APPLICATION NUMBER: US/10/164,728A
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PAM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens

```

US-10-165-067A-375

Query Match 100.0%; Score 816; DB 12; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MUNSVMMLMTALAIKFTLIDSOAQYPVNTNKGKINGLSTP.PNEILGPEQYLGVPYA 60
DB 1 MUNSVMMLMTALAIKFTLIDSOAQYPVNTNKGKINGLSTP.PNEILGPEQYLGVPYA 60
OY 61 SPTGERRFQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHMLPIWFTANLDTLMTYV 120
DB 61 SPTGERRFQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHMLPIWFTANLDTLMTYV 120
OY 121 QDQNEDCLYNIYVPTDEGANTKKNAADITSNDRGDEDEJHDQSKKPVWVYIHGGSYME 180
DB 121 QDQNEDCLYNIYVPTDEGANTKKNAADITSNDRGDEDEJHDQSKKPVWVYIHGGSYME 180
OY 181 GTGNMIDGSIILASGNYVITINRGLGLFLSTGQAAKNGYGLDQIOALRWIFENYV 240
DB 181 GTGNMIDGSIILASGNYVITINRGLGLFLSTGQAAKNGYGLDQIOALRWIFENYV 240
OY 241 AFGGDBKRVTFHGGAGAGSCVSLTSLSHYSEGUFQKALISGTAALSMWAKYQPAVYR 300
DB 241 AFGGDBKRVTFHGGAGAGSCVSLTSLSHYSEGUFQKALISGTAALSMWAKYQPAVYR 300
OY 361 LADKVCNMLDTTDMWECLEKNKYKELICOTTPATYHAFGEYVDEVIPEDEQILMEQ 360
DB 361 LADKVCNMLDTTDMWECLEKNKYKELICOTTPATYHAFGEYVDEVIPEDEQILMEQ 360
OY 361 LADKVCNMLDTTDMWECLEKNKYKELICOTTPATYHAFGEYVDEVIPEDEQILMEQ 360
DB 361 LADKVCNMLDTTDMWECLEKNKYKELICOTTPATYHAFGEYVDEVIPEDEQILMEQ 360
OY 361 GEFNLNGLMGNNGGCKFYDQGVNEDGVTPEPFSSSNPKNNKXGPECKTLRET 420
DB 361 GEFNLNGLMGNNGGCKFYDQGVNEDGVTPEPFSSSNPKNNKXGPECKTLRET 420
OY 421 IKFNYTDMADKENDETRRKTLVALFTDQWAPFAVADLHACQGSFYFAFYHHCQSEK 480
DB 421 IKFNYTDMADKENDETRRKTLVALFTDQWAPFAVADLHACQGSFYFAFYHHCQSEK 480
OY 481 KPSMAASAGDEVPYVSGIEMIGTELPSCNFSKQJNLSAVNTYWTNFAKGDQRYV 540
DB 481 KPSMAASAGDEVPYVSGIEMIGTELPSCNFSKQJNLSAVNTYWTNFAKGDQRYV 540
OY 541 PODKFTHKPRFEVAVSKYNPKDCLYJHIGKAPVRCHYATXAPLELVPHLHNL 600
DB 541 PODKFTHKPRFEVAVSKYNPKDCLYJHIGKAPVRCHYATXAPLELVPHLHNL 600
OY 601 NEIPQVASTTKVPPDMTSPFYGTFRSSPAKIMPTTSPATTPANPKHKSQDTHKTSPE 660
DB 601 NEIPQVASTTKVPPDMTSPFYGTFRSSPAKIMPTTSPATTPANPKHKSQDTHKTSPE 660
OY 661 TTULIETKRDYSTEIYIAVGSILFLNITAFALYYKKDKRHHETHRRSPQKRTTND 720
DB 661 TTULIETKRDYSTEIYIAVGSILFLNITAFALYYKKDKRHHETHRRSPQKRTTND 720
OY 721 ZAHIONEEIIMSJOMQLEHDECESLQAHDTLRLLCTCPDYTLTLRRSPDDIPMTPTT 780
DB 721 ZAHIONEEIIMSJOMQLEHDECESLQAHDTLRLLCTCPDYTLTLRRSPDDIPMTPTT 780
OY 781 MLENTLTQMQLPHTNTPSSGQNSINLPHGSHSTRV 816
DB 781 MLENTLTQMQLPHTNTPSSGQNSINLPHGSHSTRV 816

```

RESULT 36

US-10-165-067A-375

Sequence 375, Application US/10165067A

Publication No. US20030185841A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desrochers, Luc

APPLICANT: Eaton, Dan

```

APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William J.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C42
CURRENT APPLICATION NUMBER: US/10/165,067A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-165-067A-375
Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      161 GTGMMIDGSLASGANNVITINRILGILGSLTGDOAAKNGYGLLEQIOLRMIEENVG 240
Cy      241 AFGGDPKRVITIFSGGAGASCVSLLTSHYSEGLFOXAIIQSGTALSSMAVNYCPAKYTRI 300
Db      241 AFGGDPKRVITIFSGGAGASCVSLLTSHYSEGLFOXAIIQSGTALSSMAVNYCPAKYTRI 300
Cy      301 LADKVGCMMLDTTDMVECLRNKYNKELIQQITIPATYHIAFGVYIGGVYIPDDPQILMEQ 360
Db      301 LADKVGCMMLDTTDMVECLRNKYNKELIQQITIPATYHIAFGVYIGGVYIPDDPQILMEQ 360
Cy      361 GEFNYNDIMGVNGGSEIKFVDCGVNEDVDVTPNDFPSVSNNVDNLYGFEGKDTRET 420
Db      361 GEFNYNDIMGVNGGSEIKFVDCGVNEDVDVTPNDFPSVSNNVDNLYGFEGKDTRET 420
Cy      421 IKFMYTDMADKENEDETARKTLVALFTDHOVAVAAADLHAQYGSPTFYAFYHHQOSEM 480
Db      421 IKFMYTDMADKENEDETARKTLVALFTDHOVAVAAADLHAQYGSPTFYAFYHHQOSEM 480
Cy      481 KPSWADSAHGDEVYVVGIMIGPTELFSGNSEKNDVMASAVVMTWTNPAKGDPRQPV 540
Db      481 KPSWADSAHGDEVYVVGIMIGPTELFSGNSEKNDVMASAVVMTWTNPAKGDPRQPV 540
Cy      541 PCDTKFIHTKPNFEFEVAAWSKYNPKQCYLHICLKPVRDHDVATKVAEMLEVFRLHL 600
Db      541 PCDTKFIHTKPNFEFEVAAWSKYNPKQCYLHICLKPVRDHDVATKVAEMLEVFRLHL 600
Cy      601 NEIFQYVSTTKVPPPDYISFPYGTSSPAKIMPTTKRPAITPAKPKSKODPRKTPED 660
Db      601 NEIFQYVSTTKVPPPDYISFPYGTSSPAKIMPTTKRPAITPAKPKSKODPRKTPED 660
Cy      661 TTVLETRKRYSTELSTAVGASLLFLNLAFAAYKKDKRRSECHRRPSORNTYND 720
Db      661 TTVLETRKRYSTELSTAVGASLLFLNLAFAAYKKDKRRSECHRRPSORNTYND 720
Cy      721 IAHIONEIMSLQKQLEHDECELSQAHDLRLTQPPVTLTLRRSPDDIPANCPNIT 780
Db      721 IAHIONEIMSLQKQLEHDECELSQAHDLRLTQPPVTLTLRRSPDDIPANCPNIT 780
Cy      781 MIPNTLGNOPLATRTFSGGONSTNUPHGHSTTRV 816
Db      781 MIPNTLGNOPLATRTFSGGONSTNUPHGHSTTRV 816

RESULT 37
US-10-145-124A-375
Sequence 375, Application: US/10145124A
Publication No. US200101970.A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bistisreir, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivarcoff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlsem, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Christopher
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavira, Iwar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2610P1C44
CURRENT APPLICATION NUMBER: US/10/145,124A
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 09/919585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062253
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064245
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-124A-375

Query Match      100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 MUNSNNVLMKLTALAIKRTLLIDSOAOYFVNTNNGKIRGLRTPLPNEILGVEQYLGYPYA 60
Db      1 MUNSNNVLMKLTALAIKRTLLIDSOAOYFVNTNNGKIRGLRTPLPNEILGVEQYLGYPYA 60
Cy      61 SPTGERRFQPPPESSWTGIRNTQFPAAYCPQHLDBRSLLHMLPIWTFANLDTLNTYV 120
Db      61 SPTGERRFQPPPESSWTGIRNTQFPAAYCPQHLDBRSLLHMLPIWTFANLDTLNTYV 120
Cy      121 QDNEDECLYNNIYFTEDGANTKKNADITSNRGEDEDIDQNSKKPVVYIHGGSYME 180
Db      121 QDNEDECLYNNIYFTEDGANTKKNADITSNRGEDEDIDQNSKKPVVYIHGGSYME 180
Cy      181 GTGMMIDGSLASGANNVITINRILGILGSLTGDOAAKNGYGLLEQIOLRMIEENVG 240
Db      181 GTGMMIDGSLASGANNVITINRILGILGSLTGDOAAKNGYGLLEQIOLRMIEENVG 240
Cy      241 AFGGDPKRVITIFSGGAGASCVSLLTSHYSEGLFOXAIIQSGTALSSMAVNYCPAKYTRI 300
Db      241 AFGGDPKRVITIFSGGAGASCVSLLTSHYSEGLFOXAIIQSGTALSSMAVNYCPAKYTRI 300
Cy      301 LADKVGCMMLDTTDMVECLRNKYNKELIQQITIPATYHIAFGVYIGGVYIPDDPQILMEQ 360
Db      301 LADKVGCMMLDTTDMVECLRNKYNKELIQQITIPATYHIAFGVYIGGVYIPDDPQILMEQ 360
Cy      361 GEFNYNDIMGVNGGSEIKFVDCGVNEDVDVTPNDFPSVSNNVDNLYGFEGKDTRET 420
Db      361 GEFNYNDIMGVNGGSEIKFVDCGVNEDVDVTPNDFPSVSNNVDNLYGFEGKDTRET 420
Cy      421 IKFMYTDMADKENEDETARKTLVALFTDHOVAVAAADLHAQYGSPTFYAFYHHQOSEM 480
Db      421 IKFMYTDMADKENEDETARKTLVALFTDHOVAVAAADLHAQYGSPTFYAFYHHQOSEM 480
Cy      481 KPSWADSAHGDEVYVVGIMIGPTELFSGNSEKNDVMASAVVMTWTNPAKGDPRQPV 540

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DB 481 KPSWADSHGDEVPYVFGI PMIGTELFSCNFSXNDVMSLAVMTWTNTAKTGDPKPV 540
QY 541 PDKTFHTKPRREEVAVMSKYNPCQCLYHIGLKPRVCHYRATKAFMLEVPHLNL 600
DB 541 PDKTFHTKPRREEVAVMSKYNPCQCLYHIGLKPRVCHYRATKAFMLEVPHLNL 600
QY 601 NEIFQVSTTTKVPDPMTSPFYGTGRSPAKIMPTTRPATTPANNPKSKDPKGPED 660
DB 601 NEIFQVSTTTKVPDPMTSPFYGTGRSPAKIMPTTRPATTPANNPKSKDPKGPED 660
QY 661 TTVLETKRDVSTELSTVIAVGASLLFLNLIAFALYKXDKRHEHRRSPQRMNTND 720
DB 661 TTVLETKRDVSTELSTVIAVGASLLFLNLIAFALYKXDKRHEHRRSPQRMNTND 720
QY 721 IAHIONEELMSLQMKOLBHDHCEGSLQJCHTJRLTGPEDYTLTLRSPDIPMTPTIT 780
DB 721 IAHIONEELMSLQMKOLBHDHCEGSLQJCHTJRLTGPEDYTLTLRSPDIPMTPTIT 780
QY 781 MIPNTLTGMQPLHNTFTSGGQNSTNLPHGSHSTRV 816
DB 781 MIPNTLTGMQPLHNTFTSGGQNSTNLPHGSHSTRV 816

RESULT 38
US-10-160-502A-375
Sequence 375, Application US/10160302A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P
APPLICANT: Bornstein, David
APPLICANT: Destroyers, Inc
APPLICANT: Eatch, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Ford, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary R.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC57
CURRENT APPLICATION NUMBER: US/10/160,502A
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See file wrapper or PAJX.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO: 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-160-502A-375

Query Match 100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pident No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MANSNVLMMLTALAIKFTLIDSOAQYVWNTNGKIRGLRTPPLNEILGVEGYLSVPA 60
1 MANSNVLMMLTALAIKFTLIDSOAQYVWNTNGKIRGLRTPPLNEILGVEGYLSVPA 60
DB 1 MANSNVLMMLTALAIKFTLIDSOAQYVWNTNGKIRGLRTPPLNEILGVEGYLSVPA 60
QY 61 SPTGERRFOPEPPSSNTG:RNTQFANCPQHLDBRSLLHMLJINFTAKLDCIMTY 120
DB 61 SPTGERRFOPEPPSSNTG:RNTQFANCPQHLDBRSLLHMLJINFTAKLDCIMTY 120
QY 121 QDQNEDECYLYNTYPTEDGANTKKNAD:TSNRSJEDEDIHDQNSKKPWWYIHSSSYME 180
DB 121 QDQNEDECYLYNTYPTEDGANTKKNAD:TSNRSJEDEDIHDQNSKKPWWYIHSSSYME 180
QY 121 QDQNEDECYLYNTYPTEDGANTKKNAD:TSNRSJEDEDIHDQNSKKPWWYIHSSSYME 180
DB 121 QDQNEDECYLYNTYPTEDGANTKKNAD:TSNRSJEDEDIHDQNSKKPWWYIHSSSYME 180
QY 181 GTGNM:JCSIIASGVNIVYTTINRUGILGFLSTGQAKANKYGLLDQIQALRWIEENYG 240
DB 181 GTGNM:JCSIIASGVNIVYTTINRUGILGFLSTGQAKANKYGLLDQIQALRWIEENYG 240
QY 241 AFGGPKRVITFGSGAGASCVSLLT:SHYSEGLFOKAIISGSGALSSMAVNYOPAYTYC 300
DB 241 AFGGPKRVITFGSGAGASCVSLLT:SHYSEGLFOKAIISGSGALSSMAVNYOPAYTYC 300
QY 301 LADKVCNMJLDTTDMVCLRNKYNKELIQCTITPATYHIAFGVIDGVY:PDOPQ:LYKQ 360
DB 301 LADKVCNMJLDTTDMVCLRNKYNKELIQCTITPATYHIAFGVIDGVY:PDOPQ:LYKQ 360
QY 361 GEPNLYDMLGVNGCEGLKFEVDG:VQNEDEVTNDDPFSNSNVCM:YGPBEGKTLRET 420
DB 361 GEPNLYDMLGVNGCEGLKFEVDG:VQNEDEVTNDDPFSNSNVCM:YGPBEGKTLRET 420
QY 421 IKFMYTDMADEKENDETRRKTJVALFTDQWVAFAVADLAQYGSFTFYAFYHQCSEK 480
DB 421 IKFMYTDMADEKENDETRRKTJVALFTDQWVAFAVADLAQYGSFTFYAFYHQCSEK 480
QY 481 KPSWADSHGDEVPYVFGI PMIGTELFSCNFSXNDVMSLAVMTWTNTAKTGDPKPV 540
DB 481 KPSWADSHGDEVPYVFGI PMIGTELFSCNFSXNDVMSLAVMTWTNTAKTGDPKPV 540
QY 541 PDKTFHTKPRREEVAVMSKYNPCQCLYHIGLKPRVCHYRATKAFMLEVPHLNL 600
DB 541 PDKTFHTKPRREEVAVMSKYNPCQCLYHIGLKPRVCHYRATKAFMLEVPHLNL 600
QY 601 NEIFQVSTTTKVPDPMTSPFYGTGRSPAKIMPTTRPATTPANNPKSKDPKGPED 660
DB 601 NEIFQVSTTTKVPDPMTSPFYGTGRSPAKIMPTTRPATTPANNPKSKDPKGPED 660
QY 661 TTVLETKRDVSTELSTVIAVGASLLFLNLIAFALYKXDKRHEHRRSPQRMNTND 720
DB 661 TTVLETKRDVSTELSTVIAVGASLLFLNLIAFALYKXDKRHEHRRSPQRMNTND 720
QY 721 IAHIONEELMSLQMKOLBHDHCEGSLQJCHTJRLTGPEDYTLTLRSPDIPMTPTIT 780
DB 721 IAHIONEELMSLQMKOLBHDHCEGSLQJCHTJRLTGPEDYTLTLRSPDIPMTPTIT 780
QY 781 MIPNTLTGMQPLHNTFTSGGQNSTNLPHGSHSTRV 816
DB 781 MIPNTLTGMQPLHNTFTSGGQNSTNLPHGSHSTRV 816
```



Db 781 MIPNLTGMQPLHTFNTFFSGGQNSTNLPHGSTRV 8:6

## RESULT 39

US-10-165-247A-375

Sequence 375, Application US/10165247A

Publication No. US20030290321A:

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gottlieb, Mary E.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, C. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavira, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Nadler, Mary A.

APPLICANT: Pan, James J.

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Thomas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P263030141

CURRENT APPLICATION NUMBER: US/10/165,247A

CURRENT FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

Remaining Prior Application data removed - See File Wrapper or PAJX.

NUMBER OF SEQ ID NOS: 624

SEQ ID NO 375

LENGTH: 8:6

TYPE: PRT

ORGANISM: Homo sapiens

US-10-165-247A-375

Query Match 100.0%; Score 8:6; DB 12; Length 8:6;

Best Local Similarity 100.0%; P-adj No. 3;

Matches 8:6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSNVLLMTALAIKFTLIDSCAQYRVNTNYKILGJRTPLPNEILGVEQYLGVPYA 60

Db 781 MIPNLTGMQPLHTFNTFFSGGQNSTNLPHGSTRV 8:6

QY 1 MNSNVLLMTALAIKFTLIDSCAQYRVNTNYKILGJRTPLPNEILGVEQYLGVPYA 60

QY 61 SPPTGERRPOPEPSSWTGIRNTCTCPAAACPOHDEBSLHMDLIMFANIDTLYTV 120

Db 61 SPPTGERRPOPEPSSWTGIRNTCTCPAAACPOHDEBSLHMDLIMFANIDTLYTV 120

QY 121 CDQNEDELINIVPTEDGANTKKNAADITSNGBEDEDHDSKSKPVWYVHGGSYME 180

Db 121 CDQNEDELINIVPTEDGANTKKNAADITSNGBEDEDHDSKSKPVWYVHGGSYME 180

QY 181 GTGNMIGSLASTGYNTVITINRUGILCFLSTGDAKAKNGLLDQIQALNIEBNG 240

Db 181 GTGNMIGSLASTGYNTVITINRUGILCFLSTGDAKAKNGLLDQIQALNIEBNG 240

QY 241 AFGGCPKRVITPFGGAGASCVSLLTSHVSEGLPKXKIIOSGTALSSMAVYCPAKTR 300

Db 241 AFGGCPKRVITPFGGAGASCVSLLTSHVSEGLPKXKIIOSGTALSSMAVYCPAKTR 300

QY 301 LADKVGCMMLDITDMVECLRNKVKELIQOTTPATYHAFGVINDVLPDDPQILMEQ 360

Db 301 LADKVGCMMLDITDMVECLRNKVKELIQOTTPATYHAFGVINDVLPDDPQILMEQ 360

QY 361 GEFUNYDIMGVNNGEGLKRVDDGVNDEGVTNDEPDSVSNFVNDLYGIPBCKDLRET 420

Db 361 GEFUNYDIMGVNNGEGLKRVDDGVNDEGVTNDEPDSVSNFVNDLYGIPBCKDLRET 420

QY 421 IKFMYTDMADKENETRKTLVALFTDHQVAVAVADLHAQYGSPTYFAFYHGOSEM 480

Db 421 IKFMYTDMADKENETRKTLVALFTDHQVAVAVADLHAQYGSPTYFAFYHGOSEM 480

QY 481 KPSWADSAHGDVPEYVFGIMIGTLELFSNFSKNDVMISAVMTYTNFAKTGDPNQV 540

Db 481 KPSWADSAHGDVPEYVFGIMIGTLELFSNFSKNDVMISAVMTYTNFAKTGDPNQV 540

QY 541 PDKRFHTKPNRREEVAMSKYNDOLYHIGKPVDRHYATKVAFLVPHLNL 600

Db 541 PDKRFHTKPNRREEVAMSKYNDOLYHIGKPVDRHYATKVAFLVPHLNL 600

QY 601 NEIFQVSTTKVPDPMTSPFYGTRSPAKIMPTTRPAITPANPKHSKDPKCTGPD 660

Db 601 NEIFQVSTTKVPDPMTSPFYGTRSPAKIMPTTRPAITPANPKHSKDPKCTGPD 660

QY 661 TTVLETRKDYSTELSTIAVAGSLFLNLAEALYKKDKRRHETRRPSORNTND 720

Db 661 TTVLETRKDYSTELSTIAVAGSLFLNLAEALYKKDKRRHETRRPSORNTND 720

QY 721 IASTONEINSLQKQLEHDECESLQANDTLRLTGPDDYTLRLRSDDIIPZYTPYTI 780

Db 721 IASTONEINSLQKQLEHDECESLQANDTLRLTGPDDYTLRLRSDDIIPZYTPYTI 780

QY 781 MIPNLTGMQPLHTFNTFFSGGQNSTNLPHGSTRV 8:6

Db 781 MIPNLTGMQPLHTFNTFFSGGQNSTNLPHGSTRV 8:6

RESULT 40

US-09-978-194A-375

Sequence 375, Application US/09978194A

Publication No. US20030195339A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gottlieb, Mary E.

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin J.  
APPLICANT: Hilari, Kenneth J.  
APPLICANT: K.Javin, Ivar C.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
ACIDS Encoding the Same  
FILE REFERENCE: P2630P1C10  
CURRENT APPLICATION NUMBER: US/03/978,194A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 03/9,8585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062253  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064245  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-23  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077731  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078866  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
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PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05



[illegible]

/ PRIOR APPLICATION NUMBER: 60/085689  
 / PRIOR FILING DATE: 1998-05-15  
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 / PRIOR FILING DATE: 1998-05-15  
 / PRIOR APPLICATION NUMBER: 60/085560  
 / PRIOR FILING DATE: 1998-05-15  
 / PRIOR APPLICATION NUMBER: 60/085573  
 / PRIOR FILING DATE: 1998-05-15  
 / PRIOR APPLICATION NUMBER: 60/085704  
 / PRIOR FILING DATE: 1998-05-15  
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 12; Length 816;  
 Best Local Similarity 100.0%; Pctd. No. 0;  
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MUNSVMMLTALAKETLIDSOQYPPVNTNNGKIRGLRTPJNEILGVEOYLGPYA 60  
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 QY 61 SEPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHDLPIWFTANJDTLMTYV 120  
 DB 61 SEPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHDLPIWFTANJDTLMTYV 120  
 QY 121 ODONEDCCYLNIVYPTEDGANTKNADITNDGCEBDIHQSKKPVVYIHGGSYME 180  
 DB 121 ODONEDCCYLNIVYPTEDGANTKNADITNDGCEBDIHQSKKPVVYIHGGSYME 180  
 QY 181 GTGNMIDGSIASGYNVITINVRGLIGLSTGDOAKNGVLLDQIALRWIEENVG 240  
 DB 181 GTGNMIDGSIASGYNVITINVRGLIGLSTGDOAKNGVLLDQIALRWIEENVG 240  
 QY 241 AFGGPKRVITIFGSGAGASCVSLLTSHYSGLEFQKAIIGGATLSSMAVNYQPAKYTRI 300  
 DB 241 AFGGPKRVITIFGSGAGASCVSLLTSHYSGLEFQKAIIGGATLSSMAVNYQPAKYTRI 300  
 QY 301 LADKVGCMMLDTDMVECLRNKYNKELIQCTITPATYHIAFGPIVDDGVPDDPQILMEQ 360  
 DB 301 LADKVGCMMLDTDMVECLRNKYNKELIQCTITPATYHIAFGPIVDDGVPDDPQILMEQ 360  
 QY 361 GEFLLVNDIMLGVNQGEGLKPVNDGIVDNEEDGVPNDPFSVSNPVNDLYGPEBKDTLRET 420  
 DB 361 GEFLLVNDIMLGVNQGEGLKPVNDGIVDNEEDGVPNDPFSVSNPVNDLYGPEBKDTLRET 420  
 QY 421 IKFMYTDMADKENPETRKRKTLYALFTDQWAPPAVADLEHQYGSPTFYFAFYHRCQSEM 480  
 DB 421 IKFMYTDMADKENPETRKRKTLYALFTDQWAPPAVADLEHQYGSPTFYFAFYHRCQSEM 480  
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 DB 481 KPSWADSAHGDVPPVFGIPWIGPTEJSCNFSKNDVLSAVMTYWTNFAKTCOPRQPV 540  
 QY 541 FQDTPKZHTKPRFEVAMSKYNPDCQYLHIGLXPRVDDHVRATKAFWCELVPHLHNL 600  
 DB 541 FQDTPKZHTKPRFEVAMSKYNPDCQYLHIGLXPRVDDHVRATKAFWCELVPHLHNL 600  
 QY 601 NEIFQYVSTTQVPPSPDMTSFPGYGRSPAKIMPTTQSPATTPANNRPHSKDPKIKSPED 660  
 DB 601 NEIFQYVSTTQVPPSPDMTSFPGYGRSPAKIMPTTQSPATTPANNRPHSKDPKIKSPED 660  
 QY 661 TTVLETKRQVSTELSVTIAVGASLLFANLAFALYKXDKRSHETRRPSPQORTTND 720  
 DB 661 TTVLETKRQVSTELSVTIAVGASLLFANLAFALYKXDKRSHETRRPSPQORTTND 720  
 QY 721 IAHIONEELMSQKQLEHHECESLQAHDTLRLTCCPDYTLTARSPDDIPJLTPHTIT 780  
 DB 721 IAHIONEELMSQKQLEHHECESLQAHDTLRLTCCPDYTLTARSPDDIPJLTPHTIT 780  
 QY 781 MIPNTLGCQPLHTNTRSSGONSTNLPHGSTRV 816  
 DB 781 MIPNTLGCQPLHTNTRSSGONSTNLPHGSTRV 816

## RESULT 42

US-09-999-829A-375

Sequence 375, Application US/0999829A

Publication No. US20030195344A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gertsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, C. Christopher

APPLICANT: Guiney, Austin L.

APPLICANT: Hillman, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630P1C61

CURRENT APPLICATION NUMBER: US/09/999, 829A

CURRENT FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 624

Prior Application removed - See File Wrapper or Palm

SEQ ID NO 375

LENGTH: 816

TYPE: PRT

ORGANISM: Homo sapiens

US-09-999-829A-375

Query Match 100.0%; Score 816; DB 12; Length 816;

Best Local Similarity 100.0%; Pctd. No. 0;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MUNSVMMLTALAKETLIDSOQYPPVNTNNGKIRGLRTPJNEILGVEOYLGPYA 60  
 DB 1 MUNSVMMLTALAKETLIDSOQYPPVNTNNGKIRGLRTPJNEILGVEOYLGPYA 60  
 QY 61 SEPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHDLPIWFTANJDTLMTYV 120  
 DB 61 SEPTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDRSLHDLPIWFTANJDTLMTYV 120  
 QY 121 ODONEDCCYLNIVYPTEDGANTKNADITNDGCEBDIHQSKKPVVYIHGGSYME 180  
 DB 121 ODONEDCCYLNIVYPTEDGANTKNADITNDGCEBDIHQSKKPVVYIHGGSYME 180  
 QY 181 GTGNMIDGSIASGYNVITINVRGLIGLSTGDOAKNGVLLDQIALRWIEENVG 240  
 DB 181 GTGNMIDGSIASGYNVITINVRGLIGLSTGDOAKNGVLLDQIALRWIEENVG 240  
 QY 241 AFGGPKRVITIFGSGAGASCVSLLTSHYSGLEFQKAIIGGATLSSMAVNYQPAKYTRI 300  
 DB 241 AFGGPKRVITIFGSGAGASCVSLLTSHYSGLEFQKAIIGGATLSSMAVNYQPAKYTRI 300  
 QY 301 LADKVGCMMLDTDMVECLRNKYNKELIQCTITPATYHIAFGPIVDDGVPDDPQILMEQ 360  
 DB 301 LADKVGCMMLDTDMVECLRNKYNKELIQCTITPATYHIAFGPIVDDGVPDDPQILMEQ 360

361 GEFLLNDIMLVNGGEGGKFEVDGIVDNEEDGVTPNDPDESNSVSNVDMLYEGEGKOLIRST 420  
361 GEFLLNDIMLVNGGEGGKFEVDGIVDNEEDGVTPNDPDESNSVSNVDMLYEGEGKOLIRST 420  
421 IKFVYTDMDKSNPSTRKTYALTLTDHGYAPAYALDIAQYOSPTFYAFYHHQSEM 480  
421 IKFVYTDMDKSNPSTRKTYALTLTDHGYAPAYALDIAQYOSPTFYAFYHHQSEM 480  
481 KPSMADSAHGEDEVYFVGPMIGPTELESCNSKSDVNLAVMTYNTNFKTDDPPOFY 540  
481 KPSMADSAHGEDEVYFVGPMIGPTELESCNSKSDVNLAVMTYNTNFKTDDPPOFY 540  
541 PCQYKZHTKXMPFEEVANSKYNPCQLYJHIGLKPVRDHYRATKAPWELVPHLBN 630  
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661 TVVLETRKDYSTEASVTIAGASLLFLNLAFAALYKKKRRHETRRRSPGRATCND 720  
661 TVVLETRKDYSTEASVTIAGASLLFLNLAFAALYKKKRRHETRRRSPGRATCND 720  
721 IAHQNEEIKSLQMKQLEHDECESELQAHDTLCTCPEDYTLTLRSGEDIPKATPCTT 780  
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781 MIPNTLTGMQZHTFNTSGGQNSNLPFGHSTTRV 816  
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RESULT 43  
US-10-013-922A-375  
Sequence 375, Application US/10013922A  
Publication No. US20030195345A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botsstein, David  
APPLICANT: Desnoyers, Inc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Nardo, Inc  
APPLICANT: Fivazoff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottfritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paori, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids encoding the Same  
FILE REFERENCE: P2630P/C91  
CURRENT APPLICATION NUMBER: US/10/013,922A  
CURRENT FILING DATE: 2001-10-25  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250

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 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085734  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match: 100.0%; Score 816; DE 12; Length 916;  
 Best Local Similarity: 100.0%; Pct. No. 0;  
 Matches: 816; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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 1 MLNSNVLLMTALAIKFTLLDSQAQYFVWNTNKGIRGRTPLNNEICGFVEGYLGVPA 60  
 61 SPTGERFPQPEPPSSWTG:RNTTPAVNCPQHLBERSLLHMLPIWFTANDTLXTIV 120  
 61 SPTGERFPQPEPPSSWTGIRNTQPAVCPQHLBERSLLHMLPIWFTANDTLMTIV 120  
 121 QONNEDCLYNTIYPTDGNATKKNADITSNDRGEDEJHDONSKKPVWVIHGGSYME 180  
 121 QONNEDCLYNTIYPTDGNATKKNADITSNDRGEDEJHDONSKKPVWVIHGGSYME 180  
 121 GTGNMIDGSLIASYGVNIVTTINRGLIGFSTGDAKAGNYGLDDOICALZWEENVG 240  
 181 GTGNMIDGSLIASYGVNIVTTINRGLIGFSTGDAKAGNYGLDDOICALZWEENVG 240  
 181 GTGNMIDGSLIASYGVNIVTTINRGLIGFSTGDAKAGNYGLDDOICALZWEENVG 240  
 241 AFGGDPKRVTFSGSAGASCVSLLTSHYSEGLFOKAIIOGSLSSMAVNYGPAYTR: 300  
 241 AFGGDPKRVTFSGSAGASCVSLLTSHYSEGLFOKAIIOGSLSSMAVNYGPAYTR: 300  
 301 LADRVGCMULTDTTMEVCELRKNKYKELIQOTITPATYHIAFGVIDDGVIPDDQ:IMEO 360  
 301 LADRVGCMULTDTTMEVCELRKNKYKELIQOTITPATYHIAFGVIDDGVIPDDQ:IMEO 360  
 301 LADRVGCMULTDTTMEVCELRKNKYKELIQOTITPATYHIAFGVIDDGVIPDDQ:IMEO 360  
 361 GEFINYCMGVNCGEGKRFYDGVVDNEDGVTTPDDPFSVSNFVDNLGYRBEKDTLRET 420  
 361 GEFINYCMGVNCGEGKRFYDGVVDNEDGVTTPDDPFSVSNFVDNLGYRBEKDTLRET 420  
 421 IKFMYTMDADKENPETRRKTVALFTHOMVAPVADLHQAQGSPTYFAFHHCOSEM 480  
 421 IKFMYTMDADKENPETRRKTVALFTHOMVAPVADLHQAQGSPTYFAFHHCOSEM 480  
 481 KPSWADSAHGDEVYVYVGIPIWGTLEFSCNFSKNVYLSAVNMTYTNNAKGDPPQV 540  
 481 KPSWADSAHGDEVYVYVGIPIWGTLEFSCNFSKNVYLSAVNMTYTNNAKGDPPQV 540  
 540 KPSWADSAHGDEVYVYVGIPIWGTLEFSCNFSKNVYLSAVNMTYTNNAKGDPPQV 540  
 541 FODKFKITKPNREFEVYVYVGIPIWGTLEFSCNFSKNVYLSAVNMTYTNNAKGDPPQV 600  
 541 FODKFKITKPNREFEVYVYVGIPIWGTLEFSCNFSKNVYLSAVNMTYTNNAKGDPPQV 600  
 600 FODKFKITKPNREFEVYVYVGIPIWGTLEFSCNFSKNVYLSAVNMTYTNNAKGDPPQV 600  
 601 NEFOYVSTTKVPPPMSTSFYVTRSPAKIWTTPRAIITPANNPKSKDPKTKGPEO 660  
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 661 TTVLETKRDYSTSLSTIAVGAALLNLIAFAALYKCKRKHETRRSPORNTND 720  
 720 TTVLETKRDYSTSLSTIAVGAALLNLIAFAALYKCKRKHETRRSPORNTND 720  
 721 IAHIONEIMSLQKOLEHDEHCESLQADHTDLRLTCCPDYTLIRASPD:PLATPNTIT 780  
 721 IAHIONEIMSLQKOLEHDEHCESLQADHTDLRLTCCPDYTLIRASPD:PLATPNTIT 780  
 780 IAHIONEIMSLQKOLEHDEHCESLQADHTDLRLTCCPDYTLIRASPD:PLATPNTIT 780

Qy 781 MIPNLTGMOPLHTFNTFSGGQNSTNLPHGSHSTRV 816  
Db 781 MIPNLTGMOPLHTFNTFSGGQNSTNLPHGSHSTRV 816

## RESULT 44

US-10-017-086A-375  
Sequence 375, Application US//0017086A  
Publication No. US2003019474A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Boctstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David J.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT APPLICATION NUMBER: US//10/017,086A  
CURRENT FILING DATE: 2002-04-30  
Prior Application removed - See File Wrapper or Paim  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 375  
LENGTH: 816  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-017-086A-375

Query Match : 100.0%; Score 816; DB 12; Length 816;  
Best Local Similarity : 100.0%; Pred. No. C; Idels C; Gaps 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MINSNVJLMTALAIKFTLIDSOAQYVNTNGKRGSLRPLNELLGFEVGYLGPPYA 60  
Db 1 MINSNVJLMTALAIKFTLIDSOAQYVNTNGKRGSLRPLNELLGFEVGYLGPPYA 60  
Qy 61 SPTGERRFQPPPEPSSWTGSRNTGFAAVPOHLEERSJLHMJFNFANLDTMTTY 120  
Db 61 SPTGERRFQPPPEPSSWTGSRNTGFAAVPOHLEERSJLHMJFNFANLDTMTTY 120  
Qy 121 QDQNDCLYLNIYVPTGZANTKQADITNSDEGEDECHDQSKKPMVNYHGGSYME 183  
Db 121 QDQNDCLYLNIYVPTGZANTKQADITNSDEGEDECHDQSKKPMVNYHGGSYME 183  
Qy 181 GTGNMIDGSIASGVNYVITINRGLGLSTGDOAAKGVGLDQIOALRWIEENVG 243  
Db 181 GTGNMIDGSIASGVNYVITINRGLGLSTGDOAAKGVGLDQIOALRWIEENVG 243  
Qy 241 AFGGDPKRVTFEGGAGAGCVSLTLTSHYSGLFQKALIQSGTSLSSKAVNYOPAKYTRI 300  
Db 241 AFGGDPKRVTFEGGAGAGCVSLTLTSHYSGLFQKALIQSGTSLSSKAVNYOPAKYTRI 300

Qy 301 LADKGCNMLDITDNTVECLSNKXYKELIQCTTATYHAFGPYIDGDVLPDDQILMEQ 360  
Db 301 LADKGCNMLDITDNTVECLSNKXYKELIQCTTATYHAFGPYIDGDVLPDDQILMEQ 360  
Qy 361 GEFNLVYDMLGVNGGEGKFDVGSVNDSDGYTPNDPDSVSNFVDNLYGPEGKOTLRET 420  
Db 361 GEFNLVYDMLGVNGGEGKFDVGSVNDSDGYTPNDPDSVSNFVDNLYGPEGKOTLRET 420  
Qy 421 IKFMYTDADKENPETRRKTLVALFTDHWVAPPAADLHAQYSSPTFYAFYHHCQSEY 480  
Db 421 IKFMYTDADKENPETRRKTLVALFTDHWVAPPAADLHAQYSSPTFYAFYHHCQSEY 480  
Qy 481 KPSWADSAHGEVPPVFGIPMIGPTELFSCNFSKNDVYLSAVMTYATNFPAKTGDPNPQV 540  
Db 481 KPSWADSAHGEVPPVFGIPMIGPTELFSCNFSKNDVYLSAVMTYATNFPAKTGDPNPQV 540  
Qy 541 PODTKEITKRRRFEVWMSKYNKQDLYLHGLKPRVRDYSATKVAFMLVPHLNL 600  
Db 541 PODTKEITKRRRFEVWMSKYNKQDLYLHGLKPRVRDYSATKVAFMLVPHLNL 600  
Qy 601 NEIFQVSTTKVPDPDTSFPGTRSPAKMPTTRPATTPANNPKHSCDPRKTGPD 660  
Db 601 NEIFQVSTTKVPDPDTSFPGTRSPAKMPTTRPATTPANNPKHSCDPRKTGPD 660  
Qy 661 TTULIETKRDYSTELSTIANGASLFLNLAFAALYKKDKRHEHTRRSPGRNTTND 720  
Db 661 TTULIETKRDYSTELSTIANGASLFLNLAFAALYKKDKRHEHTRRSPGRNTTND 720  
Qy 721 IAHIONEIMSLQMKOLEHDECESSLOAHOTLRLTCPPDYLTLRRSPDOLPLWTNNTT 780  
Db 721 IAHIONEIMSLQMKOLEHDECESSLOAHOTLRLTCPPDYLTLRRSPDOLPLWTNNTT 780  
Qy 781 MIPNLTGMOPLHTFNTFSGGQNSTNLPHGSHSTRV 816  
Db 781 MIPNLTGMOPLHTFNTFSGGQNSTNLPHGSHSTRV 816

## RESULT 45

US-10-145-097A-375  
Sequence 375, Application US//10145097A  
Publication No. US20030194410A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Boctstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David J.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C47



CURRENT APPLICATION NUMBER: US/10/145,387A  
CURRENT FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 09/918885  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066254  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-21  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-21  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-21  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See file wrapper or PAJ.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 375  
LENGTH: 816  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-145-087A-375  
Query Match 100.0%; Score 816; EB 12; Length 816;  
Best Local Similarity 100.0%; Pred. KC. 3;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MINSNVLMKLTALAKETLLDSQACYPVNTNKGKRGATPLPNEILSPVECYLGPYA 60  
DB 1 MINSNVLMKLTALAKETLLDSQACYPVNTNKGKRGATPLPNEILSPVECYLGPYA 60  
QY 61 SPPTGERRFPQPPPPSSWTGIRNTTQPAACPGHIDERSLJHMLTMTFALDITMTTV 120  
DB 61 SPPTGERRFPQPPPPSSWTGIRNTTQPAACPGHIDERSLJHMLTMTFALDITMTTV 120  
QY 121 ODQNECCYLNIVPTDGGANTKNADITSNDRGEDEHDONSKKPPVYVHGGSYME 180  
DB 121 ODQNECCYLNIVPTDGGANTKNADITSNDRGEDEHDONSKKPPVYVHGGSYME 180  
QY 181 GTGMNIDGSLIAGYGVITINRILGILGISTGQAKNGYGLDQIALAMPEVNG 240  
DB 181 GTGMNIDGSLIAGYGVITINRILGILGISTGQAKNGYGLDQIALAMPEVNG 240  
QY 241 AFGSDPKRVTIFSGGACASVSLTSHVSESHFOKAIIOSTALSSAMVNOQAKVTEI 300  
DB 241 AFGSDPKRVTIFSGGACASVSLTSHVSESHFOKAIIOSTALSSAMVNOQAKVTEI 300  
QY 301 LADRVGCMJLDTDMVECCJRNKNYKE--TQTTTPATYH--AFGVIDGVYIPDDPCILMEQ 360  
DB 301 LADRVGCMJLDTDMVECCJRNKNYKE--TQTTTPATYH--AFGVIDGVYIPDDPCILMEQ 360  
QY 361 GEFINVDIMLVGNGSEGLKFDGVNEDGVTPNDPSSVSNVYKULXGFEKCTLAET 420  
DB 361 GEFINVDIMLVGNGSEGLKFDGVNEDGVTPNDPSSVSNVYKULXGFEKCTLAET 420  
QY 421 IKFMYTMAKDEKNEPTRRKTLVALFTDCHQVAVAPVAAADJAAQVSPFYFAFHHGQSEN 480  
DB 421 IKFMYTMAKDEKNEPTRRKTLVALFTDCHQVAVAPVAAADJAAQVSPFYFAFHHGQSEN 480  
QY 481 KPSWADSAHGDDEVYVYFQIMIGTELFSQNFSGKDEVMLEAVVMYTWYJNPAKCGQNCQV 540  
DB 481 KPSWADSAHGDDEVYVYFQIMIGTELFSQNFSGKDEVMLEAVVMYTWYJNPAKCGQNCQV 540  
QY 541 PQTTFIHTKRNFEFEAMSKYKSCQLYHJGLKPRVDRHATATKVAWLE-VPELHL 600  
DB 541 PQTTFIHTKRNFEFEAMSKYKSCQLYHJGLKPRVDRHATATKVAWLE-VPELHL 600

QY 601 NEIFQVSTTTKVPPPMTSPFYGTRRSAPAKIWPITKRAPAITPANNPKSKDPAKTGPD 660  
DB 601 NEIFQVSTTTKVPPPMTSPFYGTRRSAPAKIWPITKRAPAITPANNPKSKDPAKTGPD 660  
QY 661 TTVLETRKDYSTELSTIIVAGASLFLNLILAFALYKKOKRHECHRRSPQORNTND 720  
DB 661 TTVLETRKDYSTELSTIIVAGASLFLNLILAFALYKKOKRHECHRRSPQORNTND 720  
QY 721 IAHQNEIEMSLQKQJHEHCESSLOQHDLTURLCPEYTLTPRSFDDIPMTPTIT 780  
DB 721 IAHQNEIEMSLQKQJHEHCESSLOQHDLTURLCPEYTLTPRSFDDIPMTPTIT 780  
QY 781 MIPNTLQXQPLHTFNTFSGQNSTLPHGHSSTRV 816  
DB 781 MIPNTLQXQPLHTFNTFSGQNSTLPHGHSSTRV 816  
RESULT 46  
US-10-164-829A-375  
Sequence 375, Application US/10164829A  
Publication No. US200301094780A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsens, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavina, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William J.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids encoding the Same  
FILE REFERENCE: P263071C28  
CURRENT APPLICATION NUMBER: US/10/164,829A  
CURRENT FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: 09/918885  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-21  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-21  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-12

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/ PRIOR APPLICATION NUMBER: 60/077791
/ PRIOR FILING DATE: 1998-03-12
/ Remaining Prior Application data removed - See File Wrapper or P.A.M.
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO: 375
/ LENGTH: 816
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-164-929A-375

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Query Match      100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MINSVLLMTALAKFTLIDSOAQYPVVNTNYGKIRSLRPLPNEILGPEVGYLGVPYA 60
DB 1 MINSVLLMTALAKFTLIDSOAQYPVVNTNYGKIRSLRPLPNEILGPEVGYLGVPYA 60
QY 61 SPTGERRFPPEPPSSWTGIRNTTQFAVCPQHLDERSLHDMPLWFTANLDTMTYV 120
DB 61 SPTGERRFPPEPPSSWTGIRNTTQFAVCPQHLDERSLHDMPLWFTANLDTMTYV 120
QY 121 QONRDCUYNIVYETEGCATKKAADITNSDGEDEBCHIDQSKRPVWYHIGSSYME 180
DB 121 QONRDCUYNIVYETEGCATKKAADITNSDGEDEBCHIDQSKRPVWYHIGSSYME 180
QY 181 GTGNMIDGSLASVGNVIVITNVALGILGFLSTGQQAANKVGLDQICARVNEENVG 240
DB 181 GTGNMIDGSLASVGNVIVITNVALGILGFLSTGQQAANKVGLDQICARVNEENVG 240
QY 241 AFQSDPKAVTIFGSAAGASCVSLTLEHYSGLQKAIJSGGTLSSMAKNOYAKRTI 300
DB 241 AFQSDPKAVTIFGSAAGASCVSLTLEHYSGLQKAIJSGGTLSSMAKNOYAKRTI 300
QY 301 LADKSGCNMLDTTEVEGCAKKNYKELIQCTTPATYVIAEGPVIDEGVIEDPQIMBQ 360
DB 301 LADKSGCNMLDTTEVEGCAKKNYKELIQCTTPATYVIAEGPVIDEGVIEDPQIMBQ 360
QY 361 GEFLLVDMGVNOCSEGLKPVGDIYDMDGVTENDPDESVSNFYDNTXGPEGMDTRET 420
DB 361 GEFLLVDMGVNOCSEGLKPVGDIYDMDGVTENDPDESVSNFYDNTXGPEGMDTRET 420
QY 421 IKFWYTMADKKNPRTBRKTLVACJTHCQWAPAVAAJHACVSPFYFAYAFYHHCSEK 480
DB 421 IKFWYTMADKKNPRTBRKTLVACJTHCQWAPAVAAJHACVSPFYFAYAFYHHCSEK 480
QY 481 KFSMAASAAGCEVYVFGIPLYGPTLFSCHFSKNDVYLSAYMTYVTPAKTGDNPQV 540
DB 481 KFSMAASAAGCEVYVFGIPLYGPTLFSCHFSKNDVYLSAYMTYVTPAKTGDNPQV 540
QY 541 POCFKFHTKNEFEVAVMSKYNPKQCYLHIGLKPVRDHYAKTAFFMLEVPSJHNL 600
DB 541 POCFKFHTKNEFEVAVMSKYNPKQCYLHIGLKPVRDHYAKTAFFMLEVPSJHNL 600
QY 601 NEIFQVSTTTKVPDPDXTSPFYGRSPAKIWPITKSPATTPANNPHSGSCPXTQPED 660
DB 601 NEIFQVSTTTKVPDPDXTSPFYGRSPAKIWPITKSPATTPANNPHSGSCPXTQPED 660
QY 661 TVVLIETKRDVSTELSVTIAGASLLFNLIAFALYKKRKHETHRRSPSCRNNTND 720
DB 661 TVVLIETKRDVSTELSVTIAGASLLFNLIAFALYKKRKHETHRRSPSCRNNTND 720
QY 721 IAHICNEEISJLQMQLBHDHCESLQAHDTLRCJCPEDYLLTLRRSPDDPLMTPRTIT 780
DB 721 IAHICNEEISJLQMQLBHDHCESLQAHDTLRCJCPEDYLLTLRRSPDDPLMTPRTIT 780
QY 781 MIENITLGMQPLATENTFSGQGNSTNLPHGSHSTRV 816
DB 781 MIENITLGMQPLATENTFSGQGNSTNLPHGSHSTRV 816

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RESULT 47  
US-10-164-929A-375

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/ Sequence 375, Application US/10164929A
/ Publication No. US20030194781A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Bolstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Ford, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geiber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Guiney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavini, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Pao, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C36
/ CURRENT FILING DATE: 2001-10-19
/ PRIOR APPLICATION NUMBER: US/10/164, 929A
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066364
/ PRIOR FILING DATE: 1997-11-21
/ PRIOR APPLICATION NUMBER: 60/077450
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 60/077632
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077641
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077649
/ PRIOR FILING DATE: 1998-03-11
/ PRIOR APPLICATION NUMBER: 60/077791
/ PRIOR FILING DATE: 1998-03-12
/ Remaining Prior Application data removed - See File Wrapper or P.A.M.
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO: 375
/ LENGTH: 816
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-164-929A-375

```

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Query Match      100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MINSVLLMTALAKFTLIDSOAQYPVVNTNYGKIRSLRPLPNEILGPEVGYLGVPYA 60
DB 1 MINSVLLMTALAKFTLIDSOAQYPVVNTNYGKIRSLRPLPNEILGPEVGYLGVPYA 60
QY 61 SPTGERRFPPEPPSSWTGIRNTTQFAVCPQHLDERSLHDMPLWFTANLDTMTYV 120

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Db 61 SPTGRRRQPPSPSSMTGIRMTQPAVCPQHLDBRS.LHDM.LIWTANILTLNTV 120  
 Qy 121 OQONEDCLYNIIVPTCEGATKKNADDTISNDGCEDEHDONSKRPVYVTHGSSVWE 180  
 Db 121 OQONEDCLYNIIVPTCEGATKKNADDTISNDGCEDEHDONSKRPVYVTHGSSVWE 180  
 Qy 181 GTGNMIDGSLASVGVYVTVINRGLIGLSTGQAKNGYLLDQIOALRWIEENQ 240  
 Db 181 GTGNMIDGSLASVGVYVTVINRGLIGLSTGQAKNGYLLDQIOALRWIEENQ 240  
 Qy 241 AFGGDPKRVTFGSGAGASCVS.LTSHVSEGLFQKALIOSGALSSMVAWQPAVTE 300  
 Db 241 AFGGDPKRVTFGSGAGASCVS.LTSHVSEGLFQKALIOSGALSSMVAWQPAVTE 300  
 Qy 301 LADKVCNMLDTCEYECJRNKVKELIQOTTFATVHAFGVIDGVYVPEFQILXEO 360  
 Db 301 LADKVCNMLDTCEYECJRNKVKELIQOTTFATVHAFGVIDGVYVPEFQILXEO 360  
 Qy 361 GEFVNYTLMGVNQGELKRVGDIIVNEDGVTEKDRFSVSNVENVLXGVPEKTLRET 420  
 Db 361 GEFVNYTLMGVNQGELKRVGDIIVNEDGVTEKDRFSVSNVENVLXGVPEKTLRET 420  
 Qy 421 IKFMYTDMADKENPECEKRTLVALFTDHCQVAPAVADJHAQVGSFTYFVAFVHQCSEK 480  
 Db 421 IKFMYTDMADKENPECEKRTLVALFTDHCQVAPAVADJHAQVGSFTYFVAFVHQCSEK 480  
 Qy 481 KPSWADSAHGDVEYVFGIMISGTELFSCNFSKQDVM.SAVMTYVNTNPAKTDGQOV 540  
 Db 481 KPSWADSAHGDVEYVFGIMISGTELFSCNFSKQDVM.SAVMTYVNTNPAKTDGQOV 540  
 Qy 541 POKTFHTKRNFEETAKSKNPKDOLY.HIGLKRVRVCHRYATCAVFEVYPLHVL 600  
 Db 541 POKTFHTKRNFEETAKSKNPKDOLY.HIGLKRVRVCHRYATCAVFEVYPLHVL 600  
 Qy 601 NEIFQVSTTTKVPVPMTSFPYGTSPAKIMPTKRPATFANNPKSKSPKTKGPE 660  
 Db 601 NEIFQVSTTTKVPVPMTSFPYGTSPAKIMPTKRPATFANNPKSKSPKTKGPE 660  
 Qy 661 TVVLETKRDYSTELSVTAVGASLFLNLPAALYKXKDRHETRRPSPQRTTND 720  
 Db 661 TVVLETKRDYSTELSVTAVGASLFLNLPAALYKXKDRHETRRPSPQRTTND 720  
 Qy 721 IAHQNEIWSLQKQEHDSCESLQAHDLRLTLPDPTLLRSPDIPMTENTT 780  
 Db 721 IAHQNEIWSLQKQEHDSCESLQAHDLRLTLPDPTLLRSPDIPMTENTT 780  
 Qy 781 MIPNTLTQMOPLEHTFNTFSGQNS.TNLPCHSTTRV 816  
 Db 781 MIPNTLTQMOPLEHTFNTFSGQNS.TNLPCHSTTRV 816

APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James.  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann.  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2630P-C3  
 CURRENT APPLICATION NUMBER: US/09/978,299A  
 PRIOR FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
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 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080194  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080327  
 PRIOR FILING DATE: 1998-04-01

RESULT 48  
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 Sequence 375, Application US/09978299A  
 Publication No. US2003019435A1  
 GENERAL INFORMATION:  
 APPLICANT: Askrenazi, Avi  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bolstein, David  
 APPLICANT: Ceenoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Geisler, Hanspeter  
 APPLICANT: Geritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kijavini, Ivar J.

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? PRIOR APPLICATION NUMBER: 60/085573
? PRIOR FILING DATE: 1998-05-15
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? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085697

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Query Match 100.0% Score 816; DB 12; Length 816;
Rest Local Similarity 100.0%; Prec. No. 0; Indels 0; Gaps 0;
Matches 816; Conservative 0; Mismatches 0;

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QY 1 MNSNVLMWLTALAKFTLIDSCAQPVVNTNYKINGSLRPLPNEIGPVEQYUGVYA 60
DB 1 MNSNVLMWLTALAKFTLIDSCAQPVVNTNYKINGSLRPLPNEIGPVEQYUGVYA 60
QY 6: SPTGERRFQPEPPSSWTGIRNTGFAVPOH:DESLJHDKPIFTNIDLMRYV 120
DB 6: SPTGERRFQPEPPSSWTGIRNTGFAVPOH:DESLJHDKPIFTNIDLMRYV 120
QY 121 QONEDCLYLN:YVTEGANTKCAADITSNDGEDEDDIHQNSKKPVVYIHGSYME 180
DB 121 QONEDCLYLN:YVTEGANTKCAADITSNDGEDEDDIHQNSKKPVVYIHGSYME 180
QY 181 GTGNVYIDGSIILASYNVIVITINVRGLIGFLSTGDAKKNYGLDQICALRWIEENVG 240
DB 181 GTGNVYIDGSIILASYNVIVITINVRGLIGFLSTGDAKKNYGLDQICALRWIEENVG 240
QY 241 AFGSDPKRYTIGSSAGASCVSLTLHSYSESLFOKALIGSTALSSAANVQPAKRYR 300
DB 241 AFGSDPKRYTIGSSAGASCVSLTLHSYSESLFOKALIGSTALSSAANVQPAKRYR 300
QY 301 LADKVGCMNLDITTMVECLRNKNYKELLQOTITPATYHAFGPVIGDVPIDDPQILMEQ 360
DB 301 LADKVGCMNLDITTMVECLRNKNYKELLQOTITPATYHAFGPVIGDVPIDDPQILMEQ 360
QY 361 GEFLYND:MLSVNGGGLKFVUGIYDNEGCVTPRPFDSVSNFVNLYGYEBSKDTLRET 420
DB 361 GEFLYND:MLSVNGGGLKFVUGIYDNEGCVTPRPFDSVSNFVNLYGYEBSKDTLRET 420
QY 421 IKFYTDMADKXENPEFRKTLVALFTDHOVNPAAADLEAQQYSGPTFYFAFYHRCOSEM 480
DB 421 IKFYTDMADKXENPEFRKTLVALFTDHOVNPAAADLEAQQYSGPTFYFAFYHRCOSEM 480
QY 481 KPSWADSAGDEVVPVFGIPMIPTLESCNFSKXDVMLSAVVMWTYNFAKTGDPNPV 540
DB 481 KPSWADSAGDEVVPVFGIPMIPTLESCNFSKXDVMLSAVVMWTYNFAKTGDPNPV 540

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Qy 541 POCXFIHFKRNFEEVAMSKNYPKXQYLIHIGLKPVRDCHVRAKNVAFMLEVPEHNL 600  
Db 541 POCXFIHFKRNFEEVAMSKNYPKXQYLIHIGLKPVRDCHVRAKNVAFMLEVPEHNL 600  
Qy 601 NEFFOVSTTKYPPDMNSFRYGTGRSPAKIMPTTKKALTPANNPKSKPKHKTGPE 660  
Db 601 NEFFOVSTTKYPPDMNSFRYGTGRSPAKIMPTTKKALTPANNPKSKPKHKTGPE 660  
Qy 661 TVLITKRDYSTELSVTLAVGASLFLFNILAFALYKCKXEPHETRRPSPORXTND 720  
Db 661 TVLITKRDYSTELSVTLAVGASLFLFNILAFALYKCKXEPHETRRPSPORXTND 720  
Qy 721 IAHQNEEINSLCKOLEHDECESLQADHTLRLTTPPYTLTTPRSPDCPLXTENTT 780  
Db 721 IAHQNEEINSLCKOLEHDECESLQADHTLRLTTPPYTLTTPRSPDCPLXTENTT 780  
Qy 781 KIPNLTGMOPHTENTFSGGKSTLYLPHGASTRY 816  
Db 781 KIPNLTGMOPHTENTFSGGKSTLYLPHGASTRY 816

RESULT 49  
US-09-978-544A-375  
Sequence 375, Application US/09978544A  
Publication No. US2003019436A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvarole, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlesen, Kary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaud, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillier, Kenneth J.  
APPLICANT: Kijavyn, Ivar C.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2530P1C3  
CURRENT APPLICATION NUMBER: US/09/978,544A  
PRIOR FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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Query Match          100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
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DB 61 SPTGERFQPEPPSSWTGIRNTQFAVCPQLDESLHMLPIMFANLTLMTYV 120
QY 121 QDQNEDECLYN-YVPTEDGANTKKNADDITSENGEDED:HDQNSKKPVVYIHGSSYE 180
DB 121 QDQNEDECLYN-YVPTEDGANTKKNADDITSENGEDED:HDQNSKKPVVYIHGSSYE 180
QY 181 GTGNMIDSLASVGNVITITINRLGILGLSLGDAKKNVGLLQIALRMIEENVG 240
DB 181 GTGNMIDSLASVGNVITITINRLGILGLSLGDAKKNVGLLQIALRMIEENVG 240
QY 241 AFGDPRKVTTFGSGAGASCYSLTLTSHSEGLFOKAIIOGSLASSMAVNYQPAKYTRI 300
DB 241 AFGDPRKVTTFGSGAGASCYSLTLTSHSEGLFOKAIIOGSLASSMAVNYQPAKYTRI 300
QY 301 LADKVCNMKLDITDMVBCGLRKNKYKELIOCTITPATYHIAFPVIDGVIPDDPQIMEQ 360
DB 301 LADKVCNMKLDITDMVBCGLRKNKYKELIOCTITPATYHIAFPVIDGVIPDDPQIMEQ 360
QY 361 GEFUNYDMLVNGEGELKEVDSIVENEDGTPNDPSPSVNFNDNLYGYREGDTRRET 420
DB 361 GEFUNYDMLVNGEGELKEVDSIVENEDGTPNDPSPSVNFNDNLYGYREGDTRRET 420
QY 421 IKFMYTMDADKENPETRRKTLVAFETDQWAFAPVADLNAQVSPITYFAFYHRCSEM 480
DB 421 IKFMYTMDADKENPETRRKTLVAFETDQWAFAPVADLNAQVSPITYFAFYHRCSEM 480
QY 481 KPSWADSASHQDEVPVFGIPM:GPTLEISCNFSKQVNLAVNVTYINFAKTGDPQCPV 540
DB 481 KPSWADSASHQDEVPVFGIPM:GPTLEISCNFSKQVNLAVNVTYINFAKTGDPQCPV 540
QY 541 PCDTFIHTKPRFEFEVMSKXNPRDQYLHIGKFRYRDHYATKVAFMLEVPHLHNL 600
DB 541 PCDTFIHTKPRFEFEVMSKXNPRDQYLHIGKFRYRDHYATKVAFMLEVPHLHNL 600
QY 601 NEIPQVSTTKVPDPVTSFPYGTRRGPAKIWTYKRPATTPANNRKHGSKDPKGTGED 660
DB 601 NEIPQVSTTKVPDPVTSFPYGTRRGPAKIWTYKRPATTPANNRKHGSKDPKGTGED 660
QY 661 TTVLETRDYSSTELSVITAVGASLFLNK:LAFAALYKKDKRRHETHRRSPORNTND 720
DB 661 TTVLETRDYSSTELSVITAVGASLFLNK:LAFAALYKKDKRRHETHRRSPORNTND 720
QY 721 IAHIONEZIMSLQKLEHDEHCESS:QAHJTLRLTCPPDYTLT:RRSDGCIPLMTPTNIT 780
DB 721 IAHIONEZIMSLQKLEHDEHCESS:QAHJTLRLTCPPDYTLT:RRSDGCIPLMTPTNIT 780
QY 781 MIPNLTGMOPLTHTNTSGGQNGSTNLPHGSHSTRV 816
DB 781 MIPNLTGMOPLTHTNTSGGQNGSTNLPHGSHSTRV 816
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RESULT 50
US-09-978-665A-375
; Sequence 375, Application US/09978665A
; Publication No. US20030199437A1
; GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnuyers, Juc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Fialaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaudi, J. Christopher  
APPLICANT: Gurney, Austin J.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuc, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Rey, Margaret Ann  
APPLICANT: Shelton, David J.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P.C19  
CURRENT APPLICATION NUMBER: US/09/975,665A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-04-29

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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
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Query Match 100.0% Score 816: DB 12: Length 816:
Best Local Similarity 100.0% Pct. No. 0:
Matches 816: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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DB 241 AFGDPRKRVILFSGAGASCVSLTLTSHYSEGLFQKALIGSGTJSSMANVYQAKYTR 300
QY 301 LADKVGCMNLDTTMEWECLELNKSKYKEIQQTTTPA-YHAFGVIDGVY-PDDPQITMEQ 360
DB 301 LADKVGCMNLDTTMEWECLELNKSKYKEIQQTTTPA-YHAFGVIDGVY-PDDPQITMEQ 360
QY 361 GEFNLNPMGVNGDEGLKFDVGDVNDQCVNTCPFSNSNVDMXGPECKTJREC 420
DB 361 GEFNLNPMGVNGDEGLKFDVGDVNDQCVNTCPFSNSNVDMXGPECKTJREC 420
QY 421 IKFWYTDWADKENBETRRKTLVA-LTDHQAFAVAADLHAQYGSPTFYAFYHHCQSEM 480
DB 421 IKFWYTDWADKENBETRRKTLVA-LTDHQAFAVAADLHAQYGSPTFYAFYHHCQSEM 480
QY 481 KPSWADSAHGDVEYVYVGIEMIGPTELFSNENKNDVMASAVMTYTWTFAKTGDNPQV 540
DB 481 KPSWADSAHGDVEYVYVGIEMIGPTELFSNENKNDVMASAVMTYTWTFAKTGDNPQV 540
QY 541 PDKTKFHTKENREFEVAVSKYNPKQQLYHIGLKPVEEDYRATKVAFWLELVPHJNL 600
DB 541 PDKTKFHTKENREFEVAVSKYNPKQQLYHIGLKPVEEDYRATKVAFWLELVPHJNL 600
QY 601 NEIFQYVSTTKVPPDPMTSFPYOTRRSPAKIPTTKRPAITPANNPKSKDPKTKGPD 660
DB 601 NEIFQYVSTTKVPPDPMTSFPYOTRRSPAKIPTTKRPAITPANNPKSKDPKTKGPD 660
QY 661 TTVLIETKRDYSTELSTIYVAGASLLPLNLAFAAYKKCKRRHETRRSPQRTTND 720
DB 661 TTVLIETKRDYSTELSTIYVAGASLLPLNLAFAAYKKCKRRHETRRSPQRTTND 720
QY 721 IAH1QNEEINSLQMKQLEHQBECESLQADTLRLTPEPTTJTLRSPDDIPLMPTNTT 780
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QY 781 MIPNTLTCXPLTFENTFGSGONSINLPHGSHSTRV 816
DB 781 MIPNTLTCXPLTFENTFGSGONSINLPHGSHSTRV 816

RESULT 51
US-09-978-802A-375
Sequence 375, Application US/09978802A
Publication No. US20030199674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desrochers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geider, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kilaian, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pat, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SPTGERRFPQPEPSSWTGIRNTOTFAVCPQHLERSLJHDMJFWTANLDTMTYV 120
QY 121 QONEDCLYINLYVTEGANTKKAADITGNDGEPEDHNDGSKRPVYTHGGSYVE 180
DB 121 QONEDCLYINLYVTEGANTKKAADITGNDGEPEDHNDGSKRPVYTHGGSYVE 180
QY 181 GTGNNDFGSLASVGNVYVITINVELGIGLSTGCAKGNVSLDQIQAUKWENTW 240
DB 181 GTGNNDFGSLASVGNVYVITINVELGIGLSTGCAKGNVSLDQIQAUKWENTW 240
QY 241 AFGGPKRVTIFGSGAGASVSLTSLHSEGLCKNIGSGTSSMAVNOYAKYTRI 300
DB 241 AFGGPKRVTIFGSGAGASVSLTSLHSEGLCKNIGSGTSSMAVNOYAKYTRI 300
QY 301 LADKVGCMMDITTCWECLRNKNYKELIQGITATATVAFGPIVDDGVJDDPQILMEQ 360
DB 301 LADKVGCMMDITTCWECLRNKNYKELIQGITATATVAFGPIVDDGVJDDPQILMEQ 360
QY 361 GEFNVYJINLVGNQOEGIKFVDGIVDNDGVTTPNDPDSVSNVDKNVGRPEKCTJRET 420
DB 361 GEFNVYJINLVGNQOEGIKFVDGIVDNDGVTTPNDPDSVSNVDKNVGRPEKCTJRET 420
QY 421 IEFVYTCMAKCKENPETRKKTUVALFTTHQVAFVAAADLNAVQSPPTFYAFVPHHCOSEM 480
DB 421 IEFVYTCMAKCKENPETRKKTUVALFTTHQVAFVAAADLNAVQSPPTFYAFVPHHCOSEM 480
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DB 481 KESVADSAHGDVVPVFGIPIYIGPTELSCHFSKIDVYLSVMTVYTNFAKGDPPQPV 540
QY 541 PODKEIHTKPRFEFVAMSKYNPDQCYLJHGLKPRPADHVRATKTAFAFWELVPHJLN 600
DB 541 PODKEIHTKPRFEFVAMSKYNPDQCYLJHGLKPRPADHVRATKTAFAFWELVPHJLN 600
QY 601 NEIFQVSTTTKVPDPKXTSPFYGIRASPAKIWTPTKPAITPANNPESKDPKTPED 660
DB 601 NEIFQVSTTTKVPDPKXTSPFYGIRASPAKIWTPTKPAITPANNPESKDPKTPED 660
QY 661 TVLIETKRDYSTEJSTIAGASLLFNLIAFALYKXCKRKHETHRRSPQRNTINC 720

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DB 661 TVLIETKRDYSTEJSTIAGASLLFNLIAFALYKXCKRKHETHRRSPQRNTINC 720
QY 721 IAHIONEIWSLONKQLEHDECESSQADHTLRLTTPPYTLTRRSPDIPLXPNIT 780
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QY 781 MIPNLTGMQPLHFTNTPFGGONSTNLPJCHSTTRV 816
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? Publication No. US20030199021A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnovers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Flivaroff, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey E.
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Guiney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kijavini, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Nadler, Mary A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? TITLE OF INVENTION: Acids Encoding the Same
? FILE REFERENCE: P2630P1076
? CURRENT APPLICATION NUMBER: US/10/013, 924A
? PRIOR FILING DATE: 2002-12-10
? PRIOR APPLICATION NUMBER: 09/518585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
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? PRIOR FILING DATE: 1998-03-12
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 624
? SEQ ID NO 375
? LENGTH: 816

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TYPE: PRT
ORGANISM: Homo sapiens
US-10-013-924A-375

Query Match      100.0%; Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MINSNVLLMTALAIFKFLIDSOAGYVNTNYSKIRGLRPLPNEILIGVEQYLGYPYA 60
QY 61 SPTGERRFPQPEPPSSKGTGIRNTQFPAVCPQHLDESLHMDLPINMTNDLTMTYV 120
DB 61 SPTGERRFPQPEPPSSKGTGIRNTQFPAVCPQHLDESLHMDLPINMTNDLTMTYV 120
QY 121 QOQNEDECLYINLYVTEDEGANTKXNADDTISNDRGEFCHIDGNSKXPMVYIGSSYME 160
DB 121 QOQNEDECLYINLYVTEDEGANTKXNADDTISNDRGEFCHIDGNSKXPMVYIGSSYME 160
QY 181 GTANVIGDSILASIGNNVYITINRGLGLGTSTGDAKAKRYLLDQIQALRYIEENVG 240
DB 181 GTANVIGDSILASIGNNVYITINRGLGLGTSTGDAKAKRYLLDQIQALRYIEENVG 240
QY 241 AFGSDPKRVTTFGSGAGACVSLTLTSHYSEGLFCKATIGSTALSSKAWYCRKXTRYI 300
DB 241 AFGSDPKRVTTFGSGAGACVSLTLTSHYSEGLFCKATIGSTALSSKAWYCRKXTRYI 300
QY 361 LADKRGKCNLDITTMVEELRNKRYEELQCTITFATYVAFQPVIGDGVIFDDPQILMEQ 360
DB 361 LADKRGKCNLDITTMVEELRNKRYEELQCTITFATYVAFQPVIGDGVIFDDPQILMEQ 360
QY 361 GEFLLNYDMLGNGQECIKFYDGTVDNEDGVTPRDFDSNSNPFQNLKGRYEGDILSEI 420
DB 361 GEFLLNYDMLGNGQECIKFYDGTVDNEDGVTPRDFDSNSNPFQNLKGRYEGDILSEI 420
QY 421 IKFMYTCMAKXENPETERKTLVAFTEHQWAPAPAAALHQQVSSPTFYFAFYHCGSEM 480
DB 421 IKFMYTCMAKXENPETERKTLVAFTEHQWAPAPAAALHQQVSSPTFYFAFYHCGSEM 480
QY 481 KPMWDSAHGDEVPVFGIPIMLGPTLEFSCNFKQDVLSAVNTWTNFAKIDGPNQPV 540
DB 481 KPMWDSAHGDEVPVFGIPIMLGPTLEFSCNFKQDVLSAVNTWTNFAKIDGPNQPV 540
QY 541 PODTKFIHKPRFEVAVMSKYNPKDQYLHIGLKPVRDHYRATKVAFWLELVPHLNL 600
DB 541 PODTKFIHKPRFEVAVMSKYNPKDQYLHIGLKPVRDHYRATKVAFWLELVPHLNL 600
QY 601 NEIFCYVSTTTKVPPEKTSPPYGRSRSPAKIMPCTTKAPATTPANNPGSKDPKGTGED 660
DB 601 NEIFCYVSTTTKVPPEKTSPPYGRSRSPAKIMPCTTKAPATTPANNPGSKDPKGTGED 660
QY 661 TTVLLETGXDVSTELSVTIANGASLLFNIIAPALAYKKKKRHEHTRRSPQNTTND 720
DB 661 TTVLLETGXDVSTELSVTIANGASLLFNIIAPALAYKKKKRHEHTRRSPQNTTND 720
QY 721 IAHIONEEIMSLQKQLEHDEHCESLCAHDTLRLLCEPDYTLTARSPDQJELMTPTTIT 780
DB 721 IAHIONEEIMSLQKQLEHDEHCESLCAHDTLRLLCEPDYTLTARSPDQJELMTPTTIT 780
QY 781 MIPNTLTGMQPLHNTNFSGGCNSITNLPHGHSITRV 816
DB 781 MIPNTLTGMQPLHNTNFSGGCNSITNLPHGHSITRV 816

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APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvarci, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Hillen, Kenneth C.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C74
CURRENT APPLICATION NUMBER: US:/0/020,445A
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/362250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27

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RESULT 53
US-10-020-445A-375
Sequence 375, Application US/10020445A
Publication No. US20030198994A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

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/ PRIOR APPLICATION NUMBER: 60/079920  
/ PRIOR FILING DATE: 1998-03-30  
/ PRIOR APPLICATION NUMBER: 60/079923  
/ PRIOR FILING DATE: 1998-03-30  
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/ PRIOR FILING DATE: 1998-05-15  
/ PRIOR APPLICATION NUMBER: 60/085704  
/ PRIOR FILING DATE: 1998-05-15  
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match: 100.0%; Score 816; DB 12; Length 816;  
Best local similarity: 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUNSVMILTAIAIIFTTIDSOAQPVVNTYKTRGIRTPLEMLGPVQYGVPA 60  
Db 1 MUNSVMILTAIAIIFTTIDSOAQPVVNTYKTRGIRTPLEMLGPVQYGVPA 60  
QY 61 SPTGRRRQPPPEPSKGTGINTTFOFAVCGHJDERSLDHMLPIWTFANLDTMTV 120  
Db 61 SPTGRRRQPPPEPSKGTGINTTFOFAVCGHJDERSLDHMLPIWTFANLDTMTV 120  
QY 121 QDQNECLYINIVPTEDGANTKCNADITSDRGEDDIDQNSKKPVVYIHGGSYWE 180  
Db 121 QDQNECLYINIVPTEDGANTKCNADITSDRGEDDIDQNSKKPVVYIHGGSYWE 180  
QY 181 GTGNMIDGSLASYGAVIYITTYRIGLIGFLSTGQAKKNGVGLDQCALPMIEENVG 240  
Db 181 GTGNMIDGSLASYGAVIYITTYRIGLIGFLSTGQAKKNGVGLDQCALPMIEENVG 240  
QY 241 AFGDPRVITIFSGAGASCVSLLTSHYSEGAFQYALIQSGTALSSMAYVQPAKYTRI 300  
Db 241 AFGDPRVITIFSGAGASCVSLLTSHYSEGAFQYALIQSGTALSSMAYVQPAKYTRI 300

301 LADKVGCMMLDTTDMVECLRNKNYKELIQCTTPATYHIAFGSVIGDVI PDDPQIMEQ 360  
301 LADKVGCMMLDTTDMVECLRNKNYKELIQCTTPATYHIAFGSVIGDVI PDDPQIMEQ 360  
361 GEFANDIMLVNNOGEGELKFDVIGDVEDGVTPNDDFSVSNVNDUUYGVPEKQILRET 420  
361 GEFANDIMLVNNOGEGELKFDVIGDVEDGVTPNDDFSVSNVNDUUYGVPEKQILRET 420  
421 IKFMYTDMADKENPETRKRKTVALFTBQWAPAPVADLHAQYGSPTFYAFYHHCQSEV 480  
421 IKFMYTDMADKENPETRKRKTVALFTBQWAPAPVADLHAQYGSPTFYAFYHHCQSEV 480  
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481 KPSWADSAHGDDEVYVFGIPIMIGPTELFSCNFSKNDVMSAVMTWKNPAKTGDNQPV 540  
541 PDDTKFHTKPNRFEVAVMSKYNPKDCLYHIGLKPRVDHRYATKVAEFLVPHLNL 600  
541 PDDTKFHTKPNRFEVAVMSKYNPKDCLYHIGLKPRVDHRYATKVAEFLVPHLNL 600  
601 NEIFQVYSTTKVPFPPDMTSFPGYGRSPAKIMPTKRPAITFANPKSKXDPKCTGRED 660  
601 NEIFQVYSTTKVPFPPDMTSFPGYGRSPAKIMPTKRPAITFANPKSKXDPKCTGRED 660  
661 TTVLIEFKRQYSTELSVTIAVGASLFLFLNLAFALYKKCKRHEHTRRSPQRTITD 720  
661 TTVLIEFKRQYSTELSVTIAVGASLFLFLNLAFALYKKCKRHEHTRRSPQRTITD 720  
721 IAHIONEIMSLQMKQJFHDEHCESLQAHDTLTCPPDYTLTLRRSPDDPLMTPNIT 780  
721 IAHIONEIMSLQMKQJFHDEHCESLQAHDTLTCPPDYTLTLRRSPDDPLMTPNIT 780  
781 MIPNTLTGMOPLHTNTFSGGONSTNLPHGSHSTRV 916  
781 MIPNTLTGMOPLHTNTFSGGONSTNLPHGSHSTRV 916

RESULT 54  
US-10-017-094A-375  
Sequence 375, Application US/10017084A  
Publication No. US20030203402A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Fliviaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertelsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Hillan, Kenneth C.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Pacini, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William J.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC66  
CURRENT APPLICATION NUMBER: US/10/017.084A

CURRENT FILING DATE: 2002-04-30  
Prior application removed - See file Wrapper or Palm  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO 375  
LENGTH: 816  
TYPE: PAT  
ORGANISM: Homo sapiens  
US-10-017-084A-375

Query Match 100.0%; Score 816; DB 12; Length 816;  
Best Local Similarity 100.0%; Pred. No. C;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MUNSVMILMTALAIKFTLIDSCAQYPPVNTYKINGLRFLFNEILGVECYLGPVYA 60  
1 MUNSVMILMTALAIKFTLIDSCAQYPPVNTYKINGLRFLFNEILGVECYLGPVYA 60  
61 SPTGERFOPPEPSSMTGIRNTQCAAVCPHLDERSJLHDMPLWFTANLDTLMTYV 120  
61 SPTGERFOPPEPSSMTGIRNTQCAAVCPHLDERSJLHDMPLWFTANLDTLMTYV 120  
121 QDQNEDECLYANIYPTEDGANTKKKADDTISNDRGEDEDHCQSKKPVWYIHGSEYME 180  
121 QDQNEDECLYANIYPTEDGANTKKKADDTISNDRGEDEDHCQSKKPVWYIHGSEYME 180  
181 GTKNVIGDSIIASVGNVITINRRLGILGFSGGDAKGNVGLDQICARMEENVG 240  
181 GTKNVIGDSIIASVGNVITINRRLGILGFSGGDAKGNVGLDQICARMEENVG 240  
241 AFGDPRKVTIFSGGAGASCUSILTSGVSGFLGCKKFGOSGTLSSANVYQPAKYTRI 300  
241 AFGDPRKVTIFSGGAGASCUSILTSGVSGFLGCKKFGOSGTLSSANVYQPAKYTRI 300  
301 LADKVGCMMLDTTDMVECLRNKNYKELIQCTTPATYHIAFGSVIGDVI PDDPQIMEQ 360  
301 LADKVGCMMLDTTDMVECLRNKNYKELIQCTTPATYHIAFGSVIGDVI PDDPQIMEQ 360  
361 GEFANDIMLVNNOGEGELKFDVIGDVEDGVTPNDDFSVSNVNDUUYGVPEKQILRET 420  
361 GEFANDIMLVNNOGEGELKFDVIGDVEDGVTPNDDFSVSNVNDUUYGVPEKQILRET 420  
421 IKFMYTDMADKENPETRKRKTVALFTBQWAPAPVADLHAQYGSPTFYAFYHHCQSEV 480  
421 IKFMYTDMADKENPETRKRKTVALFTBQWAPAPVADLHAQYGSPTFYAFYHHCQSEV 480  
481 KPSWADSAHGDDEVYVFGIPIMIGPTELFSCNFSKNDVMSAVMTWKNPAKTGDNQPV 540  
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541 PDDTKFHTKPNRFEVAVMSKYNPKDCLYHIGLKPRVDHRYATKVAEFLVPHLNL 600  
541 PDDTKFHTKPNRFEVAVMSKYNPKDCLYHIGLKPRVDHRYATKVAEFLVPHLNL 600  
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601 NEIFQVYSTTKVPFPPDMTSFPGYGRSPAKIMPTKRPAITFANPKSKXDPKCTGRED 660  
661 TTVLIEFKRQYSTELSVTIAVGASLFLFLNLAFALYKKCKRHEHTRRSPQRTITD 720  
661 TTVLIEFKRQYSTELSVTIAVGASLFLFLNLAFALYKKCKRHEHTRRSPQRTITD 720  
721 IAHIONEIMSLQMKQJFHDEHCESLQAHDTLTCPPDYTLTLRRSPDDPLMTPNIT 780  
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781 MIPNTLTGMOPLHTNTFSGGONSTNLPHGSHSTRV 916  
781 MIPNTLTGMOPLHTNTFSGGONSTNLPHGSHSTRV 916

RESULT 55  
US-10-017-085A-375  
Sequence 375, Application US/10017085A

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/ Publication No. US20030204055A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Boesstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul C.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavir, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Acids Encoding the Same
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C73
/ CURRENT APPLICATION NUMBER: US/10/017.085A
/ CURRENT FILING DATE: 2002-04-30
/ Prior Application removed - File Wrapper of Palm
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO 375
/ LENGTH: 816
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-017-085A-375

Query Match      100.0% Score 816; DB 12; Length 816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUNSVMKLTALAKFLLISQAOYFVNTKRGKIRLRLPNEIGVECYLSPIYA 60
DB 1 MUNSVMKLTALAKFLLISQAOYFVNTKRGKIRLRLPNEIGVECYLSPIYA 60

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DB 61 SPTGRRPQPEPPSSSWTGTINTQFANVCGCHDDEPSLJHDMPIWFTANLDTLTYY 123

QY 121 CQNEDECLVNTIYVTEDEANTKXNDJITSNDECEDEDHONSRRPVVYHGGSYNE 190
DB 121 CQNEDECLVNTIYVTEDEANTKXNDJITSNDECEDEDHONSRRPVVYHGGSYNE 190

QY 122 CQNEDECLVNTIYVTEDEANTKXNDJITSNDECEDEDHONSRRPVVYHGGSYNE 180
DB 122 CQNEDECLVNTIYVTEDEANTKXNDJITSNDECEDEDHONSRRPVVYHGGSYNE 180

QY 131 GTGMIDGSLASVGNVYITINRYLGLSTFCQAKKNGSLDIOIALKTEENVG 240
DB 131 GTGMIDGSLASVGNVYITINRYLGLSTFCQAKKNGSLDIOIALKTEENVG 240

QY 241 AFGGPKRYTIFGSGAGASCVSLTLSSHSEGLFCKALIGSGTALSAAVYQAKYTRI 300
DB 241 AFGGPKRYTIFGSGAGASCVSLTLSSHSEGLFCKALIGSGTALSAAVYQAKYTRI 300

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DB 361 GEFJLVNIDMLGNOCGEG-KFVQGIYDNDGVT PNDGFGSVSNFVNLKGYEGKCTLRET 420

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DB 481 KPSWADSAGSEVPYVFGIEMIGTETLFCNCFKNDVMSAVVYTYTNTAKGDPNOVP 540

QY 541 FQCTFEITKPRFEVYVMSKYNKPDOLYHIGSKPRVRYATKVAFMLVPHNLT 600
DB 541 FQCTFEITKPRFEVYVMSKYNKPDOLYHIGSKPRVRYATKVAFMLVPHNLT 600

QY 601 NEIFQVSTTKVPPDMTSPFYGRSPAKIMPTKRPAITPANKSKDHPKGTGED 660
DB 601 NEIFQVSTTKVPPDMTSPFYGRSPAKIMPTKRPAITPANKSKDHPKGTGED 660

QY 661 TTVLSTKRDYSTELSVTANGASLFLNLAFAPALYKKCKRKHETRRSPQRNTND 720
DB 661 TTVLSTKRDYSTELSVTANGASLFLNLAFAPALYKKCKRKHETRRSPQRNTND 720

QY 721 IAHIONEIMSCKMKOLEHDECESLQADTLRLTCEPDYTLTLRSPPDIPMTPTIT 780
DB 721 IAHIONEIMSCKMKOLEHDECESLQADTLRLTCEPDYTLTLRSPPDIPMTPTIT 780

QY 781 MIPNTLTOMPLHPTNTFSGGQNSTNLPHGSTRV 816
DB 781 MIPNTLTOMPLHPTNTFSGGQNSTNLPHGSTRV 816

RESULT 56
US-10-017-085A-375
/ Sequence 375, Application US/10017081A
/ Publication No. US20030049684A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Boesstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul C.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavir, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Acids Encoding the Same
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C69
/ CURRENT APPLICATION NUMBER: US/10/017.081A
/ CURRENT FILING DATE: 2002-04-30
/ Prior Application removed - See File Wrapper of Palm
/ NUMBER OF SEQ ID NOS: 624
/ SEQ ID NO 375
/ LENGTH: 816
/ TYPE: PRT
/ ORGANISM: Homo sapiens

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US-10-017-081a-375

Query Match 100.0%; Score 816; DB 15; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNSNVLMTLALAIKFTLIDSOAOYPVVNTNGKIRGLRTPLEILGPVEOYLGVYPA 63  
DB 1 MLNSNVLMTLALAIKFTLIDSOAOYPVVNTNGKIRGLRTPLEILGPVEOYLGVYPA 63  
QY 61 SPTGERRFOPEPPSSMTGIRNTTQFAAVCPQHLDRSLJHMLPIVFTANLDTLMTYV 120  
DB 61 SPTGERRFOPEPPSSMTGIRNTTQFAAVCPQHLDRSLJHMLPIVFTANLDTLMTYV 120  
QY 121 QONEDCLYLNIVYTEGANTKKADDTISNDSGEDECHDQSKKPVWVYIHGGSYME 180  
DB 121 QONEDCLYLNIVYTEGANTKKADDTISNDSGEDECHDQSKKPVWVYIHGGSYME 180  
QY 181 GTGNMIDGSIILASVGNVITINRGLGFLSTGDAQAKNGGLDQIQALRWIEENVG 240  
DB 181 GTGNMIDGSIILASVGNVITINRGLGFLSTGDAQAKNGGLDQIQALRWIEENVG 240  
QY 241 AFGSDPRPVITFSSGAGASCYSLTLTSHVSEGLFOKATLQSGTALSQWVNYFAVYTR 300  
DB 241 AFGSDPRPVITFSSGAGASCYSLTLTSHVSEGLFOKATLQSGTALSQWVNYFAVYTR 300  
QY 301 LADKVGCMCLDTTQWELERKNYKEJLQCTITPAIVHAFGPIIDCVIPDDQILMEQ 360  
DB 301 LADKVGCMCLDTTQWELERKNYKEJLQCTITPAIVHAFGPIIDCVIPDDQILMEQ 360  
QY 361 GEFLNYDINLVNGGEGIKFYDGLVNDGDTPRDPRSSNFRQNLXYGEKCTLRE 420  
DB 361 GEFLNYDINLVNGGEGIKFYDGLVNDGDTPRDPRSSNFRQNLXYGEKCTLRE 420  
QY 421 IKFYTTMADKENETBRKTLVALFTDQWAPAVAAADLRCQYSPFYFAFHHQSEY 480  
DB 421 IKFYTTMADKENETBRKTLVALFTDQWAPAVAAADLRCQYSPFYFAFHHQSEY 480  
QY 481 KPSWADSAHGDEVYVYVQIGIMIGTELFCSCFNQNDVMSLVAVMTVYTNPAKTGDPNPV 540  
DB 481 KPSWADSAHGDEVYVYVQIGIMIGTELFCSCFNQNDVMSLVAVMTVYTNPAKTGDPNPV 540  
QY 541 PODCKFIHTKXNREEVAKSKYNPKDCLYJHIGKXPRYHATKXAFPLEYVPHANL 600  
DB 541 PODCKFIHTKXNREEVAKSKYNPKDCLYJHIGKXPRYHATKXAFPLEYVPHANL 600  
QY 601 NEIFQVSTTKVPPMTSEPYGTRSPAKIMPTTTPAIPANNDKSKDPMKGTGPEP 660  
DB 601 NEIFQVSTTKVPPMTSEPYGTRSPAKIMPTTTPAIPANNDKSKDPMKGTGPEP 660  
QY 661 TTUULIETKROVSTELSTIYAGASLLFLNIIAPALYYKKDKRHEHRRPSTQPNITND 720  
DB 661 TTUULIETKROVSTELSTIYAGASLLFLNIIAPALYYKKDKRHEHRRPSTQPNITND 720  
QY 721 IAHIONEEMSLQKOLEHDECESLQAHCTLRJCCPPDZTLTLRSPDDPIPLMTENTIT 780  
DB 721 IAHIONEEMSLQKOLEHDECESLQAHCTLRJCCPPDZTLTLRSPDDPIPLMTENTIT 780  
QY 781 XIPNLTIGMCPILHTFNFTSGGQNSTNLPHGSHSTRV 816  
DB 781 XIPNLTIGMCPILHTFNFTSGGQNSTNLPHGSHSTRV 816

RESULT 57  
US-10-167-749-375  
Sequence 375, Application US/10:67749  
Publication No. US20030356137A1  
GENERAL INFORMATION:  
APPLICANT: Askenazi, Av;  
APPLICANT: Baker Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geibler, Hanspeter  
APPLICANT: Gerlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David J.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic  
ACID SEQUENCE: Acids Encoding the Same  
FILE REFERENCE: P2630P1C60  
CURRENT APPLICATION NUMBER: US/10/167,749  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-27  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077921  
PRIOR FILING DATE: 1998-03-12  
Remaining Prior Application data removed - See File Wrapper or PAJL.  
NUMBER OF SEQ ID NOS: 624  
SEQ ID NO: 375  
LENGTH: 816  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-167-749-375  
Query Match 100.0%; Score 816; DB 15; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNSNVLMTLALAIKFTLIDSOAOYPVVNTNGKIRGLRTPLEILGPVEOYLGVYPA 60  
DB 1 MLNSNVLMTLALAIKFTLIDSOAOYPVVNTNGKIRGLRTPLEILGPVEOYLGVYPA 60  
QY 61 SPTGERRFOPEPPSSMTGIRNTTQFAAVCPQHLDRSLJHMLPIVFTANLDTLMTYV 120  
DB 61 SPTGERRFOPEPPSSMTGIRNTTQFAAVCPQHLDRSLJHMLPIVFTANLDTLMTYV 120  
QY 121 QONEDCLYLNIVYTEGANTKKADDTISNDSGEDECHDQSKKPVWVYIHGGSYME 180  
DB 121 QONEDCLYLNIVYTEGANTKKADDTISNDSGEDECHDQSKKPVWVYIHGGSYME 180  
QY 181 GTGNMIDGSIILASVGNVITINRGLGFLSTGDAQAKNGGLDQIQALRWIEENVG 240  
DB 181 GTGNMIDGSIILASVGNVITINRGLGFLSTGDAQAKNGGLDQIQALRWIEENVG 240

Db 191 GTGMDISILASVNVVITINRPLGISLSTDDCAKKNVGLDQICALEKIEENVG 240  
QY 241 AFGDPRKRTIFGSGAGASCVSLTLHSRSEGLFQKAI13GTLASSWAVNYCPKATYRI 300  
Db 241 AFGDPRKRTIFGSGAGASCVSLTLHSRSEGLFQKAI13GTLASSWAVNYCPKATYRI 300  
QY 301 LADKRGCMLOTTDWECCRRNNKKEIIQCTITPATYH1AGSPVJSDCVIPRQOIMXEO 360  
Db 301 LADKRGCMLOTTDWECCRRNNKKEIIQCTITPATYH1AGSPVJSDCVIPRQOIMXEO 360  
QY 361 GEFLNVCIALGVNOCSEGLKFDVGTIDNEDCGVTPNDPFSVSNFVDCN1YGVDEGCDLRE7 420  
Db 361 GEFLNVCIALGVNOCSEGLKFDVGTIDNEDCGVTPNDPFSVSNFVDCN1YGVDEGCDLRE7 420  
QY 421 IKFYITTMADKKNPRTKRTVALFTDQWAPAVAPADLHAQVGSFTYFAVYHRCQSEY 480  
Db 421 IKFYITTMADKKNPRTKRTVALFTDQWAPAVAPADLHAQVGSFTYFAVYHRCQSEY 480  
QY 481 KPSWADSAGDEVPYVFG1PM1GPELSCNFSKNDVWLSAVMTYNTNENKTECEPQV 540  
Db 481 KPSWADSAGDEVPYVFG1PM1GPELSCNFSKNDVWLSAVMTYNTNENKTECEPQV 540  
QY 541 PCCTKFIHTKPRFEBVAMSKNPPDOQLYH1GKFRYREHYRATKYAFMLELVPRLHNL 600  
Db 541 PCCTKFIHTKPRFEBVAMSKNPPDOQLYH1GKFRYREHYRATKYAFMLELVPRLHNL 600  
QY 601 NE1FQVSTTTCVPPPECTGSPFYGRRSRPAK1WPTTGA2PAT1PANNPNSKCPKKTGED 660  
Db 601 NE1FQVSTTTCVPPPECTGSPFYGRRSRPAK1WPTTGA2PAT1PANNPNSKCPKKTGED 660  
QY 661 TTVL1ETKRDYSTE1SVT1AVGASLL1FN1LA1FALYK1K1KRRETRHRSP1QRNTND 720  
Db 661 TTVL1ETKRDYSTE1SVT1AVGASLL1FN1LA1FALYK1K1KRRETRHRSP1QRNTND 720  
QY 721 IAH1QNEE1MSLQWQ1LH1QHECESS1QAHDT1RLT1CPEDY1TL1RSPDD1PLMTPTIT 780  
Db 721 IAH1QNEE1MSLQWQ1LH1QHECESS1QAHDT1RLT1CPEDY1TL1RSPDD1PLMTPTIT 780  
QY 781 M1PNTLTGMP1HT1PNTFSGGNS1NL1RSHSTTV 840  
Db 781 M1PNTLTGMP1HT1PNTFSGGNS1NL1RSHSTTV 840

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C84  
CURRENT APPLICATION NUMBER: US/10/013,922-A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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PRIOR FILING DATE: 1998-04-08



1 PRIOR APPLICATION NUMBER: 60/081049  
2 PRIOR FILING DATE: 1998-04-08  
3 PRIOR APPLICATION NUMBER: 60/081071  
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5 PRIOR APPLICATION NUMBER: 60/081195  
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7 PRIOR APPLICATION NUMBER: 60/081203  
8 PRIOR FILING DATE: 1998-04-09  
9 PRIOR APPLICATION NUMBER: 60/081223  
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14 PRIOR FILING DATE: 1998-04-15  
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16 PRIOR FILING DATE: 1998-04-15  
17 PRIOR APPLICATION NUMBER: 60/081952  
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39 PRIOR APPLICATION NUMBER: 60/083392  
40 PRIOR FILING DATE: 1998-04-29  
41 PRIOR APPLICATION NUMBER: 60/083495  
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56 PRIOR FILING DATE: 1998-04-29  
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73 PRIOR APPLICATION NUMBER: 60/084600

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4 PRIOR APPLICATION NUMBER: 60/084643  
5 PRIOR FILING DATE: 1998-05-07  
6 PRIOR APPLICATION NUMBER: 60/085339  
7 PRIOR FILING DATE: 1998-05-13  
8 PRIOR APPLICATION NUMBER: 60/085336  
9 PRIOR FILING DATE: 1998-05-13  
10 PRIOR APPLICATION NUMBER: 60/085323  
11 PRIOR FILING DATE: 1998-05-13  
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13 PRIOR FILING DATE: 1998-05-15  
14 PRIOR APPLICATION NUMBER: 60/085703  
15 PRIOR FILING DATE: 1998-05-15  
16 PRIOR APPLICATION NUMBER: 60/085689  
17 PRIOR FILING DATE: 1998-05-15  
18 PRIOR APPLICATION NUMBER: 60/085579  
19 PRIOR FILING DATE: 1998-05-15  
20 PRIOR APPLICATION NUMBER: 60/085580  
21 PRIOR FILING DATE: 1998-05-15  
22 PRIOR APPLICATION NUMBER: 60/085573  
23 PRIOR FILING DATE: 1998-05-15  
24 PRIOR APPLICATION NUMBER: 60/085704  
25 PRIOR FILING DATE: 1998-05-15  
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Sequence 375, Application US/13013929A  
Publication No. US20030372745A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvarski, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Najler, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630P1C89  
CURRENT APPLICATION NUMBER: US/10/013,929A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
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PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 100.0%; Pred. No. 0;  
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QY 61 SPTGERRRQPEPPSSWGTGINTTQFAVCCCHLDERSLHDMJPIWTAUPLMTTV 120  
Db 61 SPTGERRRQPEPPSSWGTGINTTQFAVCCCHLDERSLHDMJPIWTAUPLMTTV 120  
QY 122 QONNEDCYLNTIYVPEZGANTKXADDTISNDRGDEIHPQNSKKPMVYIHGSSYE 180  
Db 122 QONNEDCYLNTIYVPEZGANTKXADDTISNDRGDEIHPQNSKKPMVYIHGSSYE 180  
QY 181 GTGNMIDGSIILASXGVNIVITINRGLIGFISTGQAAKNGVJLDCQALRWIEENV 240  
Db 181 GTGNMIDGSIILASXGVNIVITINRGLIGFISTGQAAKNGVJLDCQALRWIEENV 240  
QY 241 AFGGDPKRTTIFGSGAGASCUSLTTSHSSEGLFQKATCGSTALSSNAVQPAKYTI 300  
Db 241 AFGGDPKRTTIFGSGAGASCUSLTTSHSSEGLFQKATCGSTALSSNAVQPAKYTI 300  
QY 301 LADKVGCMMLDTEDVCEGRNKNYKELIQOTTPATYHAFGVIDGVIPDPQILXEQ 360  
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Db 721 IAHIONEELISLOKOLEHDHCELSQANDTLRLTCPPPYTLITRRSPDIPLMTPTIT 780  
QY 791 MIPNLTGMOPLHTEFTFSGGONSTNLPHGSHSTTV 816  
Db 791 MIPNLTGMOPLHTEFTFSGGONSTNLPHGSHSTTV 816  
RESULT 60  
US-10-016--77A-375  
Sequence 375, Application US/10016:77A  
Publication No. US2003007311A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman

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APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary F.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, G. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James I.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC90
CURRENT APPLICATION NUMBER: US/10/016,77A
PRIORITY FILING DATE: 2002-04-30
Prior application removed - See file wrapper or Pam
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 375
LENGTH: 816
TYPE: PRT
ORGANISM: Homo sapiens
US-10-016-77A-375

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Query Match 100.0% Score 816; EB 15; Length 816;  
Best Local Similarity 100.0%; Fred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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361 GEFNVDIMAGVNGEGKLPVGDIVDNEQVTPNDFESVSNFVDNIYGVPESEKDT:RET 420
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541 POCFTFHTKPRFEVAVMSKYNPRDQCYJH:GLKPRVRCFVATKVAFWLEJPH:JHL 600
541 POCFTFHTKPRFEVAVMSKYNPRDQCYJH:GLKPRVRCFVATKVAFWLEJPH:JHL 600
541 POCFTFHTKPRFEVAVMSKYNPRDQCYJH:GLKPRVRCFVATKVAFWLEJPH:JHL 600

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DB 541 POCFTFHTKPRFEVAVMSKYNPRDQCYJH:GLKPRVRCFVATKVAFWLEJPH:JHL 600
QY 601 NEIFQVSTTTKVPDPMDTSFPYGRSPATINPTTKRATITPANNPNSGSDPKTGPD 660
DB 601 NEIFQVSTTTKVPDPMDTSFPYGRSPATINPTTKRATITPANNPNSGSDPKTGPD 660
QY 661 TVLLETKRDYSTELSVIAGASL:FNILAFALYKDKRRECHTRRRSPORNTND 720
DB 661 TVLLETKRDYSTELSVIAGASL:FNILAFALYKDKRRECHTRRRSPORNTND 720
QY 721 IAHIONEIMS:QMKOLEHCECESLQAHDTLR:TCPPDYCTLRSPDD:PLMTPTIT 780
DB 721 IAHIONEIMS:QMKOLEHCECESLQAHDTLR:TCPPDYCTLRSPDD:PLMTPTIT 780
QY 781 MEPTLTGMPDHTPNTSGGQNSTN:PHGSTIRV 816
DB 781 MEPTLTGMPDHTPNTSGGQNSTN:PHGSTIRV 816

```

## RESULT 61

US-13-166-709A-375

Sequence 375, Application US/10166709A

Publication No. US20030104536A1

GENERAL INFORMATION:

```

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary F.
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, G. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James I.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC90
CURRENT APPLICATION NUMBER: US/10/166,709A
PRIORITY FILING DATE: 2001-10-13
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077642
PRIOR FILING DATE: 1998-03-11

```

[illegible]

PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 816; DB 15; Length 816;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUNSVMALMTALAIKFTLLDSOAGYPTNTNKGKSGPLPNEILSPVEQYGVFA 60  
DB 1 MUNSVMALMTALAIKFTLLDSOAGYPTNTNKGKSGPLPNEILSPVEQYGVFA 60

QY 61 SPTGERRFQPPPPSSMTGIRNCTGPAVCPQHLDBESLHDXUPLWFTANLDTNXY 120  
DB 61 SPTGERRFQPPPPSSMTGIRNCTGPAVCPQHLDBESLHDXUPLWFTANLDTNXY 120

QY 121 CQCNEDCLVNIIVFTEGANTKKAACDITSDKRGDECHQCKKRWMYTHGSGYME 180  
DB 121 CQCNEDCLVNIIVFTEGANTKKAACDITSDKRGDECHQCKKRWMYTHGSGYME 180

QY 181 GTGMMTDSGLASGVNVIITINVRBLGJSLSTSDQAKNGVJLDDIOLALWLEENVG 240  
DB 181 GTGMMTDSGLASGVNVIITINVRBLGJSLSTSDQAKNGVJLDDIOLALWLEENVG 240

QY 241 AFGGDPKAVTTFSSGAGASCVSLLTSHSSEGLFQKALIOGCTALSSMAVYQPKATRI 300  
DB 241 AFGGDPKAVTTFSSGAGASCVSLLTSHSSEGLFQKALIOGCTALSSMAVYQPKATRI 300

QY 301 LADKVGCMIDTTDMVECLRNKRYKELIOOTITPATYHAFGPVTDGVPDDEPOLVMEQ 360  
DB 301 LADKVGCMIDTTDMVECLRNKRYKELIOOTITPATYHAFGPVTDGVPDDEPOLVMEQ 360

QY 361 GEFLLNDIMLGAVNOGSLKFVDSIVNEDGVTPNDPSSVNFVNUYGYEGKDTLRET 420  
DB 361 GEFLLNDIMLGAVNOGSLKFVDSIVNEDGVTPNDPSSVNFVNUYGYEGKDTLRET 420

QY 421 IKEMYTDMADKXENPERRKTVALFTCHQWVAFAVAADLAQVGSPTFYFVYHGCQSEM 480  
DB 421 IKEMYTDMADKXENPERRKTVALFTCHQWVAFAVAADLAQVGSPTFYFVYHGCQSEM 480

QY 481 KPSWADSAHGDENVYFSGIPMTGPTLFSQNTSKNDVMSAVVMYTKNFAKGTGPNCPV 540  
DB 481 KPSWADSAHGDENVYFSGIPMTGPTLFSQNTSKNDVMSAVVMYTKNFAKGTGPNCPV 540

QY 541 POSTKFIHTKPNRFEVAVSKYKPKDCLJHGLKPRVSDHRAKVAPELTVPHLHNT 600  
DB 541 POSTKFIHTKPNRFEVAVSKYKPKDCLJHGLKPRVSDHRAKVAPELTVPHLHNT 600

QY 601 NEIFQVASTTKVPPDMTSFPGYGRSRPAKIMPTTKRPAITPANPKSKPKHTGSED 660  
DB 601 NEIFQVASTTKVPPDMTSFPGYGRSRPAKIMPTTKRPAITPANPKSKPKHTGSED 660

QY 661 TTVALTEKADYSTELSVTAVGASLLFLKILAFALYKCKGRHETRRPSPQNTND 720  
DB 661 TTVALTEKADYSTELSVTAVGASLLFLKILAFALYKCKGRHETRRPSPQNTND 720

QY 721 IAHIONEIMSLCKOLFHDCEESLQAHDTLRITCPPEYTLTRRSSPDIPLVTPNIT 780  
DB 721 IAHIONEIMSLCKOLFHDCEESLQAHDTLRITCPPEYTLTRRSSPDIPLVTPNIT 780

QY 781 KIENTLTXGRLTFETTFSGGQSTNLPHGSHSTRV 816  
DB 781 KIENTLTXGRLTFETTFSGGQSTNLPHGSHSTRV 816

RESULT 62  
US-09-875-353-2  
Sequence 2, Application US/09875353  
Patent No. US20020168713A1  
GENERAL INFORMATION:  
APPLICANT: Curtiss, Roy A. J.  
TITLE OF INVENTION: 46980, A NOVEL HUMAN NEURULIGIN FAMILY  
TITLE OF INVENTION: MEYER AND USSES THEREOF

FILE REFERENCE: 10448-058901  
CURRENT APPLICATION NUMBER: US/09/875,353  
CURRENT FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: US 60/209,949  
PRIOR FILING DATE: 2000-06-06  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 816  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-875-353-2

Query Match 40.0%; Score 326; DB 13; Length 816;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 546; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 163 QNSKRPWYTHGSSYESTGTMIDGSLASGVNVIITINVRGSLGFLSTGQAKNG 222  
DB 162 QNSKRPWYTHGSSYESTGTMIDGSLASGVNVIITINVRGSLGFLSTGQAKNG 221

QY 223 YGLDQIQALRMEENVGAFGDPKAVTTFSSGAGASCVSLLTSHSSEGLFQKALIOG 282  
DB 222 YGLDQIQALRMEENVGAFGDPKAVTTFSSGAGASCVSLLTSHSSEGLFQKALIOG 281

QY 283 TALSSMAVYQPAKATRIILADKVGCMIDTTDMVECLRNKRYKELIOOTITPATYHAFG 342  
DB 282 TALSSMAVYQPAKATRIILADKVGCMIDTTDMVECLRNKRYKELIOOTITPATYHAFG 341

QY 343 PVIDGVPDDEPOLVMEQGEFLNDIMLGAVNOGSLKFVDSIVNEDGVTPNDPSSVNF 402  
DB 342 PVIDGVPDDEPOLVMEQGEFLNDIMLGAVNOGSLKFVDSIVNEDGVTPNDPSSVNF 401

QY 403 FVDNLYGYEGKDTLRETIKEMYTDMADKXENPERRKTVALFTCHQWVAFAVAADLA 461  
DB 402 FVDNLYGYEGKDTLRETIKEMYTDMADKXENPERRKTVALFTCHQWVAFAVAADLA 460

QY 462 CYGSPFYFAFYHHCQSEKKSMAHGDENVYFSGIPMTGPTLFSQNTSKNDVMSA 521  
DB 462 CYGSPFYFAFYHHCQSEKKSMAHGDENVYFSGIPMTGPTLFSQNTSKNDVMSA 520

QY 522 VMTYWTNFAKTGDPNOVPDPTKFIHTKPNRFEVAVSKYKPKDCLJHGLKPRVSDH 581  
DB 522 VMTYWTNFAKTGDPNOVPDPTKFIHTKPNRFEVAVSKYKPKDCLJHGLKPRVSDH 580

QY 582 YAKTVAPELTVPHLHNTLNEIFQVASTTKVPPDMTSFPGYGRSRPAKIMPTTKRPAI 641  
DB 582 YAKTVAPELTVPHLHNTLNEIFQVASTTKVPPDMTSFPGYGRSRPAKIMPTTKRPAI 640

QY 642 TPANPKSKDPKHTGSEDITVLIETKDYSTELSVTAVGASLLFLNIIAFALYKCKD 701  
DB 642 TPANPKSKDPKHTGSEDITVLIETKDYSTELSVTAVGASLLFLNIIAFALYKCKD 700

QY 702 KRRHETRR 709  
DB 702 KRRHETRR 709

RESULT 63  
US-09-934-323-6  
Sequence 6, Application US/09934323  
Patent No. US20020150910A1  
GENERAL INFORMATION:  
APPLICANT: Curtiss, Roy A. J.  
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYL ESTERASE  
FILE REFERENCE: 10448-081001  
CURRENT APPLICATION NUMBER: US/09/934,323  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 60/226,774  
PRIOR FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 6  
LENGTH: 550  
TYPE: PR1  
ORGANISM: Homo sapiens  
US-09-934-323-6

Query Match  
Best Local Similarity 100.0%; Score 48; DB 10; Length 550;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 557  
DB 236 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 283

RESULT 64  
US-10-274-694-12

Sequence 12, Application US/12274694  
Publication No. US20030143565A1

GENERAL INFORMATION:  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: BRUNS, Christopher M.  
APPLICANT: DAS, Deepapriya  
APPLICANT: CING, Li  
APPLICANT: ELIOTT, Vicki S.  
APPLICANT: GANDHI, Ameena R.  
APPLICANT: HAFALIA, April J.A.  
APPLICANT: KEARNEY, Liam  
APPLICANT: KHAN, Farrah A.  
APPLICANT: LAU, Preeti G.  
APPLICANT: LEE, Ernestine A.  
APPLICANT: LU, Dying Aina M.  
APPLICANT: MC, Yan  
APPLICANT: NGUYEN, Dannie B.  
APPLICANT: PATTERSON, Chandra S.  
APPLICANT: RAYKCAR, Jayalaxmi  
APPLICANT: RING, Heijun Z.  
APPLICANT: SAMUNNALA, Madhusudan M.  
APPLICANT: TANG, Y. Tom  
APPLICANT: THANGAVELU, Kavitha  
APPLICANT: THORNTON, Michael B.  
APPLICANT: TRIBOULEY, Catherine M.  
APPLICANT: WALIA, Narinder K.  
APPLICANT: XU, Yuming  
APPLICANT: YANG, Junming  
APPLICANT: YAO, Monique G.  
APPLICANT: YUE, Henry  
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES  
FILE REFERENCE: PI-0151 USA  
CURRENT APPLICATION NUMBER: US/10/274,694  
CURRENT FILING DATE: 2002-10-18  
PRIOR APPLICATION NUMBER: 60/221,837  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/220,037  
PRIOR FILING DATE: 2000-07-21  
PRIOR APPLICATION NUMBER: 60/218,946  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US01/21324  
PRIOR FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: 60/216,804  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PERL Program  
SEQ ID NO 12  
LENGTH: 801  
TYPE: PR1  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Ircycle ID No. US20030143589A1 743875CD1  
US-10-274-694-12

Query Match 5.9%; Score 45; DB 12; Length 801;

Best Local Similarity 100.0%; Pred. No. 5e-40;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 557  
DB 521 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 568

RESULT 65  
US-09-934-323-2

Sequence 2, Application US/09934323  
Patent No. US20020150910A1

GENERAL INFORMATION:  
APPLICANT: CURTIS, Roy A. C.  
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYESTERASE  
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
FILE REFERENCE: 10448-081001  
CURRENT APPLICATION NUMBER: US/09/934,323  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 60/226,774  
PRIOR FILING DATE: 2000-06-21  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 835  
TYPE: PR1  
ORGANISM: Homo sapiens  
US-09-934-323-2

Query Match 5.9%; Score 48; DB 10; Length 835;  
Best Local Similarity 100.0%; Pred. No. 5.2e-40;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 557  
DB 521 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 568

RESULT 66  
US-09-934-323-5

Sequence 5, Application US/09934323  
Patent No. US20020150910A1  
GENERAL INFORMATION:  
APPLICANT: CURTIS, Roy A. C.  
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYESTERASE  
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
FILE REFERENCE: 10448-081001  
CURRENT APPLICATION NUMBER: US/09/934,323  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 60/226,774  
PRIOR FILING DATE: 2000-06-21  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 836  
TYPE: PR1  
ORGANISM: Rattus norvegicus  
US-09-934-323-5

Query Match 5.9%; Score 48; DB 10; Length 836;  
Best Local Similarity 100.0%; Pred. No. 5.2e-40;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 557  
DB 521 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 568

RESULT 67  
US-09-964-761-46697

Sequence 46697, Application US/09964761  
Patent No. US20020048763A1  
GENERAL INFORMATION:

Query Match 5.9%; Score 48; DB 10; Length 836;  
Best Local Similarity 100.0%; Pred. No. 5.2e-40;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 557  
DB 521 CNFSKNDVMSAVVMYTNFPAKTGDPNQPVDTKFHTKRNREEV 568

RESULT 67  
US-09-964-761-46697

Sequence 46697, Application US/09964761  
Patent No. US20020048763A1  
GENERAL INFORMATION:





CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-23  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annotax Sequence Listing Engine vers. 1.1  
SEQ ID NO 34276  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC239319.2  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.6  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.61  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.7  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55  
OTHER INFORMATION: SWISSPROT HIT: P14943, EVALUATE 3.00e-14  
US-10-029-386-30476

Query Match 2.9% Score 24; DB 12; Length 61;  
Best Local Similarity 100.0%; Pred. No. 2e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 211 FLSTGDCQAKGNVGLDQICLRW 214  
|||||  
DB 1 FLSTGDCQAKGNVGLDQICLRW 24

RESULT 71  
US-09-925-297-718  
Sequence 718, Application US/0925297  
Patent No. US20020081559A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA105  
CURRENT APPLICATION NUMBER: US/09/925,297  
CURRENT FILING DATE: 2001-08-10  
PRIORITY APPLICATION NUMBER: PCT/US00/05989  
PRIORITY FILING DATE: 2000-03-08  
PRIORITY APPLICATION NUMBER: 60/124,270  
PRIORITY FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 928  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 718  
LENGTH: 359  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-297-718

Query Match 1.5% Score 12; DB 9; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 WYTNFAKTGDPN 537  
|||||  
DB 192 WYTNFAKTGDPN 203

RESULT 72  
US-09-418-176-4  
Sequence 4, Application US/09418176  
Publication No. US20030040040A1  
GENERAL INFORMATION:  
APPLICANT: Das, Goutam  
TITLE OF INVENTION: DNA Molecules for Expression of  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States

ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/418,176  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/624,398  
FILING DATE: 04-APR-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/SE96/00318  
FILING DATE: 12-MAR-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: SE 950,939-4  
FILING DATE: 24-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Thelma A. Chen Cleland  
REGISTRATION NUMBER: 40,948  
REFERENCE/DOCKET NUMBER: 1103326-0206  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8200  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 568 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary gland  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..568  
OTHER INFORMATION: /label= Variant\_C  
PUBLICATION INFORMATION:  
AUTHORS: Hansson, Lennart  
AUTHORS: Blackberg, Lars  
AUTHORS: Edvard, Michael  
AUTHORS: Sundberg, Lennart  
AUTHORS: Stromqvist, Mats  
AUTHORS: Hernell, Oile  
TITLE: Recombinant Human Milk Bile Salt-stimulated  
TITLE: Lipase  
JOURNAL: J. Biol. Chem.  
VOLUME: 268  
ISSUE: 35  
PAGES: 26692-26698  
DATE: Dec. 15-1993  
US-09-418-176-4

Query Match 1.5% Score 12; DB 11; Length 568;  
Best Local Similarity 100.0%; Pred. No. 0.0034;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 WYTNFAKTGDPN 537  
|||||  
DB 467 WYTNFAKTGDPN 478

RESULT 73  
US-10-156-932-7  
Sequence 7, Application US/10156932  
Publication No. US20030069181A1  
GENERAL INFORMATION:  
APPLICANT: Wong, Albert J.  
TITLE OF INVENTION: Alternative Splice Forms of Proteins as

TITLE OF INVENTION: Basis for Multiple Therapeutic Modalities  
FILE REFERENCE: 8321-8-  
CURRENT APPLICATION NUMBER: US/10/156,932  
CURRENT FILING DATE: 2002-05-28  
PRIOR APPLICATION NUMBER: US 60/293,792  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 82  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 7  
LENGTH: 612  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-156-932-7

Query Match: 1.5%; Score 12; DB 15; Length 612;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 526 YWTFNFAKTGDPN 537  
Db 467 YWTFNFAKTGDPN 478

RESULT 74  
US-09-418-176-3  
Sequence 3, Application US/09/18276  
Publication No. US20030040040A1  
GENERAL INFORMATION:  
APPLICANT: Das, Gouram  
TITLE OF INVENTION: DNA Molecules for Expression of  
TITLE OF INVENTION: Polypeptides  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/418,176  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/624,398  
FILING DATE: 04-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/SE96/00318  
FILING DATE: 12-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9501939-4  
FILING DATE: 24-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Thelma A. Chen Cleland  
REGISTRATION NUMBER: 40,948  
REFERENCE/DOCKET NUMBER: 1103326-0206  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8200  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 722 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:

ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary gland  
US-09-418-176-3

Query Match: 1.5%; Score 12; DB 15; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.0043;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 526 YWTFNFAKTGDPN 537  
Db 467 YWTFNFAKTGDPN 478

RESULT 75  
US-09-418-176-2  
Sequence 2, Application US/09/18176  
Publication No. US20030040040A1  
GENERAL INFORMATION:  
APPLICANT: Das, Gouram  
TITLE OF INVENTION: DNA Molecules for Expression of  
TITLE OF INVENTION: Polypeptides  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/418,176  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/624,398  
FILING DATE: 04-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/SE96/00318  
FILING DATE: 12-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9501939-4  
FILING DATE: 24-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Thelma A. Chen Cleland  
REGISTRATION NUMBER: 40,948  
REFERENCE/DOCKET NUMBER: 1103326-0206  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 819-8200  
TELEFAX: (212) 354-8113  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-418-176-2

Query Match: 1.5%; Score 12; DB 15; Length 745;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 526 YWTFNFAKTGDPN 537  
Db 490 YWTFNFAKTGDPN 501

Search completed: November 5, 2003, 15:31:28  
Job time: 46 secs



GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: November 5, 2003, 15:19:18 ; Search time 41 Seconds

(without alignments)  
5135,876 Million cell updates/sec

Title: US-09-978-423a-375

Perfect score: 816

Sequence: 1 XUNSVUJLMTALAIKFTLI.....TPGGQNSTNLPHGSTRV 816

Scoring table: OLIGO  
Gapex 60.0 , Gapext 60.0

Searched: 830525 segs, 259352604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post-Processing: Listing first 100 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_mycete:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	65.9	816	Q9N0M4	Q9N0M4 homo sapien
2	538	65.9	817	Q9ULG0	Q9ULG0 homo sapien
3	326	40.0	816	Q8NFZ3	Q8NFZ3 homo sapien
4	319	39.1	648	Q9Y2F8	Q9Y2F8 homo sapien
5	213	26.1	213	Q8NMG7	Q8NMG7 macaca mula
6	30	6.1	509	Q8N207	Q8N207 homo sapien
7	30	6.1	823	Q9UP12	Q9UP12 homo sapien
8	50	6.1	823	Q62765	Q62765 xatrus norv
9	48	5.9	134	Q8N5B6	Q8N5B6 homo sapien
10	48	5.9	553	Q9P211	Q9P211 homo sapien
11	48	5.9	835	Q8N284	Q8N284 homo sapien
12	48	5.9	836	Q62888	Q62888 xatrus norv
13	35	4.3	558	Q9N296	Q9N296 homo sapien
14	35	4.3	682	Q9P248	Q9P248 homo sapien
15	35	4.3	828	Q9N294	Q9N294 homo sapien
16	35	4.3	848	Q9N295	Q9N295 homo sapien

17	32	3.9	144	Q924X0	Q924X0 mus musculus
18	32	3.9	825	Q83YMS	Q83YMS mus musculus
19	32	3.9	828	Q9N297	Q9N297 homo sapien
20	32	3.9	848	Q62889	Q62889 xatrus norv
21	28	3.4	202	Q8NMG2	Q8NMG2 macaca mula
22	28	3.4	335	Q8NCD0	Q8NCD0 homo sapien
23	28	3.4	383	Q8BXR4	Q8BXR4 mus musculus
24	18	2.2	245	Q99K10	Q99K10 mus musculus
25	12	1.5	612	Q75612	Q75612 homo sapien
26	12	1.5	742	Q16398	Q16398 homo sapien
27	12	1.5	745	Q9UP41	Q9UP41 homo sapien
28	12	1.5	998	Q9N1D1	Q9N1D1 gorilla gor
29	11	1.3	110	Q8MXX4	Q8MXX4 plurella xy
30	11	1.3	540	Q23735	Q23735 culex quin
31	11	1.3	559	Q8BV97	Q8BV97 mus musculus
32	11	1.3	559	Q8BK48	Q8BK48 mus musculus
33	11	1.3	610	Q97110	Q97110 coligo opai
34	11	1.3	656	Q9XYA9	Q9XYA9 meloidogyne
35	11	1.3	656	Q96529	Q96529 meloidogyne
36	11	1.3	1248	Q9NCK5	Q9NCK5 drosophila
37	10	1.2	134	Q9GN02	Q9GN02 tribolium c
38	10	1.2	505	Q23736	Q23736 culex quin
39	10	1.2	540	Q91920	Q91920 culex tarsa
40	10	1.2	540	Q23734	Q23734 culex quin
41	10	1.2	593	Q9VDP5	Q9VDP5 drosophila
42	9	1.1	288	Q9UKY3	Q9UKY3 homo sapien
43	9	1.1	360	Q9UR11	Q9UR11 drosophila
44	9	1.1	469	Q8N8C8	Q8N8C8 homo sapien
45	9	1.1	497	Q97TP8	Q97TP8 clostridium
46	9	1.1	503	Q9UYU6	Q9UYU6 neisseria m
47	9	1.1	503	Q9UT77	Q9UT77 neisseria m
48	9	1.1	507	Q9V731	Q9V731 drosophila
49	9	1.1	525	Q96DN9	Q96DN9 homo sapien
50	9	1.1	533	Q8RLUC	Q8RLUC enterobacte
51	9	1.1	541	Q9V1C9	Q9V1C9 drosophila
52	9	1.1	541	Q24197	Q24197 drosophila
53	9	1.1	545	Q81034	Q81034 felis sive
54	9	1.1	549	Q8KRZ6	Q8KRZ6 vibrio harv
55	9	1.1	554	Q54936	Q54936 mus musculus
56	9	1.1	554	Q8K125	Q8K125 mus musculus
57	9	1.1	558	Q8K1R0	Q8K1R0 rattus norv
58	9	1.1	558	Q8Q2R3	Q8Q2R3 mus musculus
59	9	1.1	559	Q35533	Q35533 mesocricetu
60	9	1.1	560	Q8R097	Q8R097 mus musculus
61	9	1.1	561	Q91KJ0	Q91KJ0 mus musculus
62	9	1.1	561	Q91W60	Q91W60 mus musculus
63	9	1.1	562	Q76631	Q76631 rattus norv
64	9	1.1	562	Q924V9	Q924V9 rattus norv
65	9	1.1	564	Q9VLA4	Q9VLA4 drosophila
66	9	1.1	565	Q8TD29	Q8TD29 homo sapien
67	9	1.1	565	Q23010	Q23010 caenorhabdi
68	9	1.1	565	Q77540	Q77540 oryzolaus
69	9	1.1	565	Q95N05	Q95N05 canis fami
70	9	1.1	565	Q97582	Q97582 sus scrofa
71	9	1.1	565	Q8VCC2	Q8VCC2 mus musculus
72	9	1.1	565	Q924V8	Q924V8 mus musculus
73	9	1.1	565	Q55136	Q55136 mus musculus
74	9	1.1	565	Q91ZV9	Q91ZV9 mus musculus
75	9	1.1	565	Q35534	Q35534 mesocricetu
76	9	1.1	565	Q8VCT4	Q8VCT4 mus musculus
77	9	1.1	565	P70104	P70104 cavia porce
78	9	1.1	566	Q96EE8	Q96EE8 homo sapien
79	9	1.1	566	Q46421	Q46421 macaca fasc
80	9	1.1	567	Q9UK77	Q9UK77 homo sapien
81	9	1.1	567	Q9ULY1	Q9ULY1 homo sapien
82	9	1.1	574	Q9BMT7	Q9BMT7 drosophila
83	9	1.1	574	Q9V7J2	Q9V7J2 drosophila
84	9	1.1	676	Q9BMJ1	Q9BMJ1 schizaphis
85	9	1.1	676	Q8M335	Q8M335 aphid gossy
86	9	1.1	806	Q81P36	Q81P36 drosophila
87	9	1.1	956	Q9NKK0	Q9NKK0 drosophila
88	8	1.0	106	Q3VE32	Q3VE32 mus musculus
89	8	1.0	106	Q9CYM8	Q9CYM8 mus musculus

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90      8      1.0      125      16      08PBP0
91      8      1.2      147      11      09WT01
92      8      1.2      160      5      08WY33
93      8      1.0      177      5      061695
94      8      1.0      185      10      06H879
95      8      1.0      210      4      09NOC5
96      8      1.0      231      5      017964
97      8      1.0      283      5      08ST14
98      8      1.0      289      16      05RYF9
99      8      1.0      354      5      08MTF8
100     3      1.0      354      5      08MTF8

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## ALIGNMENTS

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RESULT 1
Q8N0M4 PRELIMINARY: PRT: 816 AA.
ID Q8N0M4
AC Q8N0M4;
CT 01-OCT-2002 (TRENBLUREL: 22, Created);
CT 01-OCT-2002 (TRENBLUREL: 22, Last sequence update);
DT 01-MAR-2003 (TRENBLUREL: 23, Last annotation update);
DE Neurotrophin X. (Human).
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue:Brain;
RA Strausberg R.;
RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RT 12.
RP SEQUENCE FROM N.A.
RA Jamaian S., Quach H., Pelicci X., Bourgeron T.;
RT "Evolution and expression of the human neurotrophin family, including
RT two private specific members on the X and Y chromosomes."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXY-ESTERASE/LIPASE FAMILY.
DR EMBL: BC034018; AA034018.1;
DR EMBL: AF376803; AA046112.1;
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PRINTS: PR01090; NEUROLIGIN.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolase.
SQ SEQUENCE 816 AA; 91915 MW; EA1320D630F76BD CRC64;

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Query Match: 65.9%; Score 538; DB 4; Length 816;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 658; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

QY 159 DHDQSKRPVYIHGSGYMEGTGMIDGSLASVNVVITINRYRLGLFSTGQA 218
DB 158 DHDQSKRPVYIHGSGYMEGTGMIDGSLASVNVVITINRYRLGLFSTGQA 217
QY 219 AKGNYGLDQIQALRKIEENVGAFGDPKRVTFSSGAGACVSLTISHYSEGFPQAI 278
DB 218 AKGNYGLDQIQALRKIEENVGAFGDPKRVTFSSGAGACVSLTISHYSEGFPQAI 277
QY 279 FOSGTAASSAVVQPAKYTRILADKYGCMILDTTNNVECCAPKRYKELIQCTITPATYH 338
DB 278 FOSGTAASSAVVQPAKYTRILADKYGCMILDTTNNVECCAPKRYKELIQCTITPATYH 337
QY 339 IAFGPIVDGVIPDPQILMEQGFLLNDMLSVNGGSAKFTGCVYDNEGVYTKCPGF 398
DB 338 IAFGPIVDGVIPDPQILMEQGFLLNDMLSVNGGSAKFTGCVYDNEGVYTKCPGF 397
QY 399 SYSNFVNLYGFEFGKDTLRETIKENVYTDMAKRPETPKTVALPFTHQVAPAVAA 457
DB 399 SYSNFVNLYGFEFGKDTLRETIKENVYTDMAKRPETPKTVALPFTHQVAPAVAA 457

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DB 398 SYSNFVNLYGFEFGKDTLRETIKENVYTDMAKRPETPKTVALPFTHQVAPAVAA 457
QY 458 DLHAQYSGFTFYFAFYHHCQSEMKRSMWASAGDEVYFGPMIGPTELFSCNFSRXDV 517
DB 458 DLHAQYSGFTFYFAFYHHCQSEMKRSMWASAGDEVYFGPMIGPTELFSCNFSRXDV 517
QY 518 MISAIVYVYTNPAKTGDPNPVDGTSYTHKPRFEVMAKSVNPDQULYHGLKPR 577
DB 518 MISAIVYVYTNPAKTGDPNPVDGTSYTHKPRFEVMAKSVNPDQULYHGLKPR 577
QY 578 VRDPRATVAFMLELVPALHNLNEIFQVSTTTKVPDPDTSFPFGTRSPAKMPTTK 637
DB 578 VRDPRATVAFMLELVPALHNLNEIFQVSTTTKVPDPDTSFPFGTRSPAKMPTTK 637
QY 638 RPAITPANNPKSKDPBKGPEDTVLLETGKDSYTESVITANGASLLPLNAAAPALY 697
DB 638 RPAITPANNPKSKDPBKGPEDTVLLETGKDSYTESVITANGASLLPLNAAAPALY 697
QY 698 YKDKRHHHTHRPSPORTTNDIAHIONEELMSQKQLEHDECELOAHDTLRITCP 757
DB 698 YKDKRHHHTHRPSPORTTNDIAHIONEELMSQKQLEHDECELOAHDTLRITCP 757
QY 758 PLYTLTRSPDDIPMTPTNTTMTPTLTGQNPULHTPNTFGSQGNSNLPKHSSTRV 816
DB 758 PLYTLTRSPDDIPMTPTNTTMTPTLTGQNPULHTPNTFGSQGNSNLPKHSSTRV 816

```

## RESULT 2

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ID Q9ULG0 PRELIMINARY: PRT: 817 AA.
AC Q9ULG0;
CT 01-MAY-2000 (TRENBLUREL: 13, Created);
CT 01-MAY-2000 (TRENBLUREL: 13, Last sequence update);
CT 01-OCT-2002 (TRENBLUREL: 23, Last annotation update);
DE Hypothetical protein KIAA1260 (Frogmont).
CR KIAA1260.
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue:Brain;
RA MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K., Kikuno R., Hirosewa X., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RC DNA Res. 6:337-345(1999).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: A003086; BA06574.1;
DR HSPB: P21836; XAA.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000460; Neurotrophin.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PRINTS: PR01090; NEUROLIGIN.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolase.
FT NON-TER
SQ SEQUENCE 817 AA; 92016 MW; D991AC6BAC378763 CRC64;

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Query Match: 65.9%; Score 538; DB 4; Length 817;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 658; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

QY 159 DHDQSKRPVYIHGSGYMEGTGMIDGSLASVNVVITINRYRLGLFSTGQA 218
DB 159 DHDQSKRPVYIHGSGYMEGTGMIDGSLASVNVVITINRYRLGLFSTGQA 218
QY 219 AKGNYGLDQIQALRKIEENVGAFGDPKRVTFSSGAGACVSLTISHYSEGFPQAI 278
DB 219 AKGNYGLDQIQALRKIEENVGAFGDPKRVTFSSGAGACVSLTISHYSEGFPQAI 278

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Qy	279	IOSGTAISSAANYVQAKKTCRILAAKXGGMJLDTTQWECRANKYKJELLQCTITATYH	3380
Db	279	IOSGTAISSAANYVQAKKTCRILAAKXGGMJLDTTQWECRANKYKJELLQCTITATYH	3380
Qy	279	IOSGTAISSAANYVQAKKTCRILAAKXGGMJLDTTQWECRANKYKJELLQCTITATYH	3380
Db	279	IOSGTAISSAANYVQAKKTCRILAAKXGGMJLDTTQWECRANKYKJELLQCTITATYH	3380
Qy	339	IATGPAVIDGVIPDDQQLIMEQGEFLANYDMUGVNOSEGKLFKVDGIVENGVYNDQF	3588
Db	339	IATGPAVIDGVIPDDQQLIMEQGEFLANYDMUGVNOSEGKLFKVDGIVENGVYNDQF	3588
Qy	339	IATGPAVIDGVIPDDQQLIMEQGEFLANYDMUGVNOSEGKLFKVDGIVENGVYNDQF	3588
Db	339	IATGPAVIDGVIPDDQQLIMEQGEFLANYDMUGVNOSEGKLFKVDGIVENGVYNDQF	3588
Qy	399	SVENFNDNYGVEGEQDTRETKKPYTDMAKKNPEIRREKTVLALPDHOMVAPVA-A	4577
Db	399	SVENFNDNYGVEGEQDTRETKKPYTDMAKKNPEIRREKTVLALPDHOMVAPVA-A	4577
Qy	399	SVENFNDNYGVEGEQDTRETKKPYTDMAKKNPEIRREKTVLALPDHOMVAPVA-A	4577
Db	399	SVENFNDNYGVEGEQDTRETKKPYTDMAKKNPEIRREKTVLALPDHOMVAPVA-A	4577
Qy	456	DLHAOYGSPTYEYAFYHHCQSEMKPSWADSAHGDEVYVFGPMIGPTELFSCNFSKDV	5177
Db	456	DLHAOYGSPTYEYAFYHHCQSEMKPSWADSAHGDEVYVFGPMIGPTELFSCNFSKDV	5177
Qy	456	DLHAOYGSPTYEYAFYHHCQSEMKPSWADSAHGDEVYVFGPMIGPTELFSCNFSKDV	5177
Db	456	DLHAOYGSPTYEYAFYHHCQSEMKPSWADSAHGDEVYVFGPMIGPTELFSCNFSKDV	5177
Qy	518	MLSAVVTYVNTNAAKSGDNPQPOCEKRIHKPRPFYVMSKYNPMDQYLHIGAKPR	5777
Db	518	MLSAVVTYVNTNAAKSGDNPQPOCEKRIHKPRPFYVMSKYNPMDQYLHIGAKPR	5777
Qy	518	MLSAVVTYVNTNAAKSGDNPQPOCEKRIHKPRPFYVMSKYNPMDQYLHIGAKPR	5777
Db	518	MLSAVVTYVNTNAAKSGDNPQPOCEKRIHKPRPFYVMSKYNPMDQYLHIGAKPR	5777
Qy	578	VROHYRATKVAFWLELVPULHNLNEIFQVSTTVYVSPDMTSPFYGRASDAKIMWTIK	6377
Db	578	VROHYRATKVAFWLELVPULHNLNEIFQVSTTVYVSPDMTSPFYGRASDAKIMWTIK	6377
Qy	578	VROHYRATKVAFWLELVPULHNLNEIFQVSTTVYVSPDMTSPFYGRASDAKIMWTIK	6377
Db	578	VROHYRATKVAFWLELVPULHNLNEIFQVSTTVYVSPDMTSPFYGRASDAKIMWTIK	6377
Qy	638	RPAITPANNPQSHKDHKTGSEDTTVLITRQDYSTEVSUVTIAGVASLLPLNTIAPALY	6977
Db	638	RPAITPANNPQSHKDHKTGSEDTTVLITRQDYSTEVSUVTIAGVASLLPLNTIAPALY	6977
Qy	638	RPAITPANNPQSHKDHKTGSEDTTVLITRQDYSTEVSUVTIAGVASLLPLNTIAPALY	6977
Db	638	RPAITPANNPQSHKDHKTGSEDTTVLITRQDYSTEVSUVTIAGVASLLPLNTIAPALY	6977
Qy	699	YKDKRHEHETHRSPSPORVITNCIAHIONEELKSLQWQLEHDEHESLQWQDITLITCP	7588
Db	699	YKDKRHEHETHRSPSPORVITNCIAHIONEELKSLQWQLEHDEHESLQWQDITLITCP	7588
Qy	699	YKDKRHEHETHRSPSPORVITNCIAHIONEELKSLQWQLEHDEHESLQWQDITLITCP	7588
Db	699	YKDKRHEHETHRSPSPORVITNCIAHIONEELKSLQWQLEHDEHESLQWQDITLITCP	7588
Qy	759	PQVTLTLASBDDIPLKMPRTITVYINTCYGMQOPATFNTSGGQNSNCPHGISTRV	8177
Db	759	PQVTLTLASBDDIPLKMPRTITVYINTCYGMQOPATFNTSGGQNSNCPHGISTRV	8177
Qy	759	PQVTLTLASBDDIPLKMPRTITVYINTCYGMQOPATFNTSGGQNSNCPHGISTRV	8177
Db	759	PQVTLTLASBDDIPLKMPRTITVYINTCYGMQOPATFNTSGGQNSNCPHGISTRV	8177

### RESULT 3

1D	Q8NFZ3	PFELIMINARV	ERT	816 AA
AC	Q8NFZ3			
2T	01-OCT-2002 (TreeBrel: 22, Created)			
DT	01-OCT-2002 (TreeBrel: 22, Last sequence update)			
DT	01-MAR-2003 (TreeBrel: 23, Last annotation update)			
DE	Neurolygin Y.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID:9606;			
RN	{1}			
RP	SEQUENCE FROM K.A.			
RA	Jamain S., Quach H., Fellous Y., Bourgeron T.,			
RT	"Evolution and expression of the human neurolygin family, including			
RT	two primate specific members on the X and Y chromosomes."			
RL	Submitted (May-2001) to the EMBL/Genbank/DBSJ databases."			
CC	1. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLSTEADSE/LIPASE FAMILY.			
DE	EMBL: AF376864; AAM4611.1;--			
DR	InterPro: IPR002018; Carboxesterase.			
CR	InterPro: IPR000460; Neurolygin.			
DR	InterPro: IPR000379; Ser esters _site.			
DR	Pfam: PF00135; Coesterase: 1.			
DR	PRINTS: PR01090; NEUROLYGIN.			
D3	PROSITE: PS00941; CARBOXYLSTEADSE_B_2; 1.			
KM	Hydrolase.			
SO	SEQUENCE	916 AA	92020 MW	FB68910773B1B5F6 CRC64:

Query Match	40.0%	Score 326;	DB 4;	Length 816;
Best Local Similarity	99.6%	Pred. No. 0;		
Matches 546;	Conservative	0;	Mismatches 1;	Indels 1;
			Gaps	1.

163 QNSKKPVMYIHGGSYMEGTGMIDGS-LASYGNVIVITINRGLGLGF-STGDQAKGN 222

Db	166	QNSKPRWVYIHGSGVEGTGNMIDGSLILASGVKIVIT-NYRLGILGFSTGQAKGN	221
Cy	223	YGLLDGICQLKRIEENVAFGGDPKRVITFGSGAGASCVLTLTSHSBSLPGKA-IIGG	282
Db	222	YGLLDGICQLKRIEENVAFGGDPKRVITFGSGAGASCVLTLTSHSBSLPGKA-IIGG	281
Cy	283	TALSSAAVNYQAKKTRILLADKNGCNMLTIDWYECRLNKNVYELLIOCTTPATYHIAFG	342
Db	282	TALSSAAVNYQAKKTRILLADKNGCNMLTIDWYECRLNKNVYELLIOCTTPATYHIAFG	341
Cy	343	PVLDGQVIRPDDPQIILMEGGFLANVYIMLGVNGEGGLKFVDDGIYDNEDGATPNPDFSVSN	402
Db	342	PVLDGQVIRPDDPQIILMEGGFLANVYIMLGVNGEGGLKFVDDGIYDNEDGATPNPDFSVSN	401
Cy	403	FVENDLYGEBGKDLIRETIKFMYITDMADKENPETRKXTLYALFTDHQWAPAVA-ADLHA	461
Db	402	FVNDLYGEBGKDLIRETIKFMYITDMADKENPETRKXTLYALFTDHQWAPAVAADLHA	461
Cy	462	QVGSPTTFYAFPIHHQOSEKPSMADSDANGDEVYVFGIPIMLGPTELSCNFSKSDWMLSA	521
Db	462	QVGSPTTFYAFPIHHQOSEKPSMADSDANGDEVYVFGIPIMLGPTELSNFSKSDWMLSA	521
Cy	522	VWVYTYNTFAKTGDPNQPPODTKTFHTKAPRFEVAMSKYNPCQJLYLHGLKPRVRDH	581
Db	522	VWVYTYNTFAKTGDPNQPPODTKTFHTKAPRFEVAMSKYNPCQJLYLHGLKPRVRDH	581
Cy	582	YRATKVAFLLELVPHLNLNLLEFQVYSTTTVPPDMTSPFYGRASPAKIWPTTKRPAI	641
Db	582	YRATKVAFLLELVPHLNLNLLEFQVYSTTTVPPDMTSPFYGRASPAKIWPTTKRPAI	641
Cy	642	TPANPKSHKDPHKIGPEDTVYLITKQDYSTEISVITAYGASILLFANLAFPAALYYKKD	701
Db	642	TPANPKSHKDPHKIGPEDTVYLITKQDYSTEISVITAYGASILLFANLAFPAALYYKKD	701
Cy	702	KRRHEFTR 705	
Db	702	KRRHEFTR 709	

## RESULT 4

ID	NAME	PRELIMINARY:	PRT:	648 AA.
CD	Q9Y2F8			
DT	Q9Y2F8			
DT	0: NOV-1999 (TREMBL)	12, Created		
DT	0: NOV-1999 (TREMBL)	12, Last sequence update		
DT	0: OCT-2002 (TrEMBL)	22, Last annotation update		
DE	Hypothetical protein KIA09951.			
CN	KIA09951.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	T-SSB=Brain;			
EX	MEDLINE=99246063; Pubmed=10231332;			
EA	Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,			
EA	Matsumura N., Tanaka A., Kotani H., Nomura N., Chaza O.,			
RT	"Prediction of the coding sequences of unidentified human genes. XIII.			
RT	The complete sequences of 100 new cDNA clones from brain which code			
RL	for large proteins in vitro.";			
CC	DNA Ref. 6:63-70(1999).			
CC	-1. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.			
DR	EMBL; AB023168; BAA76795.1; ..			
DR	HSSP; P2:836; IMAA.			
DR	InterPro; IPR002018; Carboxylesterab.			
DR	InterPro; IPR000460; Nucleosidgln.			
DR	InterPro; IPR00379; Ser_ester_site.			
DR	Pfam; PF00135; Coesterase; 1.			
DR	PRINTS; PRO1090; NEUROLIGIN.			
DR	Hypothetical protein; Hydrolase			
SO	SEQUENCE 648 AA; 72885 KM; 1A2E6727A709BFBC C6C64;			

Query Match	39.1%	Score 3.29	DB 4	Length 688
Best Local Similarity	99.6%	Pred No. 0		
Matches 539	Conservative	0	Mismatches 1	Indels 1
			Gaps 14	
QY	170	MYVYHGSGSYMGCTGNMIDSGSILASVGNVIVITINRGLIGLSTGDNAGKWCGLDQI	229	
Db	1	MYVYHGSGSYMGCTGNMIDSGSILASVGNVIVITINRGLIGLSTGDNAGKWCGLDQI	60	
QY	230	QALNRILENNVAGFGGDDPKRVYITFGSGAGACSVSLTSLSHYSGLFQKAIIOGRTLSKWA	289	
Db	61	QALNRILENNVAGFGGDDPKRVYITFGSGAGACSVSLTSLSHYSGLFQKAIIOGRTLSKWA	120	
QY	290	VNYQAKRYTILADKVGCSMLDITMVECSLRKYNKVELIQCTITPATYHAFGPTVGGEDV	349	
Db	121	VNYQAKRYTILADKVGCSMLDITMVECSLRKYNKVELIQCTITPATYHAFGPTVGGEDV	180	
QY	350	IPDDPQILMEZGFELNYDIMGVNGGSCLFKFDGAYVNRDGYTPNDCPDSVSNFVNDYVG	409	
Db	191	IPDDPQILMEZGFELNYDIMGVNGGSCLFKFDGAYVNRDGYTPNDCPDSVSNFVNDYVG	240	
QY	410	YPEKQDTRRITIKXWYITMDAKENRPTKRTVNAIFTHQWYAAVYAADLHAGYGSSTY	466	
Db	241	YPEKQDTRRITIKXWYITMDAKENRPTKRTVNAIFTHQWYAAVYAADLHAGYGSSTY	300	
QY	469	FYAFYHHCQSEKRSMAADSGADEVYFYFGIEMIGPTELFSQNFSAKQDVMLSAVMYTYWT	529	
Db	301	FYAFYHHCQSEKRSMAADSGADEVYFYFGIEMIGPTELFQNFSAKQDVMLSAVMYTYWT	360	
QY	529	NEATGDDNPQVPQDTKRIHTKPNRFEVYVANSKYKPKQDYLHILGKLRVZDHYATKVA	586	
Db	361	NEATGDDNPQVPQDTKRIHTKPNRFEVYVANSKYKPKQDYLHILGKLRVZDHYATKVA	420	
QY	589	FWLEJVPPLHNLNLEIFQVYVSTTKVPYPPDMCSFPGYTRSPAKIWPTRKRPATPANPK	648	
Db	421	FWLEJVPPLHNLNLEIFQVYVSTTKVPYPPDMCSFPGYTRSPAKIWPTRKRPATPANPK	480	
QY	649	HSKQDPKTGPDQTLVLETKKQYSSLEISVTAAGASLLPLNLIAFALYYKKDKRHHETH	709	
Db	481	HSKQDPKTGPDQTLVLETKKQYSSLEISVTAAGASLLPLNLIAFALYYKKDKRHHETH	540	
QY	709	R 709		
Db	541	R 541		
RESULT 5				
Q8WNG7				
Q8WNG7				
AC	PRELIMINARY:	PRT:	213 AA.	
DT	01-MAR-2002 (TREMBlere, 20, Created)			
DT	01-MAR-2002 (TREMBlere, 20, Last sequence update)			
DT	01-MAR-2002 (TREMBlere, 20, Last annotation update)			
DE	Neurologin 4 (fragment)			
CS	Nacaca mulatta (Rhesus macaque)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
NCBI	taxid:3554;			
EX	111			
RP	SEQUENCE FROM N. A.			
RC	TISSUE:Medial basar, hypothalamus;			
RA	Murgenast A.E., Ojeda S.R.;			
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF462606; AAL66382.1;			
NC	NON TER			
SC	SEQUENCE	213 AA:	24096 MW;	3AF221C035C660B C9C64;
Query Match	26.1%	Score 213	DB 6	Length 213
Best Local Similarity	100.0%	Pred. No. 1.7e-223		
Matches 213	Conservative	0	Mismatches 0	Indels 0
			Gaps 0	
QY	604	FGYVSTTKVYPPDMTSFFYGTNRSPAKIWPTRKRPATPANPKHSCQPKRTGGTGGCTTV	663	

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Db      1  FGVSSTTKPPPPDMTSPFGTRSPAKIMWTCTKBPACTPANNPKHSKOPHKGPEDCTV 60
Cy      564  LIEKAPYSFELSTIIVAGSLFLNLIAALYKKCKRHRHHRPSPQRNTNDIAH 723
Eb      61  LIEKAPYSFELSTIIVAGSLFLNLIAALYKKCKRHRHHRPSPQRNTNDIAH 120
Cy      724  IONEIWSLQCKLEHDECESSQADHTLRITCPDVTLLRRSPDDIPMTPTTTPIP 783
Db      121  IONEIWSLQCKLEHDECESSQADHTLLITCPDVTLLRRSPDDIPMTPTTTPIP 180
Cy      784  NTLGMOPLHTFNTFSGQNSYNIIPAGSCTRV 816
Db      181  NTLGMOPLHTFNTFSGQNSYNIIPAGSCTRV 213

RESULT 6
CEN207  PRELIMINARY;  PR7;  509 AA.
10  Q8N2Q7
AC  Q8N2Q7;
DT  01-OCT-2002 (TREMBLrel. 22, Created)
DT  01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  Hypothetical protein FLJ90041.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX  NCBI_Taxid=9606;
[1]
RE  SEQUENCE FROM N.A.
RC  ISSUED=EMBL;
RA  -Sogai T., Oka T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA  Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saito K.,
RA  Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA  Maechu Y., Oho T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA  Hattori A., Okumura K., Iwayanagi T., Niromiya K.,
RA  "NCBO human cDNA sequencing project.";
RL  Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC  -1: SMLARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/FAM5E FAMILY.
DR  EMBL; AK074522; BAC11039.1;
DR  InterPro: IPR002018; Carboxylesterase.
DR  Pfam: PF00135; Coesterase.1.
DR  PRINTS: PR01090; NEUROLIGIN.
KM  Hypothetical protein; Hydrolase.
SQ  SEQUENCE 509 AA; 57793 MW; 662170A29C877D03 CRC64;

Query Match 6.1%; Score 50; DB 4; Length 569;
Best Local Similarity: 100.0%; Pred. No. 4,4e-45;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      510  CNFSKNDVMASVVMYTWTFNFAKTCGDPNOYPODTTKTITHKPNFEEVAM 559
Db      212  CNFSKNDVMASVVMYTWTFNFAKTCGDPNOYPODTTKTITHKPNFEEVAM 261

RESULT 7
CEN207  PRELIMINARY;  PR7;  823 AA.
10  Q9UPT2
AC  Q9UPT2;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE  Hypothetical protein KIAA1070 (NeuroLigin 1).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX  NCBI_Taxid=9606;
[1]
RE  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RX  MEDLINE=99397452; PubMed=10470851;
RX  Kikuno R., Nagase T., Ishikawa K., Hiroseawa M., Miyajima N.,

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Rc DNA Res. 7:143-150(2000).
Cc -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
Cc EMBL: AB04069.3; BAA96004.1; -.
Dr HSSP: F21836; IMMA.
Dr InterPro: IPR002018; Carboxesterase3.
Dr InterPro: IPR000460; NeuroLigin.
Dr InterPro: IPR000379; Ser_ester_site.
Dr Pfam: PF00135; Coesterase; 1.
Dr PRINTS: PR01090; NEUROLIGIN.
Dr Hypothetical protein; HydroLase.
Ft NON TER
Ss SEQUENCE 682 AA; 75592 MW; 9E56DBF44F5DC31 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 4; Length 682;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 167 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 201
Db 34 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 68

RESULT 15
Q9NZ94 PRELIMINARY; PRT; 828 AA.
Ac Q9NZ94;
Dt 01-OCT-2000 (TREMBlrel. 15, Created)
Dt 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
Dt 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
De NeuroLigin 3 isoform.
Os Homo sapiens (Human).
Cc Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ck NCBI_TaxID=9606;
Cn 11
Rp SEQUENCE FROM N.A.
Rf MEDLINE=20231756; PubMed=10767552;
Ra Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.I.;
Rt "The structure and expression of the human neuroLigin-3 gene.";
Rl Gene 246:303-310(2000).
Cc -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
Cc EMBL: AF217413; AA071232.1; -.
Dr HSSP: P21836; IMMA.
Dr GeneW: HSKC14289; NLG3.
Dr InterPro: IPR002018; Carboxesterase3.
Dr InterPro: IPR000460; NeuroLigin.
Dr InterPro: IPR000379; Ser_ester_site.
Dr Pfam: PF00135; Coesterase; 1.
Dr PRINTS: PR01090; NEUROLIGIN.
Dr PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
Kw HydroLase.
Ss SEQUENCE 828 AA; 91570 MW; E72B4F3472678692 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 4; Length 828;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 167 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 201
Db 180 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 214

RESULT 16
Q9NZ95 PRELIMINARY; PRT; 848 AA.
Ac Q9NZ95;
Dt 01-OCT-2000 (TREMBlrel. 15, Created)
Dt 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
Dt 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
De NeuroLigin 3 isoform.
Os Homo sapiens (Human).
Cc Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ck NCBI_TaxID=9606;
Cn 11
Rp SEQUENCE FROM N.A.
Rf MEDLINE=20231756; PubMed=10767552;
Ra Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.I.;
Rt "The structure and expression of the human neuroLigin-3 gene.";
Rl Gene 246:303-310(2000).
Cc -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
Cc EMBL: AF217413; AA071233.1; -.
Dr HSSP: F21836; IMMA.
Dr InterPro: IPR002018; Carboxesterase3.
Dr InterPro: IPR000460; NeuroLigin.
Dr InterPro: IPR000379; Ser_ester_site.
Dr Pfam: PF00135; Coesterase; 1.
Dr PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
Kw HydroLase.
Ss SEQUENCE 848 AA; 93895 MW; B3EE2FAB7E427C82 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 4; Length 848;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 167 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 201
Db 200 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 234

RESULT 17
Q924X0 PRELIMINARY; PRT; 144 AA.
Ac Q924X0;
Dt 01-DEC-2001 (TREMBlrel. 19, Created)
Dt 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
Dt 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
De NeuroLigin 3 protein (Fragment).
Cn NEUROLIGIN 3.
Os Mus musculus (Mouse).
Cc Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Ck NCBI_TaxID=10090;
Cn 11
Rp SEQUENCE FROM N.A.
Rf STRAIN=129;
Ra Chateauet A.;
Rt "mouse neuroLigin 3";
Rl Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
Cc -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
Cc EMBL: AJ291730; CAC37694.1; -.
Dr InterPro: IPR002018; Carboxesterase3.
Dr Pfam: PF00135; Coesterase; 1.
Kw HydroLase.
Ft NON TER
Ss SEQUENCE 144 AA; 16348 MW; D4618324E8AA7727 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 11; Length 144;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 399 SVSNFVDNLYGYPEGKDTLRITIKFMYDMAD 430
Db 34 SVSNFVDNLYGYPEGKDTLRITIKFMYDMAD 65

RESULT 18
Q8BYM5 PRELIMINARY; PRT; 825 AA.
Ac Q8BYM5;
Dt 01-MAR-2003 (TREMBlrel. 23, Created)
Dt 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
Dt 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
De NEUROLIGIN 3 isoform HNL3 homolog.
Ck NCBI_TaxID=9606;
Cn 11
Rp SEQUENCE FROM N.A.
Rf MEDLINE=20231756; PubMed=10767552;
Ra Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.I.;
Rt "The structure and expression of the human neuroLigin-3 gene.";
Rl Gene 246:303-310(2000).
Cc -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
Cc EMBL: AF217413; AA071233.1; -.
Dr HSSP: F21836; IMMA.
Dr InterPro: IPR002018; Carboxesterase3.
Dr InterPro: IPR000460; NeuroLigin.
Dr InterPro: IPR000379; Ser_ester_site.
Dr Pfam: PF00135; Coesterase; 1.
Dr PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
Kw HydroLase.
Ss SEQUENCE 848 AA; 93895 MW; B3EE2FAB7E427C82 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 4; Length 848;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 167 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 201
Db 200 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 234
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Ck NCBI_TaxID=9606;
Cn 11
Rp SEQUENCE FROM N.A.
Rf MEDLINE=20231756; PubMed=10767552;
Ra Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.I.;
Rt "The structure and expression of the human neuroLigin-3 gene.";
Rl Gene 246:303-310(2000).
Cc -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
Cc EMBL: AF217413; AA071233.1; -.
Dr HSSP: F21836; IMMA.
Dr InterPro: IPR002018; Carboxesterase3.
Dr InterPro: IPR000460; NeuroLigin.
Dr InterPro: IPR000379; Ser_ester_site.
Dr Pfam: PF00135; Coesterase; 1.
Dr PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
Kw HydroLase.
Ss SEQUENCE 848 AA; 93895 MW; B3EE2FAB7E427C82 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 4; Length 848;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 167 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 201
Db 200 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 234

RESULT 17
Q924X0 PRELIMINARY; PRT; 144 AA.
Ac Q924X0;
Dt 01-DEC-2001 (TREMBlrel. 19, Created)
Dt 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
Dt 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
De NeuroLigin 3 protein (Fragment).
Cn NEUROLIGIN 3.
Os Mus musculus (Mouse).
Cc Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cc Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Ck NCBI_TaxID=10090;
Cn 11
Rp SEQUENCE FROM N.A.
Rf STRAIN=129;
Ra Chateauet A.;
Rt "mouse neuroLigin 3";
Rl Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
Cc -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
Cc EMBL: AJ291730; CAC37694.1; -.
Dr InterPro: IPR002018; Carboxesterase3.
Dr Pfam: PF00135; Coesterase; 1.
Kw HydroLase.
Ft NON TER
Ss SEQUENCE 144 AA; 16348 MW; D4618324E8AA7727 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 11; Length 144;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 399 SVSNFVDNLYGYPEGKDTLRITIKFMYDMAD 430
Db 34 SVSNFVDNLYGYPEGKDTLRITIKFMYDMAD 65

RESULT 18
Q8BYM5 PRELIMINARY; PRT; 825 AA.
Ac Q8BYM5;
Dt 01-MAR-2003 (TREMBlrel. 23, Created)
Dt 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
Dt 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
De NEUROLIGIN 3 isoform HNL3 homolog.
Ck NCBI_TaxID=9606;
Cn 11
Rp SEQUENCE FROM N.A.
Rf MEDLINE=20231756; PubMed=10767552;
Ra Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.I.;
Rt "The structure and expression of the human neuroLigin-3 gene.";
Rl Gene 246:303-310(2000).
Cc -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
Cc EMBL: AF217413; AA071233.1; -.
Dr HSSP: F21836; IMMA.
Dr InterPro: IPR002018; Carboxesterase3.
Dr InterPro: IPR000460; NeuroLigin.
Dr InterPro: IPR000379; Ser_ester_site.
Dr Pfam: PF00135; Coesterase; 1.
Dr PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
Kw HydroLase.
Ss SEQUENCE 848 AA; 93895 MW; B3EE2FAB7E427C82 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 4; Length 848;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 167 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 201
Db 200 KPMVYIHGGSYMEGTGMIDGSLASGYNIIVT 234
```

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;  
 RX MEDLINE=2254683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 DR EMBL: AC039018; BAC30207.1;  
 SQ SEQUENCE 525 AA; 91175 MW; 33F7F939B0A44CE CRC64;

Query Match 3.9%; Score 32; DB 1; Length 825;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-25;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 SVSNFVNDLYGPEGKDTRETIKFMYTDMAD 430  
 Db 409 SVSNFVNDLYGPEGKDTRETIKFMYTDMAD 440

RESULT 19  
 Q9NZ97 PRELIMINARY; PRT; 828 AA.

AC Q9NZ97;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE NeuroLigin 3 isoform HNL3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2031756; PubMed10767552;  
 RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Gims E.L.;  
 RT "The structure and expression of the human neuroLigin-3 gene";  
 RL Gene 246:303-310 (2000).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.  
 DR EMBL: AF217411; AAF71230.1;  
 DR HSSP: P37967; IQS3.  
 DR InterPro: IPR002018; Carboxylesterase3.  
 DR InterPro: IPR000460; NeuroLigin.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS: PR01090; NEUROLIGIN.  
 DR PROSITE: PS00941; CARBOXYL ESTERASE\_B\_2; 1.  
 KW Hydrolyase.  
 SQ SEQUENCE 828 AA; 91554 MW; A896C05932678CAA CRC64;

Query Match 3.9%; Score 32; DB 4; Length 828;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 SVSNFVNDLYGPEGKDTRETIKFMYTDMAD 430  
 Db 412 SVSNFVNDLYGPEGKDTRETIKFMYTDMAD 443

RESULT 20

Q62889 PRELIMINARY; PRT; 643 AA.  
 AC Q62889;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update);  
 DE NeuroLigin.3.  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Forebrain;  
 RX MEDLINE=96162010; PubMed=8576240;  
 RA Ichchenko K., Nguyen T., Sudhof T.C.;  
 RT "Structures, alternative splicing, and neurexin binding of multiple  
 RT neuroLigin.3";  
 RL J. Biol. Chem. 271:2676-2683 (1996).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.  
 DR EMBL: U01663; AAA97871.1;  
 DR HSSP: P21836; 1MAA.  
 DR InterPro: IPR002018; CarboxylesteraseB.  
 DR InterPro: IPR000460; NeuroLigin.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS: PR01090; NEUROLIGIN.  
 DR PROSITE: PS00941; CARBOXYL ESTERASE\_B\_2; 1.  
 KW Hydrolyase.  
 SQ SEQUENCE 848 AA; 93888 MW; 7520653B32535750 CRC64;

Query Match 3.9%; Score 32; DB 1; Length 848;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-25;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 SVSNFVNDLYGPEGKDTRETIKFMYTDMAD 430  
 Db 432 SVSNFVNDLYGPEGKDTRETIKFMYTDMAD 463

RESULT 21

Q8NMH2 PRELIMINARY; PRT; 202 AA.  
 AC Q8NMH2;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE NeuroLigin 3 (fragment).  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 CX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Medial basal hypothalamus;  
 RA Munganaest A.E., Ojeda S.R.;  
 RT Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL ESTERASE/LIPASE FAMILY.  
 DR EMBL: AF248501; AAL40263.1;  
 DR InterPro: IPR002018; CarboxylesteraseB.  
 DR InterPro: IPR000460; NeuroLigin.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS: PR01090; NEUROLIGIN.  
 KW Hydrolyase.  
 FT NON\_TER 1  
 FT NON\_TER 202  
 SQ SEQUENCE 202 AA; 22897 MW; 99602C5B70288C58 CRC64;

Query Match 3.4%; Score 28; DB 6; Length 202;  
 Best Local Similarity 100.0%; Pred. No. 2e-21;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 510 CNFSKQDVNLSAVVNTYWTNFAKTGDPN 537  
 Db 49 CNFSKQDVNLSAVVNTYWTNFAKTGDPN 76

RESULT 22  
 Q8NCD0 PRELIMINARY; PRT; 335 AA.  
 ID Q8NCD0

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AC Q8NCD0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein F190333.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saito K.,
RA Yamamoto T., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuhara Y., Ono T., Okano K., Yoshikawa Y., Kotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Nimomiya K.;
RT "NEO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL; AK074814; BAC11226.1;
DR InterPro; IPR002018; Carboxesterases.
DR InterPro; IPR000460; Neurolygin.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLYGIN.
DR KX Hypothetical protein; Hydrolase.
SQ SEQUENCE 335 AA; 37398 MW; 3E82B66FC5F54ED CRC64;

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Query Match 3.4%; Score 28; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 510 CNFSKNDVLSAVMTYNTNPAKTGDPN 537
DB 32 CNFSKNDVLSAVMTYNTNPAKTGDPN 58

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RESULT 23
Q8BXR4 PRELIMINARY; PRT; 383 AA.
AC Q8BXR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NEUROLYGIN 3 isoform HMD homolog (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=1246651;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK044438; BAC11918.1;
DR NCBI_TaxID=10090;
SQ SEQUENCE 383 AA; 43075 MW; D0B3E31B34D35086 CRC64;

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Query Match 3.4%; Score 28; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 510 CNFSKNDVLSAVMTYNTNPAKTGDPN 537
DB 79 CNFSKNDVLSAVMTYNTNPAKTGDPN 106

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RESULT 24
Q99K10 PRELIMINARY; PRT; 245 AA.
ID Q99K10

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AC Q99K10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to neurolygin 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL; BC005523; AAH05523.1;
DR HSSP; P30122; 2BCE.
DR MGD; MGI:2179435; N19n1.
DR InterPro; IPR002018; Carboxesterases.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00941; CARBOXYL-ESTERASE_B_2; 1.
DR KX Hydrolase.
SQ SEQUENCE 245 AA; 27130 MW; 48ED37A3433E9B5 CRC64;

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Query Match 2.2%; Score 18; DB 11; Length 245;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 167 KPVWYIHGSGSYMEGTGN 184
DB 173 KPVWYIHGSGSYMEGTGN 190

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RESULT 25
Q75612 PRELIMINARY; PRT; 612 AA.
AC Q75612;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Bile salt-dependent lipase cDNA isoform (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Pancreas;
RX MEDLINE=98447673; PubMed=9774442;
RA Pascualini E., Callot N., Panicot L., Mas E., Llobes R.,
RA Lombard C.;
RT "Molecular cloning of the oncogene isoform of the human pancreatic
RT bile salt-dependent lipase."
RL J. Biol. Chem. 273:28208-28218 (1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL; AF081673; AAC1012.1;
DR HSSP; P30122; 2BCE.
DR InterPro; IPR002018; Carboxesterases.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esters_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTERASE.
DR PROSITE; PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYL-ESTERASE_B_2; 1.
DR KX Hydrolase.
FT NON TER 1
SQ SEQUENCE 612 AA; 66363 MW; A5E9092D19390826 CRC64;

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Query Match 1.5%; Score 12; DB 4; Length 612;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 526 YWTFNPAKTGDPN 537

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Db 467 YMTNFAKTGDPN 478

## RESULT 26

016398 PRELIMINARY; PRT; 742 AA.

AC Q16398; 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Bile salt-dependent lipase.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96038931; PubMed=7576248;  
RA Roudaut S., Miralles F., Vargotat A., Escarano M.C., Lombardo E.;  
RT "Bile salt-dependent lipase transcripts in human fetal tissues."  
RL Biochim. Biophys. Acta 1264:141-150(1995).  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.  
DR EMBL: S9774; AAB35489.2; -  
DR HSSP: P30122; 28CE.  
DR InterPro: IPR002018; Carboxyl-esterase.  
DR InterPro: IPR003379; Ser-esterase.  
DR Pfam: PF00135; Coesterase; 1.  
DR PROSITE: PS00122; CARBOXYL-ESTERASE\_B\_1; 1.  
DR PROSITE: PS00941; CARBOXYL-ESTERASE\_B\_2; 1.  
KW Hydrolase.  
SQ SEQUENCE 742 AA; 78317 MW; 4D7DF66772EAC07 CRC64;

Query Match 1.5%; Score 12; DB 4; Length 742;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 526 YMTNFAKTGDPN 537  
Db 487 YMTNFAKTGDPN 498

## RESULT 27

Q9UP41 PRELIMINARY; PRT; 745 AA.

AC Q9UP41; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Carboxyl ester lipase.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96191740; PubMed=9510636;  
RA Madeyski K., Lidberg U., Bjursell G., Nilsson U.;  
RT "Structure and organization of the human carboxyl ester lipase  
locus."  
RL Mamm. Genome 9:334-338(1998).  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.  
DR EMBL: AF032711; AAC26514.1; -  
DR HSSP: P30122; 28CE.  
DR InterPro: IPR002018; Carboxyl-esterase.  
DR InterPro: IPR003379; Ser-esterase.  
DR Pfam: PF00135; Coesterase; 1.  
DR PROSITE: PS00122; CARBOXYL-ESTERASE\_B\_1; 1.  
DR PROSITE: PS00941; CARBOXYL-ESTERASE\_B\_2; 1.  
KW Hydrolase.  
SQ SEQUENCE 745 AA; 78697 MW; 0251356CC556706A CRC64;

Query Match 1.5%; Score 12; DB 4; Length 745;

Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 526 YMTNFAKTGDPN 537  
Db 490 YMTNFAKTGDPN 501

## RESULT 28

Q9NID1 PRELIMINARY; PRT; 998 AA.

AC Q9NID1; 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Carboxyl-ester lipase.  
OS Gorilla gorilla (gorilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.  
OX NCBI\_TaxID=9593;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20018178; PubMed=13548728;  
RA Madeyski K., Lidberg U., Bjursell G., Nilsson U.;  
RT "Characterization of the gorilla carboxyl ester lipase locus, and the  
appearance of the carboxyl ester lipase pseudogene during primate  
evolution."  
RL Gene 239:273-282(1999).  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.  
DR EMBL: AF206618; AAF71700.1; -  
DR HSSP: P30122; 28CE.  
DR InterPro: IPR002018; Carboxyl-esterase.  
DR InterPro: IPR003379; Ser-esterase.  
DR Pfam: PF00135; Coesterase; 1.  
DR PROSITE: PS00122; CARBOXYL-ESTERASE\_B\_1; 1.  
DR PROSITE: PS00941; CARBOXYL-ESTERASE\_B\_2; 1.  
KW Hydrolase.  
SQ SEQUENCE 998 AA; 101026 MW; 3C81AD44504EBABA CRC64;

Query Match 1.5%; Score 12; DB 6; Length 998;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 526 YMTNFAKTGDPN 537  
Db 490 YMTNFAKTGDPN 501

## RESULT 29

Q8WXX4 PRELIMINARY; PRT; 110 AA.

AC Q8WXX4; 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Esterase (Fragment) (Diamondback moth).  
OS Plutella xylostella (Diamondback moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Yponomeutoidea; Plutellidae; Plutella.  
OX NCBI\_TaxID=51655;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Sten B., Qiao C.;  
RT "cDNA cloning and characterization of Plutella xylostella esterase  
related to phosphatase insecticides resistance."  
RL Submitted (JUG-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.  
DR EMBL: AB059914; BAC10286.1; -  
DR InterPro: IPR002018; Carboxyl-esterase.  
DR InterPro: IPR003379; Ser-esterase.  
DR Pfam: PF00135; Coesterase; 1.

KM Hydrolase. 1  
 FT NON TER 1:0  
 SQ SEQUENCE 110 AA: 12002 MW: 89C2CC94343C6F76 CRC64;  
 Query Match 1.3%; Score 11; DB 5; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 0.0042;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 INVRGILGFL 212  
 DB 56 INVRGILGFL 66

RESULT 30  
 Q23735 PRELIMINARY; PRT; 540 AA.  
 ID 023735:  
 AC 023735:  
 DT 01-JAN-1998 (Tremblrel. 05, Created)  
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Esterase B1 precursor (EC 3.1.1.1).  
 OS Culex quinquefasciatus (Southern house mosquito).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.  
 NCBI\_TaxID=7176;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RES;  
 RX MEDLINE=3534253; PubMed=7530468;  
 RA Vaughan A., Rodriguez X., Hemingway C.;  
 RT "The independent gene amplification of electrophoretically  
 RT indistinguishable B esterases from the insecticide-resistant mosquito  
 RT Culex quinquefasciatus";  
 RL Biochem. J. 335:651-658(1995).  
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON  
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.  
 CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A  
 CC CARBOXYLIC ANION.  
 CC -1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF  
 CC BOTH A AND B ARE KNOWN.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/ESTERASE FAMILY.  
 DR EMBL: Z32695; CAA83644.1; -;  
 DR HSSP: P21836; TMAA;  
 DR InterPro: IPR002018; Carbestereases.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR003734; Lipase.  
 DR InterPro: IPR003739; Ser ester\_sites.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PR00876; CHOLINESTERASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00120; LIPASE\_SER; 1.  
 KW Hydrolyase; Serine esterase; Glycoprotein; Multigene family; Signal.  
 FT SIGNAL 1  
 FT CHAIN 1  
 FT ACT SITE 191 191  
 FT ACT\_SITE 442 442  
 FT DISULFID 68 81  
 FT CARBOHYD 54 54  
 FT CARBOHYD 485 485  
 SO SEQUENCE 540 AA; 63852 MW; AF4787D571EDBDCD CRC64;

Query Match 1.3%; Score 11; DB 5; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 GAFGDPKRVY 250  
 DB 176 GAFGDPKRVY 186

RESULT 31  
 Q8BM97

ID Q8BM97 PRELIMINARY; PRT; 559 AA.  
 AC Q8BM97:  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Similar to carboxylesterase precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Colon;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA The Riken Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 DR EMBL: AK035663; BAC20361.1; -;  
 SO SEQUENCE 559 AA; 62305 MW; 8C94D21522C252C4 CRC64;

Query Match 1.3%; Score 11; DB 11; Length 559;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNIYVP 135  
 DB 121 EDCLYNIYVP 131

RESULT 32  
 Q6BK48 PRELIMINARY; PRT; 559 AA.  
 ID Q6BK48:  
 AC Q6BK48:  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Similar to carboxylesterase precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium.  
 RA The Riken Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 DR EMBL: AK072498; BAC36707.1; -;  
 SO SEQUENCE 559 AA; 62317 MW; CC14C61034A122C3 CRC64;

Query Match 1.3%; Score 11; DB 11; Length 559;  
 Best Local Similarity 100.0%; Pred. No. 0.019;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNIYVP 135  
 DB 121 EDCLYNIYVP 131

RESULT 33  
 Q97110 PRELIMINARY; PRT; 610 AA.  
 ID Q97110:  
 AC Q97110:  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Acetylcholinesterase (fragment).  
 OS Loligo opalescens (California market squid).

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OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coeloidae; Neocoleoidea;
CC Decapodiformes; Scudiroidea; Loligo.
OX NCBI_TaxID=31211;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=optic lobe.
RA Talsia V., Granoso M., Appagans M., Giovannini E., Romani R., Rosi G.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF065384; AAD15886.1; -.
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carboxesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydrolyase.
FT NON_TER
SQ SEQUENCE 610 AA; 69516 MW; 53EBAFFE1112063 CRC64;

Query Match 1.3%; Score 11; DB 5; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 527 WTNFAKTGDPN 537
DQ 506 WTNFAKTGDPN 516
|||||
PRT: 656 AA.

RESULT 34
C9XYA9 PRELIMINARY; PRT: 656 AA.
ID C9XYA9
AC C9XYA9:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Acetylcholinesterase (Fragment).
CN ACHE.
OS Meloidogyne javanica (Root-knot nematode).
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
CC Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
CX NCBI_TaxID=6303;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99270313; PubMed=10340488;
RA Piote C., Arthaud L., Abad P., Rosso M.N.;
RT "Molecular cloning of an acetylcholinesterase gene from the plant
RT parasitic nematodes, Meloidogyne incognita and Meloidogyne javanica.";
RJ Mol. Biochem. Parasitol. 99:247-256(1999).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF065384; AAD25921.1; -.
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carboxesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
KM Hydrolyase.
FT NON_TER
SQ SEQUENCE 656 AA; 76061 MW; AF90A221AERFPOOC CRC64;

Query Match 1.3%; Score 11; DB 5; Length 656;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNIYVP 135
DQ 125 EDCLYNIYVP 135
|||||
PRT: 656 AA.

RESULT 35
C9NGK5 PRELIMINARY; PRT: 656 AA.
ID C9NGK5
AC C9NGK5:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Acetylcholinesterase.
CN ACHE.
OS Meloidogyne incognita (Southern root-knot nematode).
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
CC Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
CX NCBI_TaxID=6306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99270313; PubMed=10340488;
RA Piote C., Arthaud L., Abad P., Rosso M.N.;
RT "Molecular cloning of an acetylcholinesterase gene from the plant
RT parasitic nematodes, Meloidogyne incognita and Meloidogyne javanica.";
RJ Mol. Biochem. Parasitol. 99:247-256(1999).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF065384; AAD25921.1; -.
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carboxesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
KM Hydrolyase.
FT NON_TER
SQ SEQUENCE 656 AA; 75962 MW; 646C39B57ABDFE0 CRC64;

Query Match 1.3%; Score 11; DB 5; Length 656;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNIYVP 135
DQ 133 EDCLYNIYVP 143
|||||
PRT: 248 AA.

RESULT 36
C9NGK5 PRELIMINARY; PRT: 248 AA.
ID C9NGK5
AC C9NGK5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Neurotigin (CG13772 protein).
CN NEUROIGIN OR CG13772.
OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscivora;
CC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Xie W., Boulianne G.L.;
RT "cDNA (Drosophila neurotigin).";
RJ Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10711132;
RA Adams M.D., Gelinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

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RA Sutton G.C., Mortman C.R., Vandell M.D., Zhang C., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne X., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baker E.G., Heit G., Nelson C.R., Niklos G.J.G.,  
RA Abri J.F., Agbayani A., An H.-U., Andrews-Piankoff C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktiroglu L., Bessley E.M.,  
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhattacharya D., Bolshakov S.,  
RA Borikova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,  
RA Burris K.C., Busat D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Darlike C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes N., Dugan-Recha S., Dunkov B.C., Dunn P.,  
RA Durkin K.J., Evangelista C.C., Petrait C., Ferreira S., Fleischman N.,  
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
RA Gloeck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.C., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,  
RA Kimmel B.E., Kodira C.D., Kratz C., Kravitz S., Kuip D., La Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mallet E., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Meryulov G., Mishina N.V., Moberly C., Morris J., Noshirefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzay D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet C.M.,  
RA Palazzolo N., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Reinstra K., Sanders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupsek M.F., Smith T.,  
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Massaman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.P., Zaveri C.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter C.C.,  
RA "The genome sequence of *Drosophila melanogaster*.";  
RA Science 287:2185-2195 (2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Ceiniker S.E., Adams X.D., Krommiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Bhatnagar R.C., Rogers Y.,  
RA Barton J., An H., Baldwin D., Barton J., Beeson K.Y., Blaser L.A.,  
RA Carlson J.W., Center A., Champagne M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorett V., Doup L.E., Doyle C., Dreese D., Fattan D.,  
RA Fothergill S., Frise E., Galle R.F., Gary N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jalali M., Kruse D., Li P., Mallet E., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nestor K.A., Nuno C.,  
RA Paclet J., Paragas V., Park S., Patel S., Pfeiffer B.,  
RA Prounnavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svitskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.C., Venter C.C., Rubin G.M.,  
RA "Sequencing of *Drosophila melanogaster* genome.";  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu D., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker C.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Ceiniker S.E.,  
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Krommiller B., Karschal B., Milburn G., Richter U., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,  
RA "Annotation of *Drosophila melanogaster* genome.";  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Flybase:  
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.  
DR EMBL, AF251479; AAF69455.1; -

DR EMBL, AE003615; AAF52450.2; -  
DR HSSP; P37967; 10E3.  
DR Flybase; Pgm0031866; neurocligin.  
DR InterPro; IPR002018; Carboxylesterase.  
DR InterPro; IPR003379; Ser\_esterase.  
DR Pfam; PF00135; Coesterase; 1.  
DR PROSITE; PS00941; CARBOXYL-ESTERASE\_B\_2; 1.  
DR Hydrobase.  
SC SEQUENCE 1248 AA; 136844 MW; 3F95AD4289F761DF CRC64;  
Query Match 1.3%; Score 11; DB 5; Length 1248;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 125 EDCLYNTIYVP 135  
|||||  
Db 280 EDCLYNTIYVP 290  
RESULT 37  
Q9GN02  
ID Q9GN02 PRELIMINARY; PRT; 134 AA.  
AC Q9GN02;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 02-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Alpha-esterase like protein E2 (fragment).  
OS Tribolium castaneum (Red flour beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polypnaga; Cucujiformia;  
OC Tenebrionidae; Tribolium.  
CX NCBI\_TaxId=7070;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA CLAUDIANOS C., CRONE E., COPPIN C., RUSSELL R., OAKSHOTT C.,  
RA STRAIN-CA-1;  
RA "A Genomic Perspective on Mutant A-esterases and Metabolic  
RA Resistance to Organophosphates.";  
RA (in, unknown A. (eds.));  
RA PESTICIDE RESISTANCE - SPECIAL ACS MEETING 1999, PP.1-1,  
RA Unknown Publisher (2000).  
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.  
DR EMBL; AF260821; AAG2019.1; -  
DR HSSP; P37967; 10E3.  
DR InterPro; IPR002018; Carboxylesterase.  
DR Pfam; PF00135; Coesterase; 1.  
CX Hydrobase.  
DT CON TER 1 1  
FT NON TER 134 134  
SQ SEQUENCE 134 AA; 14749 MW; 3BBFBCD1E72F4375 CRC64;  
Query Match 1.2%; Score 10; DB 5; Length 134;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 203 NYRLGILGFL 212  
|||||  
Db 107 NYRLGILGFL 116  
RESULT 38  
Q23736  
ID Q23736 PRELIMINARY; PRT; 505 AA.  
AC Q23736;  
DT 01-JUN-1998 (TrEMBLrel. 05, Created)  
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Esterase B (EC 3.1.1.1) (fragment).  
OS Culex quinquefasciatus (Southern house mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.  
CX NCBI\_TaxId=7116;  
RN [1]



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RP SEQUENCE FROM N.A.
RC STRAIN=BE155;
RX MEDLINE=95:34253; PubMed=7530448;
RA Vaughan A., Rodriguez M., Hemingway J.;
RT "The independent gene amplification of electrophoretically
RT indistinguishable B esterases from the insecticide-resistant mosquito
RT Culex quinquefasciatus."
RJ Biochem. J. 305:651-658(1995).
CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A
CC CARBOXYLIC ANION.
CC -1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF
CC BOTH A AND B ARE KNOWN.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: Z22696; CAA83645.1; -.
DR HSSP: P17672; I033.
DR InterPro: IPR002018; Carbesterase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00135; Ser_estr_site.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00120; Lipase_ser.
KM Hydrolyase; Serine esterase; Glycoprotein; Multigene family.
FT NON_TER
FT ACT_SITE 156 156 BY SIMILARITY.
FT ACT_SITE 457 457 BY SIMILARITY.
FT DISULFID 30 46 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 505 AA; 56834 MW; CFF345CC86F0689 CRC64;

Query Match 1.2%; Score 10; DB 5; Length 505;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 AFGDPRKRYT 250
Db 142 AFGDPRKRYT 151

RESULT 39
P91920 PRELIMINARY; PRT; 540 AA.
AC P91920;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Esterase B3.
OS Culex tarsalis (Mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.
OX NCBI_TaxID=7177;
RN (1);
RP SEQUENCE FROM N.A.
RX MEDLINE=97385422; PubMed=9241436;
RA Wittiger C., Walker V.K.;
RT "Isolation and characterization of an unamp-lified esterase B3 gene
RT from malathion-resistant Culex tarsalis."
RL Biochem. Genet. 35:119-138(1997).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U88972; AAC33391.1; -.
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carbesterase.
DR InterPro: IPR000734; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KM Hydrolyase.
SQ SEQUENCE 540 AA; 60795 MW; CFC8AB43A17A558B CRC64;

Query Match 1.2%; Score 10; DB 5; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 AFGDPRKRYT 250
Db 177 AFGDPRKRYT 186

RESULT 40
Q23734 PRELIMINARY; PRT; 540 AA.
AC Q23734; O02537;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Esterase B2 (EC 3.1.1.1).
OS Culex quinquefasciatus (Southern house mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.
OX NCBI_TaxID=7176;
RN (1);
RP SEQUENCE FROM N.A.
RC STRAIN=BE155;
RX MEDLINE=95:34253; PubMed=7530448;
RA Vaughan A., Rodriguez M., Hemingway J.;
RT "The independent gene amplification of electrophoretically
RT indistinguishable B esterases from the insecticide-resistant mosquito
RT Culex quinquefasciatus."
RJ Biochem. J. 305:651-658(1995).
RN (2);
RP SEQUENCE FROM N.A.
RX MEDLINE=94178593; PubMed=8132048;
RA Vaughan A., Ketterman A.C., Hemingway J.;
RT "Comparisons of nucleic acid sequences of esterases from resistant and
RT susceptible strains of Culex quinquefasciatus."
RJ Biochem. Soc. Trans. 21:481S-485S(1993).
CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.
CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A
CC CARBOXYLIC ANION.
CC -1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF
CC BOTH A AND B ARE KNOWN.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: Z22694; CAA83643.1; -.
DR EMBL: Z86069; CAB06676.1; -.
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carbesterase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000739; Ser_estr_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00120; Lipase_ser.
KW Hydrolyase; Serine esterase; Glycoprotein; Multigene family.
FT ACT_SITE 191 191 BY SIMILARITY.
FT ACT_SITE 442 442 BY SIMILARITY.
FT DISULFID 68 81 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 540 AA; 60697 MW; IAOB40417CC2B70C CRC64;

Query Match 1.2%; Score 10; DB 5; Length 540;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 AFGDPRKRYT 250
Db 177 AFGDPRKRYT 186

RESULT 41
Q9VDP5 PRELIMINARY; PRT; 593 AA.
AC Q9VDP5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)

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CT 01-OCT-2002 (TRENBLER). 22, Last sequence update!
CT 01-MAR-2003 (TRENBLER). 23, Last annotation update!
DE CG5030 protein.
GN CG5030.
CS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Hersenson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q.X.,
RA Brandon R.C., Rogers Y.-H.C., Blair J.R.G., Cherge M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKillop G.L.G.,
RA Abrita C.F., Agbayani A., An H.-C., Andrews-Flandkuch C., Baldwin D.,
RA Bailew R.M., Sasu A., Baxendale C., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhargava D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck C., Brockstein P., Broctler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chardas I.,
RA Cherry J.M., Cawley S., Dabike C., Davenport L.S., Davies P.,
RA dePablo B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M.,
RA Dodson K., Doup L.E., Jones M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali N., Kalush F., Karpen S.H., Ke Z., Kesteven J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Moharry C., Morris J., Moshrefi A.,
RA Mount S.W., Moy M., Murphy B., Murphy L., Munz D.W., Nelson C.,
RA Nelson D.R., Nelson K.A., Nixon K., Ruskert D.R., Packer J.K.,
RA Palazolo R., Pittman G.S., Pat S., Pollard J.D., Puri V., Reese M.G.,
RA Reiner K., Remington K., Sanders R.D.C., Scheeler F., Shat H.,
RA Shue B.C., Siden-Klaras I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Switskar R., Tector C., Turner R., Venter A., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri U.S., Zhan X., Zhang G., Zhao C., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter C.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson C.W., Center A., Champe M., Davenport L.R., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dyrenke D., Farfan D.,
RA Ferreira C., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez K., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali N., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson X.A., Nunoo C.,
RA Paclob J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Switskar R., Tector C., Tyer D.,
RA Williams S.M., Zaveri U.S., Smith H.O., Venter C.C., Rubin G.M.,
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Mista S., Crosby M.A., Mathews B.B., Bayraktaroglu L., Campbell K.,
RA Hradsky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson C.W., Celniker S.E.,

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RA Clamp V., Dysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA Seale S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Murgall C.J., Lewis S.F.,
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.C.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Flybase:
RC Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AEO03729; AAF55745.2; -.
DR HSSP: P21816; IMAA.
DR Flybase: FBgn0038776; CG5030.
DR InterPro: IPR002018; Carboxylesterase.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00941; CARBOXYLESTERASE_2; 1.
KM Hydrolyase.
SO SEQUENCE 593 AA; 65726 MW; F0296DC1FB98F4C CRC64;

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Query Match 1.2%; Score 10; DB 5; Length 593;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 203 NYRGLIGFL 212
DB 234 NYRGLIGFL 243

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RESULT 42
09UXY3 PRELIMINARY; PRT; 288 AA.
AC 09UXY3;
DT 01-MAY-2000 (TRENBLER). 13, Created
DT 01-MAY-2000 (TRENBLER). 13, Last sequence update)
DT 01-MAR-2002 (TRENBLER). 20, Last annotation update)
DE Carboxylesterase-related protein.
OS Homo sapiens (human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RC Yeh B., Matney L., Yang D.;
RA Yeh B., Matney L., Yang D.;
RT "Human placental carboxylesterases: enzymatic characterization,
RT molecular cloning and evidence for the existence of multiple forms."
CC Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF106005; AAF14185.1; -.
DR HSSP: P37967; 1QEZ3.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estr_5ite.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYLESTERASE_2; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_2; 1.
KM Hydrolyase.
SQ SEQUENCE 288 AA; 30886 MW; 8F4C3BDE531BE9E CRC64;

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Query Match 1.1%; Score 9; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 125 EDCGYLNIY 133
DB 116 EDCGYLNIY 124

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## RESULT 43

Q99R1 PRELIMINARY: PRT: 360 AA.  
 AC Q99R1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Alpha-esterase 4 (Fragment).  
 GN ALPHA-EST4 OR AE4.  
 OS Drosophila simulans (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7240;  
 OK [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Robin G.C., Russell R.J., Oakeshott J.G.;  
 RT "The evolution of an alpha-esterase pseudogene inactivated in the  
 RL Drosophila melanogaster lineage."  
 CC Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/F-LIPASE FAMILY.  
 DR EMBL: AF159418; AAD49433...  
 DR HSRP: P30122; 28CE.  
 DR P1: P03027806; Desimalpha-Est4.  
 DR InterPro: IPR002018; Carboxesterase3.  
 DR Pfam: PF00335; Coesterase; 1.  
 KW Hydrolyase.  
 FT NON TER 1 1  
 FT 360 360  
 SQ SEQUENCE 360 AA; 40175 MW; 65D6D0ABECAD0F5D CRC64;

Query Match  
 Best Local Similarity 1.1%; Score 9; DB 5; Length 360;  
 Matches 9; Conservative 100.0%; Pred.No. 1.9; Mismatches 0; Indels 0; Gaps 0;

Qy 168 PMVYIHG3 176  
 Db 97 PMVYIHG3 95

## RESULT 44

Q8N8C PRELIMINARY: PRT: 469 AA.  
 AC Q8N8C;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein F433678.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 OK [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Tissue-Strain;  
 RA Kawachi T., Sugiyama A., Takeoto M., Sugiyama T., Tite R.,  
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,  
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
 RA Magatsuna M., Murakawa K., Karahori K., Takahashi-Fujii A., Oshima A.,  
 RA Suzuki Y., Sugano S., Nagahari K., Masuno Y., Nagai K., Isegai T.;  
 RT "NEO human cDNA sequencing project."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/F-LIPASE FAMILY.  
 DR EMBL: AK030997; BAC03565.1;  
 DR InterPro: IPR002018; Carboxesterase3.  
 DR Pfam: PF00335; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_2; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hypothetical protein; Hydrolyase.  
 SQ SEQUENCE 469 AA; 52312 MW; 7A18F68C10A9033 CRC64;

Query Match  
 Best Local Similarity 1.1%; Score 9; DB 4; Length 469;  
 Matches 9; Conservative 100.0%; Pred.No. 2.5; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYNLY 133  
 Db 13 EDCLYNLY 21

## RESULT 45

Q97TP8 PRELIMINARY: PRT: 497 AA.  
 AC Q97TP8;  
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Para-nitrobenzyl esterase, a/b hydrolyase.  
 GN CAPC050.  
 OS Clostridium acetobutylicum.  
 CC Plasmid pSOL1.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 NCBI\_TaxID=1488;  
 OK [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RA MEDLINE=21359325; PubMed=1146286;  
 RA Neilling J., Berton G., Melchenko M.V., Makarova K.S., Zeng C.,  
 RA Gibson R., Lee H.M., Dubois J., Liu D., Hitt J., Wolf Y.I.,  
 RA Tatunov R.L., Sabatne F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 PT bacterium Clostridium acetobutylicum."  
 RL J. Bacteriol. 183:4823-4838(2001).  
 DR EMBL: AE001438; AK76796.1;  
 DR InterPro: IPR002018; CarboxesteraseB.  
 DR Pfam: PF00335; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 KW Hydrolyase; Plasmid; Complete proteome.  
 SQ SEQUENCE 497 AA; 55902 MW; AF46CFC5CABFECC18 CRC64;

Query Match  
 Best Local Similarity 1.1%; Score 9; DB 16; Length 497;  
 Matches 9; Conservative 100.0%; Pred.No. 2.6; Mismatches 0; Indels 0; Gaps 0;

Qy 529 NFAKTGDPN 537  
 Db 442 NFAKTGDPN 450

## RESULT 46

Q9JYU6 PRELIMINARY: PRT: 503 AA.  
 AC Q9JYU6;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Lysyl-tRNA synthetase, heat inducible.  
 GN NMB1425.  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 NCBI\_TaxID=491;  
 OK [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=MC58 / Serogroup B;  
 RA MEDLINE=20175735; PubMed=10710307;  
 RA Tette-in H., Saunders N.D., Heidelberg J., Jeffries A.C., Nelson K.E.,  
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
 RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,  
 RA Halt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

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RA  Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,
RA  Cotton X.D., Utterback T.R., Khouri H., Qin H., Yamathavan C.,
RA  Gali J., Scarfate V., Maignan V., Pizze M., Grandi G., Sun H.,
RA  Smith H.C., Fraser C.M., Moxon E.R., Rappold R., Vetter J.C.;
RA  "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT  MC59."
RL  Science 287:1809-1815(2000).
CC  -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC  PROPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID);
CC  -1- CATALYTIC ACTIVITY: ATP + L-ASPARAGINE +
CC  TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-
CC  ASPARAGINYL-TRNA(ASN));
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY);
CC  -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY);
CC  -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC  -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR  EMBL: A0302491; AAF41786.1; -.
DR  HSSP: P14825; 1E10.
DR  TIGR: MMB1425; -.
DR  InterPro: IPR004364; trna-synt_2.
DR  InterPro: IPR002312; trna-synt_1ys_2.
DR  InterPro: IPR002313; trna-synt_1ys_2.
DR  InterPro: IPR004365; trna-anti_1.
DR  InterPro: IPR004365; trna-anti_1.
DR  Pfam: PF00152; trna-synt_2; 1.
DR  Pfam: PF01336; trna-anti; 1.
DR  PRINTS: PRO1042; TRNASYNTHASP.
DR  PRINTS: PRO0982; TRNASYNTHLVS.
DR  TIGRFS: TIGR00499; 1ys_bact; 1.
DR  PROSITE: PS50862; AA TRNA_LIGASE_1; 1.
KW  ATP-binding; Aminoacyl-TRNA synthetase; Ligase; Protein biosynthesis;
KW  Complete proteome.
SQ  SEQUENCE 503 AA; 57311 MW; 28CEC53DA02346C6 CRC64;

Query Match 1.1%; Score 9; DB 16; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 456 AADLHAQYG 464
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|||
DB 46 AADLHAQYG 54

RESULT 47
Q9UT77 PRELIMINARY; PRT; 503 AA.
ID Q9UT77;
AC Q9UT77;
DT 01-OCT-2003 (TrEMBLrel. 15, Created)
DT 01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lysyl-TRNA synthetase (EC 6.1.1.6).
GN LYS OR NMA1658.
OS Neisseria meningitidis (serogroup A).
CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
CC Neisseriaceae; Neisseria.
CX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Fairhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Harrison N., Holroyd S.,
RA Jagsis K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream V.A., Rutherford K.W., Simmonds M., Skelton C.,
RA Whitehead S., Spratt B.G., Baxell B.G.;
RA "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC PYROPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID);
CC -1- CATALYTIC ACTIVITY: ATP + L-ASPARAGINE +
CC TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-

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CC ASPARAGINYL-TRNA(ASN)).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY);
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY);
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR  EMBL: A163756; CAB84866.1; -.
DR  HSSP: P14825; 1E10.
DR  InterPro: IPR004364; trna-synt_2.
DR  InterPro: IPR002312; trna-synt_1ys_2.
DR  InterPro: IPR002313; trna-synt_1ys_2.
DR  InterPro: IPR004365; trna-anti_1.
DR  InterPro: IPR004365; trna-anti_1.
DR  Pfam: PF00152; trna-synt_2; 1.
DR  Pfam: PF01336; trna-anti; 1.
DR  PRINTS: PRO1042; TRNASYNTHASP.
DR  PRINTS: PRO0982; TRNASYNTHLVS.
DR  TIGRFS: TIGR00499; 1ys_bact; 1.
DR  PROSITE: PS50862; AA TRNA_LIGASE_1; 1.
DR  ATP-binding; Aminoacyl-TRNA synthetase; Ligase; Protein biosynthesis;
KW  Complete proteome.
SQ  SEQUENCE 503 AA; 57264 MW; 381891348F9D0543 CRC64;

Query Match 1.1%; Score 9; DB 16; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 456 AADLHAQYG 464
|||
|||
|||
DB 46 AADLHAQYG 54

RESULT 48
Q9V7J1 PRELIMINARY; PRT; 507 AA.
ID Q9V7J1;
AC Q9V7J1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
DE CG9424 protein.
GN CG9424.
OS Drosophila melanogaster (fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams V.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Kuanaites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang C., Chen L.X.,
RA Brannon R.C., Rogers Y.H.C., Blasei R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Millos G.L.G.,
RA Abril J.F., Abpayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakerdale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brandler D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brocette P.,
RA Burris K.C., Busam M.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Davis A.D., Dew C., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.S., Garg N.S., Gilbert W.M., Glasser K.,
RA Gocke A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeok P., Lei Y., Levitsky A.A., Li Y., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny J.M., Nelson J.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
 RA Palazzolo Y., Pittman G.S., Pat S., Pollard J., Puri V., Reese Y.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spiedling A.C., Stapleton M., Stinson R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach C.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 RL Science 287:2185-2195 (2000).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AEC3808: AAF58062.1; -  
 DR HSSP: P21316: IMA.  
 DR Flybase: FBgn003476; CG8424.  
 DR InterPro: IPR002618; CarboxylesteraseB.  
 DR InterPro: IPR000734; Lipase.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR PROSITE: PS0120; LIPASE\_SER; 1.  
 DR Hydrobase.  
 KW SEQUENCE 507 AA: 55988 MW: 976358481854357 CRC64:

Query Match 1.1%; Score 9; DB 5; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 2.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 168 PMVYTHGG 176  
 119 PMVYTHGG 126

RESULT 49  
 096DN9 PRELIMINARY; PRT; 525 AA.  
 ID 096DN9;  
 AC 096DN9;  
 DT 01-DEC-2001 (TrEMBLrel. 13, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein Flj1547.  
 DE Hypothetical protein Flj1547.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eultheria; Primates; Catarrhini; Hominoidea; Homo.  
 CC NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Niimiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,  
 RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Karihara K.,  
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie K.,  
 RA Otsuki T., Sato H., Nakamitsu A., Ishii S., Yamamoto U., Isoco Y.,  
 RA Kawai-Hiro Y., Sato K., Nishikawa T., Kitura K., Yamashita H.,  
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,  
 RA Kanohori K., Takahashi-Tajiri A., Oshima A., Sugiyama A., Kawakami B.,  
 RA Suzuki Y., Sugano S., Nagahara K., Masuro Y., Nagai K., Isogai T.,  
 RT NEBO human cDNA sequencing project.  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AK056109; BAB71094.1; -  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR PROSITE: PS0120; LIPASE\_SER; 1.  
 DR Hydrobase.  
 KW SEQUENCE 525 AA: 58200 MW: 772487838422F215 CRC64:

Query Match 1.1%; Score 9; DB 4; Length 525;  
 Best Local Similarity 100.0%; Pred. No. 2.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 2Y 125 EDCYLYNY 133  
 119 EDCYLYNY 127

RESULT 50  
 096LUD PRELIMINARY; PRT; 533 AA.  
 ID 096LUD;  
 AC 096LUD;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Paraben-hydrolyzing esterase precursor.  
 GN PBA.  
 OS Enterobacter cloacae.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Enterobacter.  
 CC NCBI\_TaxID=550;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=EW.  
 RA Valkova R., Lepine F., Boile C., Dupont X., Vilmoux R.,  
 RA "giba, a gene coding for an esterase hydrolyzing parabens in E.  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL: AY077721; AA482802.1; -  
 DR InterPro: IPR002018; CarboxylesteraseB.  
 DR InterPro: IPR000379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 DR Hydrobase; Signal.  
 KW SIGNAL 31  
 KW SEQUENCE 533 AA: 57922 MW: 520084F969E093BA CRC64:

Query Match 1.1%; Score 9; DB 2; Length 533;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 526 YMTNFAKTG 534  
 476 YMTNFAKTG 486

RESULT 51  
 096VIC PRELIMINARY; PRT; 541 AA.  
 ID 096VIC;  
 AC 096VIC;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Alpha-Est4 protein (RED07760p).  
 GN ALPHA-EST4 OR CG1082.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCBI\_TaxID=7227;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=BERKELEY.  
 RA MEDLINE=20196006; Pubmed=10711132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril C.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Batley R.M., Baau A., Bakerdale J., Bayraktaroglu L., Beasley E.M.,

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RA Beeson K.Y., Benos P.V., Berman B.F., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busar D.A., Butler H., Cadden S., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dabke C., Davenport L.B., Davies P.,
RA de Pablos A., Delcher A., Deng Z., Nays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Domes W., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hock C.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Idenwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mcherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moehrer A.,
RA Mount S.M., Moy M., Murphy B., Murphy C., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet C.M.,
RA Palazolo M., Pittman G.S., Fan S., Pollard J., Put V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Swirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.V., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan W., Zhang Q., Zhao Q., Zheng L.,
RA Zheng X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agdayan A., Carlson J.,
RA Chame M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kromtiller B., Li P., Liao G.,
RA Miranda A., Mungall C.T., Nunco J., Paclet J., Pargass V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBD databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/FAMILY.
DR EMBL: AEO03671; AAF5405.1; -
DR EMBL: AY070981; AAL46603.1; -
DR HSSP: P30122; 2BCE
DR Flybase: FBgn015572; alpha-Est4.
DR InterPro: IPR02018; Carboxylesterase.
DR InterPro: IPR00379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
KM Hydrolase.
SQ SEQUENCE 541 AA; 61305 MW; C39282265AC72EFD CRC64;

Query Match 1.1%; Score 9; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PWMVYIHGG 176
DB 104 PWMVYIHGG 112

RESULT 52
Q24197 PRELIMINARY; PRT; 541 AA.
AC Q24197;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Alpha esterase.
OS ALPHA-EST4 OR AE4 OR CG1082.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota, Metazoa, Artropoda, Hexapoda, Insecta, Pterygota,
OC Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
OC Ephydroidea, Drosophilidae, Drosophila.

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CX NCBI_TaxID=1227;
RN [1]
RP SEQUENCE FROM N.A.
RA Robit C.;
CC Submitted (MAR-1996) to the EMBL/GenBank/DBD databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: U51046; AB01145.1; -
DR HSSP: P30122; 2BCE.
DR Flybase: FBgn0015572; apha-Est4.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
KM Hydrolase.
SQ SEQUENCE 541 AA; 61277 MW; 7C6D6BE0690A4C33 CRC64;

Query Match 1.1%; Score 9; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PWMVYIHGG 176
DB 104 PWMVYIHGG 112

RESULT 53
Q81034 PRELIMINARY; PRT; 545 AA.
AC Q81034;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-KAR-2003 (TEMBLrel. 23, Last annotation update)
DE Carboxylesterase-like urinary excreted protein.
GN CAUXIN.
OS Felis silvestris catus (Cat).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eulacerta, Carnivora, Fissipedia, Felidae, Felis.
CX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Miyazaki M., Kamie K., Soeta S., Taiba H., Yamashita T.;
RT "Molecular cloning and characterization of a novel carboxylesterase-
RT like protein that is physiologically present at high concentrations in
RT the urine of domestic cats (Felis catus).";
RJ Biochem. J. 0:0-0(2002).
DR EMBL: AB045377; BAC22577.1; -
SQ SEQUENCE 545 AA; 60505 MW; 9F73FA693D271FA9 CRC64;

Query Match 1.1%; Score 9; DB 6; Length 545;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYDNIY 133
DB 119 EDCLYDNIY 127

RESULT 54
Q3KR26 PRELIMINARY; PRT; 549 AA.
AC Q3KR26;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Vest.
OS Vibrio harveyi.
OC Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
OC Vibrionaceae, Vibrio.
CX NCBI_TaxID=669;
RN [1]
RP SEQUENCE FROM N.A.
RA Teo J.W.P., Poh C.L., Zhang L.H.;
RT "Cloning and expression of Vibrio harveyi lipase.";

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RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF521299; AAM77904.1; -.
DR InterPro; IPR002018; Carboxesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolyase.
SQ SEQUENCE 549 AA; 60613 MW; 67CDBA5A30DC429F CRC64;

Query Match 1.1%; Score 9; DB 1; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 EDCLYLNLY 210
DB 164 INYRLGILG 172

RESULT 55
ID 054936 PRELIMINARY; PRT; 554 AA.
AC 054936;
CT 01-AUG-1998 (TrEMBLrel. 07, Created)
CT 01-AUG-1998 (TrEMBLrel. 27, Last sequence update)
CT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Carboxylesterase precursor.
GN ESI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CPL; TISSUE=Lung;
RC MEDLINE=99032675; PubMed=9815115;
RA Krishnasamy S., Teng A.L., Dhond R., Schultz R.M., Gross N.J.;
RT "Molecular cloning, characterization, and differential expression
RT pattern of mouse lung surfactant convertase.";
RL Am. J. Physiol. 275:1269-1275(1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF034435; AAC04708.1; -.
DR HSSP; P37967; 1OE3.
DR MGD; MGI:95420; Est.
DR InterPro; IPR002018; Carboxesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR KM Hydrolyase. Signal.
FT SIGNAL 18 POTENTIAL.
FT CHAIN 19 554 CARBOXYLESTERASE.
SQ SEQUENCE 554 AA; 61140 MW; FEFBE9A8EE74975 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 554;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNLY 133
DB 114 EDCLYLNLY 122

RESULT 56
ID 08K125 PRELIMINARY; PRT; 554 AA.
AC 08K125;
CT 01-OCT-2002 (TrEMBLrel. 22, Created)
CT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
CT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to esterase 1.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Liver;
RA Straussberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; BC026907; AAH26907.1; -.
DR InterPro; IPR002018; Carboxesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR KM Hydrolyase.
SQ SEQUENCE 554 AA; 61020 MW; 592A9C4705FC8F5E CRC64;

Query Match 1.1%; Score 9; DB 1; Length 554;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNLY 133
DB 114 EDCLYLNLY 122

RESULT 57
ID 08K380 PRELIMINARY; PRT; 558 AA.
AC 08K380;
CT 01-OCT-2002 (TrEMBLrel. 22, Created)
CT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
CT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Carboxylesterase isoenzyme.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RA Sanghani S.P., Davis W.I., Mahenholz A., Boston W.F.;
RT "Identification of the members of rat liver carboxylesterase family by
RT mass spectroscopy: cloning of a new isoenzyme.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AY034877; AAK61610.1; -.
DR InterPro; IPR002018; Carboxesterase.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR KM Hydrolyase.
SQ SEQUENCE 558 AA; 61802 MW; FB267DD19581106 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 558;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNLY 133
DB 120 EDCLYLNLY 128

RESULT 58
ID 08Q2R3 PRELIMINARY; PRT; 558 AA.
AC 08Q2R3;
CT 01-JUN-2002 (TrEMBLrel. 21, Created)
CT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
CT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to carboxylesterase 2 (intestinal, liver) (expressed sequence
DE A1266984) (Similar to liver carboxylesterase precursor).
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GN A1265984.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Liver;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=22354683; PubMed=246685.;
RA The FANTOM Consortium;
RL The RIKEN Genome Exploration Research Group Phase 1 & 2 Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,773 full-length cDNAs."
RJ Nature 420:563-571(2002).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY
DR EMBL; BC024491; AAH24491.1; -
DR EMBL; BC024517; AAH24517.1; -
DR EMBL; BC025537; AAH25537.1; -
DR EMBL; BC025812; AAH25812.1; -
DR EMBL; BC026643; AAH26643.1; -
DR EMBL; BC031295; AAH31295.1; -
DR EMBL; BC024082; AAH24082.1; -
DR EMBL; AK078953; BAC27476.1; -
DR MGI; MGI:2142491; A266984.
DR InterPro: IPR002013; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 558 AA; 61940 MW; 961A06BDC92E3FD CRC64;

Query Match 1.1%; Score 9; DB 11; Length 588;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCUYNLY 133
DB 120 EDCUYNLY 128

RESULT 59
035533 PRELIMINARY; PRT; 559 AA.
AC 035533;
DT 01-JAN-1998 (TRENKLEI. 05, Created)
DT 01-JAN-1998 (TRENKLEI. 05, Last sequence update)
DT 01-MAR-2003 (TRENKLEI. 23, Last annotation update)
DE Carboxylesterase precursor (EC 3.1.1.3) (Alc-esterase) (B-esterase)
DE (MONOALTYRASE) (Cocaine esterase) (PROCAINE esterase) (METHYLBUTYRASE).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

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CC Mesocricetus.
CX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SYRIAN GOLDEN; TISSUE=Liver;
RA Sone T., Wang C.Y.;
RT "Mitochondrial amides and carboxylesterases."
RL (in) Gengenrich F.P. (eds.);
RL Comprehensive toxicology, pp.3:265-281, Elsevier Science,
RL Oxford (1997).
CC -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL + A
CC CARBOXYLIC ANION.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; D53577; BAA23605.1; -
DR HSSP; P37967; 10E3.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase.1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 559 CARBOXYLESTERASE.
SQ SEQUENCE 559 AA; 62126 MW; 5B6BD4F9A47C6AD8 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 559;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCUYNLY 133
DB 121 EDCUYNLY 129

RESULT 60
08R097 PRELIMINARY; PRT; 560 AA.
AC 08R097;
DT 01-JUN-2002 (TRENKLEI. 21, Created)
DT 01-JUN-2002 (TRENKLEI. 21, Last sequence update)
DT 01-OCT-2002 (TRENKLEI. 22, Last annotation update)
DE Hypothetical 62.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; BC027185; AAH27185.1; -
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase.1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 560 AA; 62735 MW; 3B8E56DC9FB108B5 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCUYNLY 133
DB 122 EDCUYNLY 130

RESULT 61

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Q91WU0
ID Q91WU0 PRELIMINARY; PRT: 561 AA.
AC Q91WU0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 61.6 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
CC Submitted (SEP-2001) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EXBL: BC034479; AAH34479.1; -.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000866; Est_target.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
DR PROSITE: PS00941; EP_TARGET; 1.
KW Hypothetical protein; Hydrolyase.
SQ SEQUENCE 561 AA; 62612 MW; 10013143A797868 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLYNLY 133
DB 114 EDCYLYNLY 122

RESULT 62
Q91WU0 PRELIMINARY; PRT: 561 AA.
AC Q91WU0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to carboxylesterase 2 (intestine, liver) (Hypothetical
protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
CC Submitted (OCT-2001) to the EMBL/GenBank/DDJ databases.
CC [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
CC Submitted (JUN-2002) to the EMBL/GenBank/DDJ databases.
CC [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Colon;
RA Strausberg R.;
CC Submitted (JUL-2002) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
EMBL: BC015290; AAH15290.1; -.

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DR EMBL: BC024552; AAH24552.1; -.
DR EMBL: BC031170; AAH31170.1; -.
DR EMBL: BC034178; AAH34178.1; -.
DR EMBL: BC034180; AAH34180.1; -.
DR EMBL: BC034191; AAH34191.1; -.
DR MGD: KGI:2385905; Cest2.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
KW Hypothetical protein; Hydrolyase.
SQ SEQUENCE 561 AA; 62469 MW; F793967A646EB728 CRC64;

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Query Match 1.1%; Score 9; DB 11; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLYNLY 133
DB 123 EDCYLYNLY 131

RESULT 63
Q76631 PRELIMINARY; PRT: 561 AA.
AC Q76631;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Carboxylesterase precursor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR; TISSUE=liver;
RA Sone T., Sawada T., Kunimoto T., Takabatake E., Wang C.Y., Isobe M.;
CC Submitted (JAN-1998) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL: AB010635; BAA25692.1; -.
DR EMBL: AB010570; BAA25690.1; -.
DR EMBL: AB010559; BAA25680.1; COINED.
DR EMBL: AB010560; BAA25690.1; COINED.
DR EMBL: AB010561; BAA25690.1; COINED.
DR EMBL: AB010562; BAA25690.1; COINED.
DR EMBL: AB010563; BAA25690.1; COINED.
DR EMBL: AB010564; BAA25690.1; COINED.
DR EMBL: AB010565; BAA25690.1; COINED.
DR EMBL: AB010566; BAA25690.1; COINED.
DR EMBL: AB010567; BAA25690.1; COINED.
DR EMBL: AB010568; BAA25690.1; COINED.
DR EMBL: AB010569; BAA25690.1; COINED.
DR HSSP: P37967; IOB3.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
KW Hydrolyase; Signal.
FT SIGNAL 1
FT CHAIN 27
SQ SEQUENCE 561 AA; 62189 MW; 13BF365F5063379 CRC64;

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Query Match 1.1%; Score 9; DB 11; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLYNLY 133
DB 123 EDCYLYNLY 131

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RESULT 64
ID Q924V9 PRELIMINARY: PRT: 562 AA.
AC Q924V9:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2002 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Carboxylesterase R1.
GN CESRL1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar; TISSUE=Liver;
RA Hosokawa M., Hadame A., Shirizu T., Takahashi D., Satoh T., Chiba K.;
RT "Molecular cloning and expression of cDNA encoding microsomal acyl-CoA
hydrolyase from rat liver.";
RJ Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AB023630; BA060697.1; -.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
KM Hydrolyase.
SQ SEQUENCE 562 AA; 62305 MW; 82475E22703BD33B CRC64;

Query Match 1.1%; Score 9; DB 1; Length 562;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCVYENIY 133
Db 124 EDCVYENIY 122

RESULT 65
ID Q9VLA4 PRELIMINARY: PRT: 564 AA.
AC Q9VLA4:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG3841 protein.
GN CG3841.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscivora;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=BRKLEY;
RA MEDUNNE=20196006; PubMed=10731132;
RA Adams M.C., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gale R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zheng X., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Chapple W., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter S.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-Y., Andrews-Pfarkoch C., Baldwin D.,
RA Balilew R.M., Basu P., Baxendale J., Bayraktaroglu L., Beasly E.V.,
RA Beeson K.Y., Benson P.V., Berman B.P., Bhargava J., Bolshakov S.,
RA Borchen D., Borchen W.R., Bowck J., Brockstein P., Brooker P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Danke C., Davernport L.B., Davies P.,
RA de Fabros B., Belcher A., Deng Z., Mays A.D., New I., Dietz S.M.,

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RA Dörsen K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.C., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klip D., Lai Z.,
RA Lasko F., Lei Y., Levitsky A.A., Li C., Li Z., Liang Y., Lin X.,
RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.X., Moy M., Murphy B., Murphy D., Nuzny D.X., Nelson J.L.,
RA Nelson J.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.V.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slater E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massaman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri U.S., Zhan Y., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RJ Science 287:2185-2195(2000)
CC - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AB003625; AF52791.1; -.
DR HSSP: P37967; 1OE3.
DR Flybase: FBgn0032131; CG3841.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KM Hydrolyase.
SQ SEQUENCE 564 AA; 62785 MW; 9A6E2A29B7592C09 CRC64;

Query Match 1.1%; Score 9; DB 5; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PVMVYIHGG 176
Db 120 PVMVYIHGG 128

RESULT 66
ID C6TD29 PRELIMINARY: PRT: 565 AA.
AC C6TD29:
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Brain carboxylesterase hb2.
GN CES_HBR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Hosokawa M., Mori M., Ogasawara Y., Komori C., Tsukada E., Chiba K.;
RT "cDNA cloning and expression of carboxylesterase isozymes from human
brain.";
RJ Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mori M., Hosokawa M., Tsukada E., Ogasawara Y., Chiba K.;
RT "cDNA cloning and stable expression of human brain carboxylesterase
isozymes";
RJ Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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DR EMBL; AB025027; BAB5656.1;
DR InterPro; IPR002018; CarboxylaseB.
DR InterPro; IPR000379; Ser esterase site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYL-ESTERASE_B_2; 1.
DR Hydrolyase.
SQ SEQUENCE 565 AA; 61962 MW; E255244C2CA9A1E CRC64;

Query Match 1.1%; Score 9; DB 4; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNITY 133
DB 114 EDCLYNITY 122

RESULT 67
Q23010 PRELIMINARY; PRT; 565 AA.
AC Q23010;
CT 01-NOV-1996 (TREMBLrel. 01, Created)
CT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE K1139.1 protein.
GN K1139.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6219;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,
RA Bonfield C., Burton J., Connell X., Copsey T., Cooper J., Coulson A.,
RA Craxton K., Dear S., Du Z., Durbin R., Favello A., Fulton D.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan N.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Smailton N., Smith A., Sornhamer E., Staden R., Stinson J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
RA Watson A., Weinstock L., Wilkinson-Spratt J., Wolfdmeyer P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome I:: of C.
RT elegans.";
RL Nature 366:32-38(1994).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Greco, T., Bradshaw H.;
RT "The sequence of C. elegans cosmid K1139.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterson R.;
RT "-1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
RT -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL; U64853; AAB04976.1;
DR HSSP; P37967; 10E3.
DR WormPep; K1139.1; CE07374.
DR InterPro; IPR002018; CarboxylaseB.
DR InterPro; IPR000379; Ser esterase site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR Hydrolyase.
SQ SEQUENCE 565 AA; 63560 MW; 388039A1DF17503 CRC64;

Query Match 1.1%; Score 9; DB 5; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 203 NYRGLIGF 211
DB 157 NYRGLIGF 165

RESULT 68
Q07540 PRELIMINARY; PRT; 565 AA.
AC Q07540;
CT 01-NOV-1998 (TREMBLrel. 08, Created)
CT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Liver carboxylesterase (EC 3.1.1.1).
DE Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98297515; PubMed=9635592;
RA Potter P.M., Pawlik C.A., Morton C.L., Naeye C.W., Danks N.K.;
RT "Isolation and partial characterization of a cDNA encoding a rabbit
RT liver carboxylesterase that activates the prodrug rimotetan (CPT-
RT 22777)."
R1 Cancer Res. 58:2646-2651(1998).
CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EXBL; AFG36930; AAC39258.1;
DR HSSP; P21836; 1MAH;
DR InterPro; IPR002018; CarboxylaseB.
DR InterPro; IPR000379; Ser esterase site.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYL-ESTERASE_B_2; 1.
DR Hydrolyase.
SQ SEQUENCE 565 AA; 62291 MW; CAC61400CC81D2F CRC64;

Query Match 1.1%; Score 9; DB 6; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNITY 133
DB 114 EDCLYNITY 122

RESULT 69
Q095N05 PRELIMINARY; PRT; 565 AA.
AC Q095N05;
CT 01-DEC-2001 (TREMBLrel. 19, Created)
CT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Carboxylesterase D1.
GN CESD1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21217951; PubMed=11339814;
RA Hosokawa M., Suzuki K., Takahashi D., Mori M., Satch T., Chiba K.;
RT "Purification, Molecular Cloning, and Functional Expression of Dog
RT Liver Microsomal acyl-CoA Hydrolyase: A Member of the Carboxylesterase
RT Multigene Family."
R1 Arch. Biochem. Biophys. 389:245-253(2001).
CC -1 SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
DR EMBL; AB023629; BAB0696.1;
DR InterPro; IPR002018; CarboxylaseB.
DR InterPro; IPR000379; Ser esterase site.
DR Pfam; PF00135; Coesterase; 1.

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DR PROSITE: PS00122; CARBOXYLESTERASE_B_1;
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 565 AA; 62000 MW; 985AA4222FEF37H CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 6; Length 565;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNTY 133
Db 114 EDCLYLNTY 122

RESULT 70
097582 PRELIMINARY; PRT; 565 AA.
AC 097582;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Carboxylesterase.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactylia; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestinal mucosa;
RX MEDLINE=99013456; Pubmed=799112;
RA David L. Guo X.G., Villard C., Moulin A., Puigserver A.;
RT "Purification and molecular cloning of porcine intestinal glycerol-
ester hydrolase--evidence for its identity with carboxylesterase.";
RL Eur. J. Biochem. 257:142-148 (1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF064741; AAC70613.1;
DR HSP: P2:836; IMAA
DR InterPro: IPR000218; CarboxylesteraseB.
DR InterPro: IPR003379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 565 AA; 61712 MW; 77935CC3D93FDC CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 6; Length 565;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNTY 133
Db 114 EDCLYLNTY 122

RESULT 71
08VCC2 PRELIMINARY; PRT; 565 AA.
AC 08VCC2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Carboxylesterase 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

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SE SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: BC021150; AA421150.1;
DR EMBL: BC026897; AA426897.1;
DR MGD: MG1:68378; Cesi1.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 565 AA; 62679 MW; 21F3B0184C2E881 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 565;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNTY 133
Db 114 EDCLYLNTY 122

RESULT 72
0924V8 PRELIMINARY; PRT; 565 AA.
AC 0924V8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Carboxylesterase MHI (EC 3.1.1.1).
GN CEB3 OR CESMHI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL; TISSUE=Liver;
RA Hosokawa M., Nakamura T., Nakata F., Takahashi D., Sakae N., Satoh T.,
RA Chiba K.;
RT "Purification, molecular cloning and expression of cDNA encoding
peroxisome proliferator inducible carboxylesterase isozymes from
RT C57BL/6 mouse liver.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AB023611; BA860698.1;
DR MGD: MG1:214820; Cesi3.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR003379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 565 AA; 61810 MW; AC122636F265D34C CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 565;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNTY 133
Db 114 EDCLYLNTY 122

RESULT 73
05136 PRELIMINARY; PRT; 565 AA.
AC 05136;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

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DT 01-OCT-2002 (TRENBLREL. 22, last annotation update)
DE Carboxylesterase precursor (EC 3.1.1.1).
CN CEST OR EX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBAF1J;
RX MEDLINE=98234306; PubMed=9565681;
RA Klinghaus P., Sector J., Asmann G.;
RT "Cloning and sequencing of a novel murine liver carboxylesterase
RT cDNA."
RL Biochim. Biophys. Acta 1397:175-179(1998).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: Y12887; CAZ3388.1; -.
DR HSP: P37967; J0E3.
DR MGD: MGI:98378; Cest1.
DR InterPro: IPR002018; Carbestereas.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PSC0122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
RW Hydrolyase; Signal.
FT SIGNAL.
FT SEQUENCE 565 AA; 62722 MW; B55A5A15C27B79 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCCLYNLY 133
DB 114 EDCCLYNLY 122

RESULT 74
Q91ZV9 PRELIMINARY; PRT; 565 AA.
ID Q91ZV9;
AC Q91ZV9;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DR 01-DEC-2001 (TRENBLREL. 19, last sequence update)
DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
DE Triacylglycerol hydrolase (EC 3.1.1.1).
GN CEST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=129/J; TISSUE=Liver;
RX MEDLINE=21363045; PubMed=11470237;
RA Dolinsky V.W., Spidone S., Lehner R., Vance D.E.;
RT "The cloning and expression of a murine triacylglycerol hydrolase cDNA
RT and the structure of its corresponding gene."
RL Biochim. Biophys. Acta 1532:162-172(2001).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF378751; AAK5067.1; -.
DR MGD: MGI:2148202; Cest3.
DR InterPro: IPR002018; Carbestereas.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PSC0122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
RW Hydrolyase.
FT SEQUENCE 565 AA; 61887 MW; 2ADF9725721DF9A CRC64;

Query Match 1.1%; Score 9; DB 11; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 125 EDCCLYNLY 133
DB 114 EDCCLYNLY 122

RESULT 75
Q35534 PRELIMINARY; PRT; 565 AA.
ID Q35534;
AC Q35534;
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
DE Carboxylesterase precursor (EC 3.1.1.1).
GN CARBOXYLESTERASE.
CS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=Syrian golden; TISSUE=Liver;
RA Sene T., Ishida Y., Takahatake E., Wang C., Isobe N.;
RT "Cloning and expression of a hamster liver cDNA encoding a novel
RT carboxylesterase which catalyzes the activation of carcinogenic
RT ary-hydroxamic acids."
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: D50578; BAA23604.1; -.
DR HSP: P21836; 1MAH.
DR InterPro: IPR002018; Carbestereas.
DR InterPro: IPR003379; Ser_estr_site.
DR Pfam: PF00135; Coesterase_1.
DR PROSITE: PSC0122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
RW Hydrolyase; Signal.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE 565 AA; 62165 MW; 8273233A59DF1ED0 CRC64;

Query Match 1.1%; Score 9; DB 11; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: November 5, 2003, 15:25:15  
 Job time : 47 secs

GenCore version 3.1.6  
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OW protein - protein search, using sw model

Run on: November 5, 2003, 15:22:08 / Search time 17 seconds

(without alignments)  
2257.282 Million cell updates/sec

Title: US-09-978-423a-375

Perfect score: 816  
Sequence: 1 MLNSVLMVLTALAKETLI.....TFSGGQNSTMLPRGHSTRV 816

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	65.9	816	1	NLG4_HUMAN
2	326	40.0	816	1	NLG4_HUMAN
3	213	26.1	213	1	NLG4_HUMAN
4	50	6.1	816	1	NLG4_HUMAN
5	50	6.1	816	1	NLG4_HUMAN
6	50	6.1	816	1	NLG4_HUMAN
7	48	5.9	816	1	NLG4_HUMAN
8	48	5.9	816	1	NLG4_HUMAN
9	35	4.3	816	1	NLG4_HUMAN
10	32	3.9	816	1	NLG4_HUMAN
11	32	3.9	816	1	NLG4_HUMAN
12	28	3.4	202	1	NLG3_MOUSE
13	28	1.5	742	1	EST1_HUMAN
14	14	1.2	540	1	EST1_HUMAN
15	9	1.1	532	1	EST2_RABIT
16	9	1.1	533	1	EST2_RABIT
17	9	1.1	549	1	EST2_RABIT
18	9	1.1	554	1	EST2_RABIT
19	9	1.1	556	1	EST2_RABIT
20	9	1.1	561	1	EST1_MOUSE
21	9	1.1	561	1	EST1_MOUSE
22	9	1.1	561	1	EST1_MOUSE
23	9	1.1	561	1	EST1_MOUSE
24	9	1.1	562	1	EST2_MOUSE
25	9	1.1	562	1	EST2_MOUSE
26	9	1.1	566	1	EST1_MOUSE
27	9	1.1	567	1	EST1_MOUSE
28	9	1.1	597	1	EST1_MOUSE
29	9	1.1	620	1	ACE1_MOUSE
30	9	1.1	620	1	ACE1_MOUSE
31	8	1.0	382	1	GP18_MOUSE
32	8	1.0	506	1	CYP11_MOUSE
33	8	1.0	563	1	LIP1_MOUSE

34	8	1.0	563	1	LIP2_MOUSE
35	8	1.0	581	1	ACES_MOUSE
36	8	1.0	586	1	ACES_MOUSE
37	8	1.0	590	1	ACES_MOUSE
38	8	1.0	599	1	ACES_MOUSE
39	8	1.0	612	1	ACES_MOUSE
40	8	1.0	629	1	ACES_MOUSE
41	8	1.0	664	1	ACES_MOUSE
42	8	1.0	782	1	ACES_MOUSE
43	8	1.0	837	1	ACES_MOUSE
44	8	1.0	912	1	ACES_MOUSE
45	8	1.0	918	1	ACES_MOUSE
46	8	1.0	2144	1	GLI1_MOUSE
47	8	1.0	2766	1	GLI1_MOUSE
48	8	0.9	52	1	LHA_MOUSE
49	7	0.9	127	1	Y55E_MOUSE
50	7	0.9	133	1	Y55E_MOUSE
51	7	0.9	141	1	Y55E_MOUSE
52	7	0.9	141	1	Y55E_MOUSE
53	7	0.9	141	1	Y55E_MOUSE
54	7	0.9	141	1	Y55E_MOUSE
55	7	0.9	141	1	Y55E_MOUSE
56	7	0.9	141	1	Y55E_MOUSE
57	7	0.9	159	1	Y55E_MOUSE
58	7	0.9	198	1	Y55E_MOUSE
59	7	0.9	199	1	Y55E_MOUSE
60	7	0.9	204	1	Y55E_MOUSE
61	7	0.9	205	1	Y55E_MOUSE
62	7	0.9	208	1	Y55E_MOUSE
63	7	0.9	234	1	Y55E_MOUSE
64	7	0.9	262	1	Y55E_MOUSE
65	7	0.9	270	1	Y55E_MOUSE
66	7	0.9	270	1	Y55E_MOUSE
67	7	0.9	271	1	Y55E_MOUSE
68	7	0.9	272	1	Y55E_MOUSE
69	7	0.9	274	1	Y55E_MOUSE
70	7	0.9	274	1	Y55E_MOUSE
71	7	0.9	282	1	Y55E_MOUSE
72	7	0.9	295	1	Y55E_MOUSE
73	7	0.9	307	1	Y55E_MOUSE
74	7	0.9	341	1	Y55E_MOUSE
75	7	0.9	352	1	Y55E_MOUSE
76	7	0.9	357	1	Y55E_MOUSE
77	7	0.9	357	1	Y55E_MOUSE
78	7	0.9	419	1	Y55E_MOUSE
79	7	0.9	439	1	Y55E_MOUSE
80	7	0.9	461	1	Y55E_MOUSE
81	7	0.9	461	1	Y55E_MOUSE
82	7	0.9	461	1	Y55E_MOUSE
83	7	0.9	489	1	Y55E_MOUSE
84	7	0.9	505	1	Y55E_MOUSE
85	7	0.9	505	1	Y55E_MOUSE
86	7	0.9	505	1	Y55E_MOUSE
87	7	0.9	526	1	Y55E_MOUSE
88	7	0.9	533	1	Y55E_MOUSE
89	7	0.9	550	1	Y55E_MOUSE
90	7	0.9	551	1	Y55E_MOUSE
91	7	0.9	554	1	Y55E_MOUSE
92	7	0.9	554	1	Y55E_MOUSE
93	7	0.9	557	1	Y55E_MOUSE
94	7	0.9	565	1	Y55E_MOUSE
95	7	0.9	574	1	Y55E_MOUSE
96	7	0.9	581	1	Y55E_MOUSE
97	7	0.9	584	1	Y55E_MOUSE
98	7	0.9	602	1	Y55E_MOUSE
99	7	0.9	607	1	Y55E_MOUSE
100	7	0.9	611	1	Y55E_MOUSE

## ALIGNMENTS

RESULT 1

NLG4 HUMAN  
 ID NLG4 HUMAN STANDARD: PRT: 816 AA.  
 AC DBMCM4; C9ULG9;  
 CT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Neuroigin 4 precursor (Neurigin X) (HMLX).  
 GN NLG4 OR KIAA26C.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND DISBASE.  
 RX PubMed=12669065;  
 RA Jarrin S., Quach H., Betancur C., Rastam M., Colineaux C.,  
 RA Gillberg I.C., Soderstrom H., Gatos B., Leboyer X., Gillberg C.,  
 RA Bougeron T., Nyden A., Philippe A., Cohen D., Chabane N.,  
 RA Moutereau S., Moutereau M.C., Briche A., Spohnheim E., Spix and T.,  
 RA Skjeldal O.H., Coleman M., Pearl P.L., Cohen I.L., Tsaluris C.,  
 RA Zappella M., Menchetti G., Pampella A., Aschauer H., Van Milderger L.,  
 RA "Mutations of the X-linked genes encoding neuroigin NLG3 and NLG4  
 PT are associated with autism";  
 PI Nat. Genet. 34:27-29(2003).  
 RA [2]  
 RE SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20039619; PubMed=10574462;  
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirokawa N., Koyama N.,  
 RA Chana O.;  
 RA "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RN DNA Res. 6:337-345(1999).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22399257; PubMed=7477932;  
 RA Strussberg R.L., Feinsold E.A., Grouse L.H., Derge J.G.,  
 RA Altschuler R.D., Collins F.S., Wagner L., Schmitt C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,  
 RA Dzhapenko L., Marusina K., Farmer A.A., Rubin G.W., Hong T.,  
 RA Stalderon M., Soares M.B., Bonaldi M.F., Casavant T.L., Schreier T.E.,  
 RA Brownstein M.J., Ustin T.S., Tostiyuki S., Cantini P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Adams R.D., Kallaby S.C.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Yalox J.A., Garatarte F.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.Y., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faley T., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.V.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Stallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP INTERACTION WITH DLG4.  
 RX PubMed=9278515;  
 RA Irie M., Hata Y., Takeuchi M., Ichitkenko K., Toyoda A., Hirao K.,  
 RA Takai Y., Rosahl T.W., Suedhof T.C.;  
 RT "Binding of neuroigin to PSD-95";  
 RL Science 277:1511-1515(1997).  
 RN [5]  
 RP INTERACTION WITH DLG4, AND TISSUE SPECIFICITY.  
 RX PubMed=1168788;  
 RA Bolliger M.F., Frei K., Winterhalter K.H., Gloor S.N.;  
 RT "Identification of a novel neuroigin in humans which binds to PSD-95  
 RL Biochem. J. 356:581-588(2001).  
 CC -!- FUNCTION: Putative neuronal cell surface protein involved in cell-

CC cell-interactions.  
 CC -!- SUBUNIT: Interacts through its C-terminus with DLG4/PSD-95 third  
 CC P22 domain.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. (Potential).  
 CC -!- TISSUE SPECIFICITY: Expressed at highest levels in heart.  
 CC Expressed at lower levels in liver, skeletal muscle and pancreas  
 CC and at very low levels in brain.  
 CC -!- DISEASE: Defects in NLG4 may be the cause of X-linked autism  
 CC [MIM:306425]; a pervasive developmental disorder (PDD),  
 CC prototypically characterized by impairments in reciprocal social  
 CC interaction and communication, restricted and stereotyped patterns  
 CC of interests and activities, and the presence of developmental  
 CC abnormalities by 3 years of age.  
 CC -!- DISEASE: Defects in NLG4 may be the cause of Asperger syndrome  
 CC (AS), a form of childhood autism.  
 CC -!- SIMILARITY: Belongs to the type-B carboxy/esterase/lipase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AF376803; AAA66112.1; -  
 CC EMBL: AB03086; BAA6574.1; ALT -NT.  
 CC EMBL: BC034018; AAA34018.1; -  
 CC HSSP: P21836; IMAA.  
 CC Genbank: HGNC:14287; NLG4.  
 CC XIM: J30427; -  
 CC XIM: J30425; -  
 CC InterPro: IPR002018; Carboxesterab.  
 CC InterPro: IPR000460; Neuroigin.  
 CC InterPro: IPR000379; Ser ester\_site.  
 CC Pfam: PF03135; Coesteraseg; -  
 CC PRINTS: PR01090; NEUROIGIN.  
 CC PROSITE: PS00941; CARBOXYLESTERASE\_3\_2; -  
 CC Cell adhesion; Glycoprotein; Signal; Transmembrane.  
 CC FT SIGNAL 1 43  
 CC FT CHAIN 1 816 NEUROIGIN 4.  
 CC FT DOMAIN 44 675 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 677 697 POTENTIAL.  
 CC FT CYTOPLASMIC (POTENTIAL).  
 CC FT DISULFID 110 146 BY SIMILARITY.  
 CC FT DISULFID 306 317 BY SIMILARITY.  
 CC FT CARBOHYD 476 510 BY SIMILARITY.  
 CC FT CARBOHYD 102 102 N-LINKED (GLCNAC...); (POTENTIAL).  
 CC FT CARBOHYD 511 511 N-LINKED (GLCNAC...); (POTENTIAL).  
 CC SO SEQUENCE 816 AA; 91915 MW; EA1320D690F76BBD CRC64;  
 CC  
 CC Query Match 65.9%; Score 518; DB 1; Length 816;  
 CC Best Local Similarity 99.8%; Pred. No. 0;  
 CC Matches 658; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 CC  
 CC 155 DHDNNSKRPVNYHGGSSYEGGNMIDGSLASXGVYITINRGLIGFSTGDOA 218  
 CC 158 DHDNNSKRPVNYHGGSSYEGGNMIDGSLASXGVYITINRGLIGFSTGDOA 217  
 CC 219 AKGVGLDQIALFWIEENYGAFGDQPKRTTIPSGASASCVSLTLTSHSEGLFQKAT 278  
 CC 218 AKGVGLDQIALFWIEENYGAFGDQPKRTTIPSGASASCVSLTLTSHSEGLFQKAT 277  
 CC 279 IOSGALSSMAVNYOPAKYTRILADKVCNKLTTDNYECIRKNVKEIIQTTTPATYH 338  
 CC 278 IOSGALSSMAVNYOPAKYTRILADKVCNKLTTDNYECIRKNVKEIIQTTTPATYH 337  
 CC 339 IAFGVIGSDVPEDDPOLMEGEPFLANDIMLVNNGVSGELFVGVGVNEDGVPNPDF 398  
 CC 338 IAFGVIGSDVPEDDPOLMEGEPFLANDIMLVNNGVSGELFVGVGVNEDGVPNPDF 397  
 CC 399 SVSNFVDNLVGYPECKDRLRETIKFMYTDMAKDKNPRTKRTVALFTDHWAPAVA-A 457

DB 398 SVSNFVNDLYGSPGCKTJRETIKEMVTDMAKRENTRRKTLVALFTTHQVAFVATA 457  
QY 458 DHAQYGSPTTYFAFYAHQSEMKPSMDSAGDEVPVYVGGIPLMGPTLPSCHESANDY 517  
DB 458 DHAQYGSPTTYFAFYAHQSEMKPSMDSAGDEVPVYVGGIPLMGPTLPSCHESANDY 517  
QY 518 MSAVMTWTNTNPAKTGDPNQPVDPTKFIHTKPRFEFVMSKYNPKDQLYHIGAKPR 577  
DB 518 MSAVMTWTNTNPAKTGDPNQPVDPTKFIHTKPRFEFVMSKYNPKDQLYHIGAKPR 577  
QY 578 VEDHVRATKVAWMLSLVPHLNLNFIQVYSTTVVPPPECTSPRYGTRSPAKIWTTK 637  
DB 578 VEDHVRATKVAWMLSLVPHLNLNFIQVYSTTVVPPPECTSPRYGTRSPAKIWTTK 637  
QY 638 RPAITFANNPKSKDPKTKGPDPTVLLLETGRDYSLEDSVIAVAGASLFLFNIAFALY 697  
DB 638 RPAITFANNPKSKDPKTKGPDPTVLLLETGRDYSLEDSVIAVAGASLFLFNIAFALY 697  
QY 698 YKKDXRHEHTRHRRSPQRTVNDIAHIONEBSIQLMKOLEHDECELSQADTLRLTCP 757  
DB 698 YKKDXRHEHTRHRRSPQRTVNDIAHIONEBSIQLMKOLEHDECELSQADTLRLTCP 757  
QY 758 PNYTLTFRSPDIPCLNTENTITNPNLTGMPCHENTSSGGONSNIPLHSGSTRV 816  
DB 758 PNYTLTFRSPDIPCLNTENTITNPNLTGMPCHENTSSGGONSNIPLHSGSTRV 816

## RESULT 2

NGUY\_HUMAN STANDARD: PRT: 816 AA.

AC Q8NF23, Q9YZF8, (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Neurotigin 4, Y-linked precursor (Neurotigin Y).  
GN NGUY OR KIA0695..  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catartini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN 1)  
RX SEQUENCE FROM N.A. (ISOFORM 1).  
RP PubMed=12669065;  
RA Jamain S., Quach H., Betancur C., Rastan M., Colinaux C.,  
RA Silberberg I.C., Soderstrom H., Giroux B., Leboyer M., Gillberg C.,  
RA Bouteiron T., Nyden A., Philippe A., Cohen D., Chabane N.,  
RA Mouton-Rozeon V.C., Brice A., Sponheim E., Spunkland I.,  
RA Skjeldal O.H., Coleman M., Pearl P., Cohen I.L., Teouais J.,  
RA Zappella M., Menchetti G., Pompella A., Aschauer H., Van Nieuwenegem L.,  
RT "Mutations of the X-linked genes encoding neurotigin NGUY and NIGM4  
RT are associated with autism".  
RL Nat. Genet. 34:27-29(2003).  
RN 2)  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC -ISSUE=Brain;  
RA MEDLINE=99246063; PubMed=10231032;  
RA Nagase T., Iseikawa K.-I., Suyama M., Kikuno R., Hirasawa W.,  
RA Miyajima K., Tanaka A., Kotani H., Kozura K., Ohara O.,  
RT "Prediction of the coding sequences of unidentified human genes. XIII.  
RT The complete sequences of 106 new cDNA clones from brain which code  
RT for large proteins in vitro".  
RL CNA Res. 6:63-70(1999).  
CC -1- FUNCTION: Putative neuronal cell surface protein involved in cell-  
CC cell-interactions.  
CC -1- STRUCT: Interacts through its C-terminus with DCAF-95 third  
CC PD2 domain (by similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q8NF23-1; Sequence=D:spliced;  
CC Name=2;  
CC IsoId=Q8NF23-2; Sequence=VSP\_007537;

CC Note=No experimental confirmation available;  
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

CC EMBL: AF376604; AA046113.2;  
CC EMBL: AB023168; BA076795.1;  
CC InterPro: IPR002018; Carboxylesterase.  
CC InterPro: IPR004600; Neurotigin.  
CC InterPro: IPR003799; Ser\_esterase.  
CC Pfam: PF00135; Coesterase; 1.  
CC PRINTS: PR01090; NEUROLIGIN.  
CC PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
CC Cell adhesion; Glycoprotein; signal; Transmembrane;  
CC Alternative splicing.  
CC FT SIGNAL 43  
CC CHAIN 44 816 POTENTIAL.  
CC DOMAIN 44 676 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 677 697 POTENTIAL.  
CC DOMAIN 698 816 CYTOPLASMIC (POTENTIAL).  
CC DISULFID 110 146 BY SIMILARITY.  
CC DISULFID 306 317 BY SIMILARITY.  
CC DISULFID 476 510 BY SIMILARITY.  
CC CARBOHYD 102 102 N-LINKED (GLCNAc...) (POTENTIAL).  
CC FT CARBOHYD 511 511 N-LINKED (GLCNAc...) (POTENTIAL).  
CC FT VARSPLIC 1 168 Missing (in isoform 2).  
CC FT SQ SEQUENCE 816 AA; 92020 MW; F86893073B1BBF6 CRC64;

Query Match 40.0%; Score 326; DB 1; Length 816;  
Best Local Similarity 99.6%; Pred. No. 0;

Matches 546; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 163 QNSKRPVWYIHGSGYMEGTGMI DGSILASGVNVIYITINVRIGLIGFLSTGQAAKN 222  
DB 162 QNSKRPVWYIHGSGYMEGTGMI DGSILASGVNVIYITINVRIGLIGFLSTGQAAKN 221  
QY 223 YGLDQIQALRKLEENVAFGDPKRVVTFSSGAGASVSLTSHSESGFQAAIIOSG 282  
DB 222 YGLDQIQALRKLEENVAFGDPKRVVTFSSGAGASVSLTSHSESGFQAAIIOSG 281  
QY 283 TALSSMAVNYCPAKYTRILADKVGQNM LDTDMECLENKYKELIQOTTIPATYHIAFG 342  
DB 282 TALSSMAVNYCPAKYTRILADKVGQNM LDTDMECLENKYKELIQOTTIPATYHIAFG 341  
QY 343 PVIDGQVLPDQFQILMEGFLNLTDMIGVNGSGGLKFGVDSIVNEGCVTFPNDPDSVSN 402  
DB 342 PVIDGQVLPDQFQILMEGFLNLTDMIGVNGSGGLKFGVDSIVNEGCVTFPNDPDSVSN 401  
QY 403 FVNDLYGPRGKDTLRETIKEMVTDMAKRENTRRKTLVALFTDHQVAFVATAADLHA 461  
DB 402 FVNDLYGPRGKDTLRETIKEMVTDMAKRENTRRKTLVALFTDHQVAFVATAADLHA 461  
QY 462 QVGSPTTYFAFYAHQSEMKPSMDSAGDEVPVYVGGIPLMGPTLPSCHESANDY 521  
DB 462 QVGSPTTYFAFYAHQSEMKPSMDSAGDEVPVYVGGIPLMGPTLPSCHESANDY 521  
QY 522 VNMVTVTNPAKTGDPNQPVDPTKFIHTKPRFEFVMSKYNPKDQLYHIGAKPRVDRH 581  
DB 522 VNMVTVTNPAKTGDPNQPVDPTKFIHTKPRFEFVMSKYNPKDQLYHIGAKPRVDRH 581  
QY 582 YKATVAEMLSLVPHLNLNFIQVYSTTVVPPPECTSPRYGTRSPAKIWTTKPAI 641  
DB 582 YKATVAEMLSLVPHLNLNFIQVYSTTVVPPPECTSPRYGTRSPAKIWTTKPAI 641  
QY 642 TPANNPKSKDPKTKGPDPTVLLLETGRDYSLEDSVIAVAGASLFLFNIAFALYKKD 701  
DB 642 TPANNPKSKDPKTKGPDPTVLLLETGRDYSLEDSVIAVAGASLFLFNIAFALYKKD 701



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642 IPANNPKHSHKSPHNGIPEDTIVLTETKADYSIEVTVAVGASLFLNLAFAALYYKKD 70:
CY 702 KRRETHR 709
DB 702 KRRETHR 709

RESULT 3
NCBI_MACNU
ID NCBI_MACNU STANDARD: PRT: 213 AA.
AC Q9MMG7:
DT 15-SEP-2003 (rel. 42, Created);
DT 15-SEP-2003 (rel. 42, Last sequence update);
DT 15-SEP-2003 (rel. 42, Last annotation update);
DE Neuroligin 4 (Fragment).
GN NCNG4.
OS Macaca mulatta (Rhesus macaque);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN 1:
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RA Mungest A.E., Ojeda S.R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBCP databases.
CC - FUNCTION: Putative neuronal cell surface protein involved in cell-
CC cell-interactions (by similarity).
CC - SUBMIT: Interacts through its C-terminus with DISC4/PSD-95 third
CC PDZ domain (by similarity).
CC - SIMILARITY: Belongs to the type-B carboxy-peptidase/ligase family.
CC This SNIS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb.ch).
CC
DR EMBL: AF462636; AAL66382.1;
DR PROSITE: PS00941; CARBOXYPEPTIDASE_B_2: PARTIAL.
KM Cell adhesion; Transmembrane.
FT NON_TER 1
FT DOMAIN <1 73 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 74 94 POTENTIAL.
FT DOMAIN 95 213 CYTOPLASMIC (POTENTIAL).
SO SEQUENCE 213 AA: 24036 MW; CAF21610035C660B CRC64;

Query Match 26.1%; Score 213; DB 1; Length 213;
Best Local Similarity 100.0%; Pred.No. 1.4e-212;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID NCBI_HUMAN STANDARD: PRT: 840 AA.
AC Q9N07: Q9N072;
DT 15-SEP-2003 (rel. 42, Created);
DT 15-SEP-2003 (rel. 42, Last sequence update);
DT 15-SEP-2003 (rel. 42, Last annotation update);
DE Neuroligin 1 precursor.
GN NCNG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1:
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA MEDLINE=99397452; PubMed=10470851;
RX Kikuno R., Nagase T., Shikawa K.-I., Hirosawa Y., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RN 2:
RX DNA Res. 6:197-205 (1999).
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Endothelium;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feilgenfeldt E.A., Grosse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang C., Hsieh F.,
RA Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshynski S., Carrinzi P., Prange C.,
RA Raha S.S., Loque, J.N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Sosak S.A., McEwan P.C., McKernan K.J., Malek C.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muey W.M., Soergers E.O., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting Y., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Bittencourt A.C., Krzywicki M.T., Skalski U., Smalins D.E.,
RA Schenker A., Schein C.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN 3:
RX Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE OF 315-823 FROM N.A.
RC TISSUE=Embryo;
RA Itoigai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saito K.,
RA Yamamoto C., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Hattori Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "XEDD human cDNA sequencing project.";
RN 4:
RX Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RP CONCEPTUAL TRANSLATION (ISOFORM 1).
RA Roehrer B.;
RN 5:
RX Unpublished observations (MAY-2003).
RP INTERACTION WITH DISC4.
RX PubMed=9278515;
RA Irie M., Hata Y., Takeuchi M., Ichtchenko K., Toyoda A., Hirao K.,
RA Takai Y., Rosahl T.W., Suedhof T.C.;
RT "Binding of neuroligins to PSD-95.";
RN 6:
RX Science 277:1511-1515 (1997).
RP FUNCTION.
RX PubMed=10892652;
RA Scheiffele P., Fan J., Cho J., Fetter R., Serafini T.;
RT "Neuroligin expressed in nonneuronal cells triggers presynaptic
RT development in contacting axons.";
RN 7:
RX Cell 101:657-669 (2000).

```

CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in  
CC cell-cell interactions by forming intercellular junctions through  
CC binding to beta-neurexins. Seems to play role in formation or  
CC maintenance of synaptic junctions. In vitro, triggers the de novo  
CC formation of presynaptic structures. May be involved in  
CC specification of excitatory synapses.  
CC -1- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and  
CC neuexin 3-beta (By similarity). Interacts through its C-terminus  
CC with DLG4/PSD-95 third PDZ domain.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Enriched in  
CC synaptic plasma membranes and clustered in synaptic clefts and  
CC postsynaptic densities (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q99K10-1; Sequence=D:displayed;  
CC Note=No experimental confirmation available;  
CC Name=2;  
CC IsoId=Q99K10-2; Sequence=VSP\_007527;  
CC -1- PTM: N- and O-glycosylated (By similarity).  
CC -1- SIMILARITY: Belongs to the type-B carboxy-esterase/lipase family.  
CC -----  
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CC -----  
CC EMBL: AB028993; BAA33022.1;  
CC EMBL: BC032555; AAH32555.1;  
CC EMBL: AK074522; BAC11039.1; AL2\_1117.  
CC HSPB: P21836; 1MAA.  
CC DR HSPB: HSPB:14291; NLGN1.  
CC DR MIM: 600568;  
CC DR InterPro: IPR002218; CarboxylesteraseB.  
CC DR InterPro: IPR000460; NeuroLigin.  
CC DR InterPro: IPR000379; Ser\_esterase.  
CC DR Pfam: PF00135; Coesterase; 1.  
CC DR PRINTS: PR01080; NEUROLIGIN.  
CC DR PROSITE: PS00941; CARBOXYESTERASE\_3\_2; 1.  
CC KM Cell adhesion; Glycoprotein; Signal; Transmembrane;  
CC KM Alternative splicing.  
CC FT SIGNAL 45  
CC FT CHAIN 46  
CC FT DOMAIN 46  
CC FT TRANSMEM 695  
CC FT DOMAIN 7-6  
CC FT DISULFID 1-2  
CC FT DISULFID 3-9  
CC FT DISULFID 359  
CC FT DISULFID 543  
CC FT CARBOHYD 103  
CC FT CARBOHYD 303  
CC FT CARBOHYD 340  
CC FT CARBOHYD 544  
CC FT VARPPLIC 181  
CC FT CONFIDICT 711  
CC SC SEQUENCE 940 AA; 93835 MW; A3FE21716F62DE29 CEC64;  
Query Match 6.1%; Score 50; DB 1; Length 940;  
Best Local Similarity 100.0%; Pred. No. 3.7e-43;  
Matches 50; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
OY 510 CFEKNDVYLSAVNTYWTNPAKTGPRQPVQCTKTKTKNFEEVAV 553  
DB 543 CFEKNDVYLSAVNTYWTNPAKTGPRQPVQCTKTKTKNFEEVAV 592  
RESULT 5  
NG1\_MOUSE STANDARD: PRT; 843 AA.  
ID NG1\_MOUSE

AC Q99K10;  
CC 15-SEP-2003 (Rel. 42, Created)  
CC 15-SEP-2003 (Rel. 42, Last sequence update)  
CC 15-SEP-2003 (Rel. 42, Last annotation update)  
CC NEUOLIGIN\_1 precursor.  
CC NLGN1 OR KIAA1370.  
CC Mus musculus (mouse).  
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CC NCBI\_TaxID=10090.  
CC (1)  
CC SEQUENCE FROM N.A. (ISOFORM 1).  
CC TISSUE=Brain;  
CC MEDLINE=22579291; PubMed=12693551;  
CC Okazaki N., Kikuno R., Ohara R., Iizawa H., Yusa S.,  
CC Nakajima D., Nagase T., Ohara R., Koga H.,  
CC Prediction of the coding sequences of 400 mouse KIAA-homologous  
CC cDNAs identified by screening of terminal sequences of cDNA clones  
CC randomly sampled from size-fractionated libraries.";  
CC [2]  
CC SEQUENCE FROM N.A. (ISOFORM 2).  
CC MEDLINE=22388257; PubMed=1247932;  
CC Strussberg R., Feingold E.A., Grouse L.H., Derge J.G.,  
CC Krasner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
CC Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,  
CC Brownstein M.J., Usdin T.B., Yoshizaki S., Carrinci P., Prange C.,  
CC Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
CC Fahy J., Heltzer E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
CC Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
CC Blakesley R.C., Grimwood J., Green E.D., Dickson M.C.,  
CC Rodriguez A.W., Touchman J.W., Schmutz J., Myers R.M.,  
CC Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smatius D.E.,  
CC Scherch A., Schein J.F., Jones S.J.M., Marra M.A.,  
CC "Generation and initial analysis of more than 15,000 full-length human  
CC and mouse cDNA sequences.";  
CC Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
CC (3)  
CC TISSUE SPECIFICITY.  
CC PubMed=11329178;  
CC Gilbert M., Smith J., Roskams A.J., Auld J.V.,  
CC "NeuroLigin 3 is a vertebrate gliotactin expressed in the olfactory  
CC ensheathing glia: a growth-promoting class of macroglia.";  
CC Glia 34:155-164(2001).  
CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in  
CC cell-cell interactions by forming intercellular junctions through  
CC binding to beta-neurexins. Seems to play role in formation or  
CC maintenance of synaptic junctions. In vitro, triggers the de novo  
CC formation of presynaptic structures (By similarity). May be  
CC involved in specification of excitatory synapses.  
CC -1- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and  
CC neuexin 3-beta, and through its C-terminus with DLG4/PSD-95 third  
CC PDZ domain (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Enriched in  
CC synaptic plasma membranes and clustered in synaptic clefts and  
CC postsynaptic densities (By similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC Note=No experimental confirmation available;  
CC IsoId=Q99K10-1; Sequence=D:displayed;  
CC Name=2;  
CC IsoId=Q99K10-2; Sequence=VSP\_007528, VSP\_007529, VSP\_007530;  
CC Note=No experimental confirmation available;  
CC -1- TISSUE SPECIFICITY: Expressed in olfactory bulb.  
CC -1- PTM: N- and O-glycosylated (By similarity).  
CC

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CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL: AK122433; BAC65715.1; ALT_INIT.
DR EXBL: BC005523; AAH05523.1; ..
DR HSSP: P30122; 28CE.
DR MGD: MGI:2179435; N.gn1.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000460; Neuro1igin.
DR InterPro: IPR000379; Ser esterase_site.
DR Pfam: PF00135; Coesterase; ..
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
KW Alternative splicing.
FT SIGNAL 1
FT CHAIN 45
FT DOMAIN 46 843
FT TRANSMEM 46 697
FT TRANSMEM 698 718
FT DOVAIN 719 843
FT CARBOHYD 109 109
FT CARBOHYD 303 303
FT CARBOHYD 343 343
FT CARBOHYD 547 547
FT DISULFID 117 153
FT DISULFID 342 353
FT DISULFID 512 546
FT VASPLC 165 184
FT VASPLC 235 269
FT TITRTISRAVACALRTKGGCFPRQATKKE (in isoform 2);
FT VARSPLC 270 843
FT SEQUENCE 843 AA; 94149 MW; 69E50703CF7D251F CRC64;
SQ
Query Match 6.1%; Score 50; DB 1; Length 843;
Best Local Similarity 100.0%; Pred. No. 3.7e-03;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 510 CNFSNDVMSAVVMTWTWTFNFAKCGDPNQPVCOTKFRITKPRNFEEVAV 559
DB 546 CNFSNDVMSAVVMTWTWTFNFAKCGDPNQPVCOTKFRITKPRNFEEVAV 595
RESULT 6
N_G1_RAT
ID N_G1_RAT STANDARD; PRT; 843 AA.
AC Q62765;
DT 15-SEP-2003 (Rel. 42; Created)
DT 15-SEP-2003 (Rel. 42; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Neuro1igin 1 precursor (Neuro1igin I).
GN NLGN1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2, 3 AND 4), PARTIAL SEQUENCE,
RP CHARACTERIZATION, AND INTERACTION WITH NEUREXIN 1-BETA.
RC TISSUE=Brain;
RX MEDLINE=95254653; PubMed=7736595;
RX Ichtchenko K., Hata Y., Nguyen T., Ullrich B., Missler M., Xoomaw C.,
RX Suedhof T.C.;
RX "Neuro1igin 1: a splice site-specific ligand for beta-neurexins";

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RU Cell 81:435-443(1995).
RN [2]
RP INTERACTION WITH NEUREXIN 1-BETA, AND FUNCTION.
RX MEDLINE=97467410; PubMed=9325340;
RA Nguyen T., Suedhof T.C.;
RA "Binding properties of neuro1igin 1 and neuroxin 1beta reveal function
RA as heterophilic cell adhesion molecules.";
RL J. Biol. Chem. 272:26032-26039(1997).
RN [3]
RP BLOCKAGE OF N-TERMINUS, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN
RP 2-BETA AND NEUREXIN 3-BETA.
RX MEDLINE=96162010; PubMed=8576240;
RA Ichtchenko K., Nguyen T., Suedhof T.C.;
RA "Structures, alternative splicing, and neuroxin binding of multiple
RA neuro1igins.";
RL J. Biol. Chem. 271:2676-2682(1996).
RN [4]
RP TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX PubMed=9927700;
RX Song U.-Y., Ichtchenko K., Suedhof T.C., Brose N.;
RX "Neuro1igin 1 is a postsynaptic cell-adhesion molecule of excitatory
RX synapses.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1100-1105(1999).
RN [5]
RP TISSUE SPECIFICITY.
RX PubMed=11329178;
RA Gilbert M., Smith J., Roskams A.J., And V.J.;
RA "Neuro1igin 3 is a vertebrate gliotactin expressed in the olfactory
RA ensheathing glia, a growth-promoting class of macroglia.";
RL Glia 34:151-164(2001).
RN [6]
RP FUNCTION: Neuronal cell surface protein thought to be involved in
RP cell-cell interactions by forming intercellular junctions through
RP binding to beta-neurexins. Seems to play role in formation or
RP maintenance of synaptic junctions. In vitro, triggers the de novo
RP formation of presynaptic structures (By similarity). May be
RP involved in specification of excitatory synapses.
RN [7]
RP SUBUNIT: Interacts with neuroxin 1-beta isoforms 3/beta 4B5A and
RP 4/beta 4B5B. Interacts with neuroxin 2-beta isoforms 3/beta 4B5A,
RP 4/beta 4B5B, 7/beta 4B5A6 and 8/beta 4B5B6. Interacts with
RP corresponding neuroxin 3-beta isoforms. Interacts through its C-
RP terminus with DLG4/PSD-95 third PDZ domain (By similarity).
RN [8]
RP SUBCELLULAR LOCATION: Type I membrane protein. Enriched in
RP synaptic plasma membranes and clustered in synaptic clefts and
RP postsynaptic densities. Colocalized with DLG4/PSD-95 and
RP WMAPR1/glutamate (WMDA) receptor subunit zeta 1.
RN [9]
RP ALTERNATIVE PRODUCTS:
RP Event=Alternative splicing; Named isoforms=4;
RP Name=1;
RP IsoId=Q62765-1; Sequence=Displayed;
RP Name=2;
RP IsoId=Q62765-2; Sequence=VSP_007531; VSP_007532;
RP Note=No experimental confirmation available;
RP Name=3;
RP IsoId=Q62765-3; Sequence=VSP_007532;
RP Name=4;
RP IsoId=Q62765-4; Sequence=VSP_007531;
RN [10]
RP TISSUE SPECIFICITY: Expressed in brain, almost exclusively in
RP neurons, and spinal chord.
RN [11]
RP DEVELOPMENTAL STAGE: Expression is low in embryonic brains (E12-
RP E16) but increases dramatically after birth (postnatal days P0-P3)
RP and reaches a plateau during the period when most synapses are
RP formed (P5-P8).
RN [12]
RP PTM: N- and O-glycosylated.
RN [13]
RP PTM: The N-terminus is blocked.
RN [14]
RP SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
RN [15]
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RP or send an email to license@isb-sib.ch).

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RN [1]
RP INTERACTION WITH DLG4.
RX PubMed=9278515;
RA Irie Y., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,
RA Takai Y., Rosahl T.W., Suedhof T.C.;
RT "Binding of neuroligins to PSD-95."
RL Science 277:1511-1515(1997).
RF .
RE FUNCTION:
RX PubMed=10892652;
RA Scheiffele P., Fan J., Choeh J., Fetter R., Serafini T.;
RT "Neuroigin expressed in nonneuronal cells triggers presynaptic
RT development in contacting axons."
RL Cell 101:657-669(2000).
CC -- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell interactions by forming intercellular junctions through
CC binding to beta-neurexins. Seems to play role in formation or
CC maintenance of synaptic junctions. In vitro, triggers the de novo
CC formation of presynaptic structures.
CC -- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and
CC neuexin 3-beta (by similarity). Probably interacts through its C-
CC terminus with DGK/PD-95 third PDZ domain.
CC -- SIMILARITY LOCATION: Type I membrane protein (Potential).
CC -- SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announc/
CC or send an email to license@isb-sib.ch).
CC -----
DR EXBL: AF376802; AAA6111.1; -
DR EMBL: AB037787; BAA92604.1; -
DR HSSP: P21836; INKA.
DR Genew: HGNC:14290; NLGN2.
DR MIM: 606479; -
DR InterPro: IPR002019; CarbesteraseB.
DR InterPro: IPR000460; Neuroligin.
DR InterPro: IPR003379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PRINTS: PRO1090; NEUROLOGIN.
DR ProSITE: PS00941; CARBOXYLESTERASE_B_2.1.
KW Cell adhesion; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 15
FT CHAIN 1 635
FT DOMAIN 15 677
FT TRANSMEM 678 698
FT TRANSMEM 699 835
FT DOMAIN 836 855
FT 7-SULFID 106 141
FT FT DISULFID 317 328
FT DISULFID 487 521
FT CARBOHYD 98 98
FT CARBOHYD 136 136
FT CARBOHYD 522 522
SQ GARBHYD 835 AA; 90819 MW; 359938630193587 CRC64;
SEQUENCE

Query Match 5.9%; Score 48; DB 1; Length 835;
Best Local Similarity 100.0%; Freq. No. 4,3e-41;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

521 CNPSKDVMLSAVNMTWTWTFPAKTGPDPNGVPCDDTKFTITKRNPREEV 557
|||||
AC Q62888; STANDARD; PRT; 836 AA.
ID _NLGN2_RAT
AC Q62888;
ID 15-SEP-2003 (rel. 42, Created)
ID 15-SEP-2003 (rel. 42, Last sequence update)

```

DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE NeuroLigin 2 precursor.  
 GN NLGN2.  
 CS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF N-TERMINUS, TISSUE  
 RP SPECIFICITY, AND INTERACTION WITH NEUREXIN 1-BETA, NEUREXIN 2-BETA AND  
 RP NEUREXIN 3-BETA.  
 RC TISSUE=Forebrain;  
 RX MEDLINE=96162010; PubMed=9576240;  
 RA Ichtchenko K., Nguyen T., Suedhof T.C.,  
 RT "Structures, alternative splicing, and neurexin binding of multiple  
 RT neuroLigins";  
 RL J. Biol. Chem. 277:2676-2682(1996).  
 RN (2)  
 RP TISSUE SPECIFICITY.  
 RX PubMed=11329178;  
 RA Gilbert M., Smith J., Postkams A.O., Auld V.J.;  
 RT "NeuroLigin 3 is a vertebrate gliotactin expressed in the olfactory  
 RT ensheathing glia, a growth-promoting class of "macroglia";  
 RL Glia 34:151-164(2001).  
 CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in  
 CC cell-cell interactions by forming intercellular junctions through  
 CC binding to beta-neurexins. Seems to play role in formation or  
 CC maintenance of synaptic structures. In vitro, triggers the de novo  
 CC formation of presynaptic structures (By similarity).  
 CC -1- SUBUNIT: Interacts with neurexin 1-beta isoforms 3/Beta 4B5A and  
 CC 4/Beta 4B5B. 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with  
 CC neurexin 3-beta. Probably interacts through its C-terminus with  
 CC DLG4/PSD-95 third PDZ domain (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named Isoform=2;  
 CC Name=1;  
 CC IsoId=Q62888-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q62888-2; Sequence=VSP 007533;  
 CC -1- TISSUE SPECIFICITY: Expressed in brain, spinal chord and dorsal  
 CC root ganglion.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -----  
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 CC -----  
 DR EMBL: U41662; AAA97870.1; -;  
 DR HSPB: P37967; IOE3.  
 DR InterPro: IPR002013; Carboxylesterase.  
 DR InterPro: IPR000460; NeuroLigin.  
 DR InterPro: IPR003379; Ser\_estr\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS: PR01090; NEUROLIGIN.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; -;  
 KM Cell adhesion; Glycoprotein; Signal; Transmembrane;  
 KW Alternative splicing.  
 FT SIGNAL 1 14  
 FT CHAIN 15 836  
 FT DOMAIN 15 678  
 FT TRANSMEM 679 699  
 FT DOMAIN 700 836  
 FT DISULFID 106 144  
 FT DISULFID 317 328  
 FT DISULFID 487 522  
 FT CARBOHYD 98 98  
 FT CARBOHYD 136 136  
 N-LINKED (GLCNAC...); (POTENTIAL).  
 N-LINKED (GLCNAC...); (POTENTIAL).  
 N-LINKED (GLCNAC...); (POTENTIAL).

FT CARBOHYD 522 522 N-LINKED (GLCNAC...); (POTENTIAL).  
 FT VARSPLIC 153 169 Missing (in isoform 2).  
 FT FTID=VSP\_007533.  
 SC SEQUENCE 836 AA; 90961 MW; 1AD51CB1BE4BF9CF CRC64;  
 Query Match 5.9%; Score 48; DB 1; Length 836;  
 Best Local Similarity 100.0%; Pred. No. 4,3e-41;  
 Matches 48; Conservative 0; Indels 0; Gaps 0;  
 510 CNFSNDMLSAVMTYNTNPAKTGDPQOPQDPQKPIHTKPNRFEV 557  
 521 CNFSNDMLSAVMTYNTNPAKTGDPQOPQDPQKPIHTKPNRFEV 568  
 RESCUT 9  
 ID NLG3 HUMAN STANDARD; PRT; 848 AA.  
 AC Q9NZ34; Q9NZ34; Q9NZ35; Q9NZ36; Q9NZ37; Q9NZ48;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE NeuroLigin 3 precursor (Gliotactin homolog).  
 GN NLGN3 OR NL3 OR KIAA1482.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=20231756; PubMed=10767552;  
 RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin P.Y., Gims E.I.;  
 RT "The structure and expression of the human neuroLigin-3 gene";  
 RL Gene 246:303-310(2000).  
 RN (2)  
 RP SEQUENCE OF 12-848 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=20277482; PubMed=10819333;  
 RA Nagase T., Kikuno R., Ichikawa K., Hirosewa Y., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XVII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RL for large proteins in vitro.";  
 RL DNA Res. 7:143-150(2000).  
 RN (3)  
 RP SEQUENCE OF 410-848 FROM N.A.  
 RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
 RA Yamamoto Y., Wakamatsu A., Nakamura Y., Kojima S., Nagabari K.,  
 RA Kasuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
 RA Hattori A., Okumura K., Iwayanagi T., Niimoriya K.;  
 RT "NEO human cDNA sequencing project.";  
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.  
 RN (4)  
 RP INTERACTION WITH DLG4.  
 RX PubMed=9278515;  
 RA Irie M., Hata Y., Takeuchi M., Ichtchenko K., Toyoda A., Hirao K.,  
 RA Takai Y., Rosahl T.W., Suedhof T.C.;  
 RT "Binding of neuroLigins to PSD-95.";  
 RL Science 277:1511-1515(1997).  
 RN (5)  
 RP VARIANT X-LINKED AUTISM CYS-451.  
 RX PubMed=12669065;  
 RA Jamain S., Quach H., Betancur C., Rastam M., Colineaux C.,  
 RA Gillberg I.C., Soderstrom H., Gires B., Leboyer M., Gillberg C.,  
 RA Bourgeron T., Nyden A., Philippe A., Cohen D., Chabane N.,  
 RA Mouren-Simeoni M.C., Brice A., Sponheim E., Spunkland L.,  
 RA Skjeldal O.H., Coleman M., Pearl P.L., Cohen I.L., Tsiftouris J.,  
 RA Zappella M., Menchetti G., Pompella A., Aschauer H., Van Maldergem T.;  
 RT "Mutations of the X-linked genes encoding neuroLigins NLGN3 and NLGN4  
 RT are associated with autism.";  
 RL Nat. Genet. 34:27-29(2003).  
 CC -1- FUNCTION: Neuronal cell surface protein thought to be involved in  
 CC cell-cell interactions by forming intercellular junctions through  
 CC binding to beta-neurexins. May play a role in formation or

RESULT 10	NCBI_MOUSE	STANDARD:	PRG:	825 AA:
AC	OBRYM5: OBRYM4:			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
FT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DE	Neuro-1,igin 3 precursor (G1otactin homolog)			
GN	Neuro-1,igin 3 precursor (G1otactin homolog)			
OS	Mus musculus (Mouse)			
CC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
CC	Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus.			
OX	NCBI_TaxID=10990;			
EN	11			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN=C57BL/6J; TISSUE=Hypothalamus, and Retina;			
RX	MEDLINE=22354683; PubMed=1246851;			
RA	Chazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikaido I., Otsu N., Saito R., Suzuki T., Yamazaki T., Miyamoto T.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenck G., Gajdarski T.,			
RA	Belldrelli R., Hall D.P., Holt C., Hume D.A., Quackenbush D.,			
RA	Schirrali L.M., Karpman A., Matsuda H., Batalov S., Betsel K.W.,			
RA	Blake J.A., Bixby D., Busic V., Chochia C., Corbani L.E., Cousins S.,			
RA	Dalla E.E., Dragani T.A., Fletcher C.F., Forrest A., Prazar K.S.,			
RA	Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustinech S., Hirokawa N., Jackson I.J., Jarvis E.D.,			
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,			
RA	Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,			
RA	Maglott D.R., Malraiz L., Marchionni L., McKenzie L., Miki H.,			
RA	Nagatsuma T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,			
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,			
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,			
RA	Sandelin A., Schneider C., Sempke C.A., Setou Y., Shimada K.,			
RA	Sutiana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,			
RA	Veratini R., Wagner L., Walsby J., Wang Y., Watanabe Y., Wells C.,			
RA	Willing L.G., Wyszewski B., Yamaguchi M., Yang L., Yang L.,			
RA	Yan Z., Yanolun M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,			
RA	Hirozane-Kikuchi T., Kono H., Nakamura M., Sakazume N., Sato K.,			
RA	Shiraki T., Maki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,			
RA	Hara A., Hashizume W., Imciani K., Ishii Y., Itoh M., Kagawa I.,			
RA	Myazaki A., Sakai K., Sasaki D., Shibata K., Shiragawa A.,			
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers T.,			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573 (2002).			
RN	12			
RP	TISSUE SPECIFICITY, AND DEVELOPMENTAL STGE.			
RA	PubMed=11329178;			
RA	Gilbert M., Smith J., Roskams A.J., Auld V.J.;			
RT	"Neuro-1,igin 3 is a vertebrate gliotactin expressed in the olfactory			
RT	enkephalin gliotactin, a growth-promoting class of macroglia."			
RL	Glia 34:151-164 (2001).			
CC	-1- FUNCTION: Neuronal cell surface protein thought to be involved in			
CC	cell-cell interactions by forming intercellular junctions through			
CC	binding to beta-neurexins. May play a role in formation or			
CC	maintenance of synaptic junctions. May also play a role in glia-			
CC	glia or glia-neuron interactions in the developing peripheral			
CC	nervous system.			
CC	-1- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and			
CC	neuexin 3-beta, and probably through its C-terminus with			
CC	DUGA/PSD-95 third PDZ domain (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).			
CC	-1- TISSUE SPECIFICITY: Expressed in olfactory bulb and olfactory			
CC	epithelium. Found in olfactory ensheathing glia but not in			
CC	olfactory neurons, and in developing peripheral glia.			
CC	-1- DEVELOPMENTAL STGE: Detected at embryonic day E11 and postnatal			
CC	day P1 in retinal astrocytes, spinal chord astrocytes and Schwann			
CC	cells of the dorsal root ganglion.			
CC	-1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.			



```

DE  Neurotigin 3 (Glialectin homolog) (Fragment).
CN  NLGN3.
OS  Macaca mulatta (Rhesus macaque).
CC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  Mammalia; Eutheria; Primates; Catarrhini; Corcolithectidae;
CC  Cercopitheciinae; Macaca.
CN  NCBI_TaxID=9544;
RX  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Hypothalamus;
RA  Mendenhall A.E., Ojeda S.R.;
RL  Submitted (SEP-2001) to the EMBL/GenBank/DBS databases.
CC  -1- FUNCTION: Neuronal cell surface protein thought to be involved in
CC  cell-cell interactions by forming intercellular junctions through
CC  binding to beta-neurexins. May play a role in formation or
CC  maintenance of synaptic junctions. May also play a role in glia-
CC  glia or glia-neuron interactions in the developing peripheral
CC  nervous system.
CC  -1- SUBUNIT: Interacts with neuexin 1-beta, neuexin 2-beta and
CC  neuexin 3-beta, and probably through its C-terminus with
CC  DLG4/PSD-95 third PDZ domain (5% similarity).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC  -1- SIMILARITY: Belongs to the type-B carboxylesterase/-lipase family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  the European Bioinformatics Institute. There are no restrictions on its
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF424950; AAL40263.1; -
DR  InterPro: IPR02015; Carboxesterases.
DR  InterPro: IPR000463; Neurotigin.
DR  Pfam: PF00135; Coesterase; 1.
DR  PRINTS: PR01090; NEUROIGLIN.
DR  PROSITE: PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW  Cell adhesion; Glycoprotein.
FT  NON TER 1 1
FT  DOMAIN <1 >202 EXTRACELLULAR (POTENTIAL).
FT  DISULFID 15 49 BY SIMILARITY.
FT  CARBOHYD 50 50 N-LINKED (GLCNAC... ) (POTENTIAL).
FT  NON TER 202 202
SQ  SEQUENCE 202 AA; 22897 MW; 996C2C5B7C28E158 CRC64;

Query Match 3.4%; Score 28; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.8e-2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY  510 CNEKQDVMLSAVMTYTNFAKTGDPN 537
DB  49 CNEKQDVMLSAVMTYTNFAKTGDPN 76

RESULT 13
BAL_HUMAN STANDARD; FRT; 742 AA.
AC  p19835;
CD  01-FEB-1991 (Rel. 17, Created;
CD  01-APR-1993 (Rel. 25, Last sequence update);
CD  15-SEP-2003 (Rel. 42, Last annotation update);
CD  15-SEP-2003 (Rel. 42, Last annotation update);
DE  Bile-salt-activated lipase precursor (EC 3.1.1.3) (EC 3.1.1.13) (SAL)
DE  (Bile-salt-activated lipase) (BSAL) (Carboxyl ester lipase) (Sterol
DE  esterase) (Cholesterol esterase) (Pancreatic lysophospholipase).
GN  CEL OR BAL.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC  TISSUE=Mammary gland;

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```

RX  MEDLINE=91062144; PubMed=1698625;
RA  Nilsson J., Blaaberg U., Carlsson P., Enerbaeck S., Hennell O.,
RA  Bjursell G.;
RA  "cDNA Cloning of human-milk bile-salt-stimulated lipase and evidence
RA  for its identity to pancreatic carboxylic ester hydrolase.";
RT  Eur. J. Biochem. 192:543-550(1990).
EN  (2)
RP  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC  TISSUE=pancreas;
RA  MEDLINE=91092392; PubMed=2265692;
RA  Hul D.Y., Kiesel J.A.;
RA  "Sequence identity between human pancreatic cholesterol esterase and
RA  bile salt-stimulated milk lipase.";
RT  FEBS Lett. 276:131-134(1990).
EN  (3)
RP  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC  TISSUE=Mammary gland;
RA  MEDLINE=9105134; PubMed=1988041;
RA  Baba T., Downs D., Jackson K.W., Tang J., Wang C.-S.;
RA  "Structure of human milk bile salt activated lipase.";
RT  Biochemistry 30:500-510(1991).
EN  (4)
RP  SEQUENCE FROM N.A.
RA  MEDLINE=92347859; PubMed=1639390;
RA  Lidberg U., Nilsson J., Stromberg K., Stenman G., Sahlin P.,
RA  Enerbaeck S., Bjursell G.;
RA  "Genomic organization, sequence analysis, and chromosomal
RA  localization of the human carboxyl ester lipase (CEL) gene and a
RA  cell-like (CEL) gene.";
RT  Genomics 13:630-640(1992).
EN  (5)
RP  PARTIAL SEQUENCE, AND ACTIVE SITE.
RA  MEDLINE=91122282; PubMed=1991511;
RA  Christie D.L., Cleverly D.R., O'Connor C.J.C.;
RA  "Human milk bile-salt stimulated lipase. Sequence similarity with rat
RA  lysophospholipase and homology with the active site region of
RA  cholinesterases.";
RT  FEBS Lett. 276:190-194(1991).
EN  (6)
RP  CARBOHYDRATE-LINKAGE SITES.
RA  MEDLINE=9538331; PubMed=7654718;
RA  Wang C.S., Dashi A., Jackson K.W., Yeh J.C., Cummings R.D.,
RA  Tang J.;
RA  "Isolation and characterization of human milk bile salt-activated
RA  lipase C-cell fragment.";
RT  Biochemistry 34:10639-10644(1995).
EN  (7)
RP  STRUCTURE OF N-LINKED CARBOHYDRATES.
RA  MEDLINE=99150217; PubMed=10024650;
RA  Mechref Y., Chen P., Novotny M.V.;
RA  "Structural characterization of the N-linked oligosaccharides in bile
RA  salt-stimulated lipase originating from human breast milk.";
RT  Glycobiology 9:227-234(1999).
EN  (8)
RP  -1- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT
RP  WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION OF
RP  DIETARY TRIGLYCERIDES.
CC  -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC  fatty acid anion.
CC  -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC  acid.
CC  -1- ENZYME REGULATION: ACTIVATED BY BILE SALTS CONTAINING A 7-HYDROXYL
CC  GROUP.
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=long;
CC  isoId=p19835-1; Sequence=Displayed;
CC  Name=short;
CC  isoId=p19835-2; Sequence=VSP_001463;
CC  -1- TISSUE SPECIFICITY: MAMMARY GLAND, AND PANCREAS.
CC  -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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DR EMBL: X54457; CAA36325.1; ALT\_INIT.  
 DR EMBL: M85201; AAA52014.1; -  
 DR EMBL: M54994; AAA53211.1; -  
 DR EMBL: M94579; AAA51973.1; ALT\_INIT.  
 DR PDB: 1F6W; 18-OCT-00.  
 DR GlycoSuiteDB; S19835; -  
 DR Gene: HGN:1848; CEL.  
 DR MIM: 114840; -  
 DR InterPro: IPR0320-8; Carboxylesterases.  
 DR InterPro: IPR00379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1;  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydroxylase; Serine esterase; Lipid degradation; Glycoprotein; Repeat;  
 KW Signal; Alternative splicing; 3D-structure.  
 FT SIGNAL 1 20  
 FT CHAIN 1 20  
 FT DOMAIN 21 742  
 FT ACT\_SITE 214 214  
 FT ACT\_SITE 340 340  
 FT ACT\_SITE 455 455  
 FT DISULFID 84 100  
 FT DISULFID 266 277  
 FT CARBOHYD 207 207  
 FT CARBOHYD 553 553  
 FT CARBOHYD 563 563  
 FT CARBOHYD 579 579  
 FT CARBOHYD 596 596  
 FT CARBOHYD 607 607  
 FT CARBOHYD 618 618  
 FT CARBOHYD 623 623  
 FT CARBOHYD 643 643  
 FT CARBOHYD 651 651  
 FT CARBOHYD 662 662  
 FT COMAIN 734 734  
 FT REPEAT 555 555  
 FT REPEAT 570 570  
 FT REPEAT 581 581  
 FT REPEAT 592 592  
 FT REPEAT 603 603  
 FT REPEAT 613 613  
 FT REPEAT 624 624  
 FT REPEAT 635 635  
 FT REPEAT 646 646  
 FT REPEAT 657 657  
 FT REPEAT 668 668  
 FT REPEAT 679 679  
 FT REPEAT 680 680  
 FT REPEAT 691 691  
 FT REPEAT 702 702  
 FT REPEAT 713 713  
 FT REPEAT 724 724  
 FT REPEAT 734 734  
 FT VARSPLIC 430 435  
 SO SEQUENCE 742 AA; 78345 MW; 1A0C23D8C8C2859 CRC64;  
 Missing (in isoform short).  
 Query Match 1.5%; Score 12; DB 1; Length 742;  
 Best Local Similarity 100.0%; Pred. No. 0.00079;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

EST1\_CULP;  
 70 EST1\_CULP1 STANDARD; PRT; 540 AA.  
 AC P16954;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Esterase B1 precursor (EC 3.1.1.1).  
 GN BL  
 OS Culex pipiens (house mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culex.  
 OX NCBI\_TaxID=7175;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN-TM-R;  
 RX MEDLINE=90207238; PubMed=2320576;  
 RA Moulos C., Fauguin Y., Agarwal M., Lemieux E., Herzog M.,  
 RA Abadon M., Baysse-Arnaout V., Hyten O., de Saint Vincent B.R.,  
 RA Georgiou G.P., Pasteur N.;  
 RT "Characterization of amplification core and esterase B1 gene  
 RT responsible for insecticide resistance in Culex."  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:2574-2578 (1990).  
 RL  
 CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON  
 CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.  
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 CC -1- MISCELLANEOUS: THERE ARE TWO SUCH ESTERASES: A AND B. ALLELES OF  
 CC BOTH A AND B ARE KNOWN.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -----  
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DR EMBL: M32328; AAA28389.1; -  
 DR PIR: A35986; A35986.  
 DR HSSD: P21836; IMAA.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR00379; Ser\_estrs\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; FALSE NEG.  
 KW Hydroxylase; Serine esterase; Glycoprotein; Multigene family; Signal.  
 FT SIGNAL 1 7  
 FT CHAIN 1 540  
 FT ACT\_SITE 191 191  
 FT ACT\_SITE 442 442  
 FT DISULFID 68 81  
 FT CARBOHYD 452 452  
 SO SEQUENCE 540 AA; 60806 MW; F73B25B9A757C95 CRC64;  
 Query Match 1.2%; Score 10; DB 1; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 0.071;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 AFGDPRKVT 250  
 DB 177 AFGDPRKVT 186  
 RESULT 15  
 EST2\_RABIT  
 10 EST2\_RABIT STANDARD; PRT; 532 AA.  
 AC P14543;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Liver carboxylesterase 2 (EC 3.1.1.1).  
 OS Oryctolagus cuniculus (Rabbit).

RESULT 14

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=8930866; PubMed=2745458;  
 RA Ozois J.;  
 RT "Isolation, properties, and the complete amino acid sequence of a  
 second form of 60-kDa glycoprotein esterase. Origin of the  
 60-kDa protein in the microsomal membrane."  
 RL J. Biol. Chem. 264:12533-12545(1989).  
 CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN  
 THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.  
 CC CATALYTIC ACTIVITY: A carboxylic ester + H<sub>2</sub>O = an alcohol + a  
 carboxylic anion.  
 CC SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic  
 reticulum.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR PIR: A34329; A34329.  
 DR HSP: P37967; 10E3.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_ests\_site.  
 DR Pfam: PF00135; Coesterase.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_2; 1.  
 KM Glycoprotein; Hydrolyase; Serine esterase; Endoplasmic reticulum;  
 KM Pyridolone carboxylic acid. PYRIDOLONE CARBOXYLIC ACID.  
 FT MCDRES 201 201  
 FT ACT\_SITE 201 201  
 FT ACT\_SITE 430 430  
 FT DISULFID 69 96  
 FT DISULFID 251 264  
 FT SITE 529 532  
 FT SITE 249 249  
 FT CARBOHYD 363 363  
 SQ SEQUENCE 532 AA; 59058 MW; C57DD676A13A932 CRC64;  
 Query Match 1.1%; Score 9; DB 1; Length 532;  
 Best Local Similarity 100.0%; Pred. No. 0.76;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCVLYNLY 133  
 DB 94 EDCVLYNLY 102  
 RESULT 16  
 EST: RABIT STANDARD; PRT: 539 AA.  
 ID EST1\_RABIT  
 AC P:2337;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Liver carboxylesterase 2 (EC 3.1.1.1).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN (1)  
 RP SEQUENCE.  
 RC MEDLINE=8913943; PubMed=3343253;  
 RA Kozra G., Ozois J.;  
 RT "Complete covalent structure of 60-kDa esterase isolated from  
 2,3,7,8-tetrachlorodibenzo-p-dioxin-induced rabbit liver  
 microsomes."  
 RL J. Biol. Chem. 263:3486-3493(1988).  
 RN (2)  
 RP SEQUENCE OF 1-70 AND 532-539.  
 RX MEDLINE=88033124; PubMed=3567634;  
 RA Ozois J.;  
 RT "Isolation and characterization of a 60-kilodalton glycoprotein  
 esterase from liver microsomal membranes.";

RL J. Biol. Chem. 262:15316-15321(1987).  
 CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN  
 THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.  
 CC CATALYTIC ACTIVITY: A carboxylic ester + H<sub>2</sub>O = an alcohol + a  
 carboxylic anion.  
 CC SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic  
 reticulum.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 DR PIR: A29923; A29923.  
 DR HSP: P21836; 1MAH.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000379; Ser\_ests\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_2; 1.  
 KM Glycoprotein; Hydrolyase; Serine esterase; Endoplasmic reticulum.  
 FT ACT\_SITE 195 195  
 FT ACT\_SITE 441 441  
 FT DISULFID 69 98  
 FT DISULFID 247 258  
 FT SITE 536 539  
 FT CARBOHYD 61 61  
 FT CARBOHYD 363 363  
 SQ SEQUENCE 539 AA; 59539 MW; 98C72BC36A9B0BD CRC64;  
 Query Match 1.1%; Score 9; DB 1; Length 539;  
 Best Local Similarity 100.0%; Pred. No. 0.77;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCVLYNLY 133  
 DB 96 EDCVLYNLY 104  
 RESULT 17  
 EST: RAT STANDARD; PRT: 549 AA.  
 ID EST1\_RAT  
 AC P10953; O63106; O64626;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Liver carboxylesterase 1 precursor (EC 3.1.1.1) (Carboxylesterase ES-1)  
 DE (E1) (ES-THET)  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-48.  
 RC STRAIN=Sprague-Dawley; Tissue=Liver;  
 RX MEDLINE=89174514; PubMed=3235453;  
 RA Takagi Y., Kotohashi K., Kawabata S., Go M., Omura T.;  
 RT "Molecular cloning and nucleotide sequence of cDNA of microsomal  
 carboxylesterase B1 of rat liver."  
 RL J. Biochem. 104:801-806(1988).  
 RN (2)  
 RP SEQUENCE OF 10-549 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=89350119; PubMed=2973335;  
 RA Long R.M., Satch H., Martin B.M., Kimura S., Gonzalez F.J., Pohl L.R.;  
 RT "Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence  
 for a multigene family."  
 RL J. Biochem. Biophys. Res. Commun. 156:966-973(1988).  
 RN (3)  
 RP SEQUENCE OF 13-549 FROM N.A.  
 RC STRAIN=Sprague-Dawley; Tissue=Liver;  
 RX MEDLINE=94274701; PubMed=8006016;  
 RA Alexson S.E.H., Finlay T.H., Helman U., Svensson L.T., Diezfauy R.,  
 Eggersten G.;  
 RT "Molecular cloning and identification of a rat serum carboxylesterase  
 expressed in the liver."  
 RL J. Biol. Chem. 269:17118-17124(1994).  
 CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN

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CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL: M20629; AAA43871.1; -
DR EMBL: D36629; BAA6310.1; -
DR EMBL: D00362; BAA20565.1; -
DR EMBL: X78489; CAA5241.1; -
DR PIR: A31584; A31584.
DR HSSP: P21836; 1MAH.
DR InterPro: IPR002018; Carboxylesterase.
DR Pfam: PF00315; Coesterase; 1; _site.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 549 LIVER CARBOXYLESTERASE 1.
FT ACT_SITE 221 221 BY SIMILARITY.
FT ACT_SITE 453 453 BY SIMILARITY.
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 273 284 BY SIMILARITY.
FT SITE 546 549 PRESENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 476 476 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 372 372 P -> L.
FT CONFLICT 48 48 A -> R (IN REF. 3).
FT CONFLICT 174 175 IW -> FG (IN REF. 2).
FT CONFLICT 250 250 V -> L (IN REF. 2).
FT CONFLICT 399 399 K -> N (IN REF. 1).
FT CONFLICT 504 504 K -> E (IN REF. 1).
FT CONFLICT 512 513 LC -> FE (IN REF. 3).
SQ SEQUENCE 549 AA; EC174 MW; 18D6A586DA50E862 CRC64;

Query Match: 1.1%; Score 9; DB 1; Length 549;
Best Local Similarity 100.0%; Pred No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNTY 133
DB 114 EDCLYLNTY 122

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=91169540; PubMed=1840565;
RA Owen M., Tappern K., Meda S., Elliott R.W., Stephenson D.A.,
RA Grant S.G., Garschow R.E.,
RT "Characterization of a murine cDNA encoding a member of the
RT carboxylesterase multigene family."
RL Genomics 9:344-354 (1991).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL: M57960; AAA63297.1; -
DR PIR: A39060; A39060.
DR HSSP: P37967; 1Q83.
DR MGD: MGI:95420; E81.
DR InterPro: IPR02018; Carboxylesterase.
DR Pfam: PF00315; Coesterase; 1; _site.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 554 LIVER CARBOXYLESTERASE.
FT ACT_SITE 221 221 BY SIMILARITY.
FT ACT_SITE 453 453 BY SIMILARITY.
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 273 284 BY SIMILARITY.
FT SITE 551 554 PRESENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 377 377 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 554 AA; 61140 MW; 8A826D553DC8F69 CRC64;

Query Match: 1.1%; Score 9; DB 1; Length 554;
Best Local Similarity 100.0%; Pred No. 0.79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNTY 133
DB 114 EDCLYLNTY 122

```

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RESULT 19
EST2 CAEEL
ID EST2 CAEEL STANDARD; PRT; 556 AA.
AC 007085; D16351;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Esterase CMO6B1 (EC 3.1.1.1).
GN F31H6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodidae; Pelodidae; Pelodidae; Pelodidae; Pelodidae;
CX NCBI_TaxID=6239;
RN [1]

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BX MEDLINE=94033620. Pubmed=8239278;
RA Fecor X., Cousin X., Tourant J.-P., Thierry-Mieg D., Arpagaus M.;
RT "cDNA sequence, gene structure, and cholinesterase-like domain of an
AT esterase from Caenorhabditis elegans mapped to chromosome V";
RL DNA Seq. 3:347-356(1993).
RN [2]
R2 SEQUENCE FROM N.A.
R3 STRAIN=Bristol NZ;
R4 Jones K., Woldemann P.;
RL Submitted (Aug-1997) to the EMBL/GenBank/CDL databases.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC. ATTACHED TO THE INNER SIDE OF
CC THE MEMBRANE BY A LIPID ANCHOR.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC -----
CC EXBL: X66104; CAA46599.1; ..
CC EXBL: AFO6437; AAB65887.1; ..
CC PIR: A56690; A56690.
CC PIR: T31783; T31783.
CC HSSP: P37967; 10E3.
CC WormPep: P13463; CE09375.
CC InterPro: IPR002018; Carboxylesterase.
CC InterPro: IPR00379; Ser_estrs_site.
CC Pfam: PF00135; Coesterase_1.
CC PROSITE: PSC0122; CARBOXYLESTERASE_3_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_3_2; FALSE NEG.
CC HydroLase; Serine esterase; Myristate; Membrane.
CC INT MET 0 POTENTIAL.
CC LIPID 1 MYRISTATE (POTENTIAL).
CC ACT_SITE 207 207 BY SIMILARITY.
CC ACT_SITE 330 330 BY SIMILARITY.
CC ACT_SITE 445 445 BY SIMILARITY.
CC DISULFID 75 97 BY SIMILARITY.
CC CONFLICT 542 556 NMSERRSRQRFNPF -> ELYGKKKSKAK (IN REF.
CC SEQUENCE 556 AA; 62391 MW; 4635E5B2428DB99B CRC64;
SO
Query Match 1.1%; Score 9; DB 1; Length 556;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 168 PMVYIHGG 176
DB 117 PMVYIHGG 125

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RT "Cloning and sequence analysis of a hamster liver cDNA encoding a
RL novel putative carboxylesterase";
RL Biochim. Biophys. Acta 1207:138-142(1994).
CC -1- FUNCTION: INVOLVED IN THE DEOXYFLAVONOID XENOBIOLOGICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EXBL: D28566; BAA05913.1; ..
CC PIR: S47655; S47655.
CC HSSP: P37967; 10E3.
CC InterPro: IPR002018; Carboxylesterase.
CC InterPro: IPR00379; Ser_estrs_site.
CC Pfam: PF00135; Coesterase_1.
CC PROSITE: PSC0122; CARBOXYLESTERASE_3_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_3_2; 1.
CC Glycoprotein; HydroLase; Serine esterase; Endoplasmic reticulum;
CC signal; Multigene family.
CC SIGNAL 1 27 POTENTIAL.
CC CHAIN 28 561 LIVER CARBOXYLESTERASE.
CC ACT_SITE 227 227 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC ACT_SITE 459 459 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC DISULFID 95 122 BY SIMILARITY.
CC DISULFID 280 291 BY SIMILARITY.
CC SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).
CC CARBOHYD 276 276 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 362 362 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 561 AA; 62330 MW; 46B11E42475321 CRC64;
SO
Query Match 1.1%; Score 9; DB 1; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 125 EDCYLYNLY 133
DB 120 EDCYLYNLY 128

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RESULT 20
EST1_MESAU STANDARD; PRT: 561 AA.
ID EST1_MESAU STANDARD; PRT: 561 AA.
AC 064419;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase precursor (EC 3.1.1.1).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetidae;
OC Mesocricetus.
CX NCBI_TaxID=10366;
RN [1]
R2 SEQUENCE FROM N.A.
R3 STRAIN=Syrian golden; TISSUE=Liver;
R4 MEDLINE=94338665; Pubmed=8043605;
R5 Sore T., Isobe M., Takabatake E., Wang C.Y.;

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RESULT 21
EST1_RAT STANDARD; PRT: 561 AA.
ID EST1_RAT STANDARD; PRT: 561 AA.
AC 063108;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 3 precursor (EC 3.1.1.1) (Carboxylesterase ES-3)
DE (B1 5.5 esterase) (ES-H-EL).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
R2 SEQUENCE FROM N.A.
R3 STRAIN=Sprague-Dawley; TISSUE=Liver;
R4 MEDLINE=95032008; Pubmed=7945287;
R5 Robbi M., Beaufay H.;
R6 "Cloning and sequencing of rat liver carboxylesterase ES-3 (egagyn)";
R7 Biochem. Biophys. Res. Commun. 203:1404-1411(1994).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
CC THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.

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RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; Tissue=Liver;
RX MEDLINE=35050819; Pubmed=7961958;
RA Yang B., Yang D., Brady M., Parkinson A.;
RT "Rat kidney carboxylesterase. Cloning, sequencing, cellular
localization, and relationship to rat liver hydrolyase."
R. Biol. Chem. 269:29688-29696(1994).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE
ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@sib-sib.ch).
CC EMBL: J13698; AAA64633.1; -.
DR HSSP: P21836; IMAH.
DR InterPro: IPR002818; Carboxylesterase.
DR InterPro: IPR003986; ER_target.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolyase; Serine esterase; Endoplasmic reticulum;
KW signal; Multigene family.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 19 561 LIVER CARBOXYLESTERASE B-1.
FT ACT_SITE 221 221 BY SIMILARITY.
FT ACT_SITE 466 466 BY SIMILARITY.
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 273 284 BY SIMILARITY.
FT SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 561 AA: 62494 MW: 61301336CB96C9 CACG64;

Query Match 1.1%; Score 9; DB 1; Length 561;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCVLYNLY 133
DB 114 EDCVLYNLY 122

RESULT 24
ES22 MOUSE STANDARD: PRT; 562 AA.
AC 064176;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 22 precursor (EC 3.1.1.1) (Eggsen; Esterase-
DE 22) (Es-22).
CN ES22.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10290;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=9247141; Pubmed=3783403;
RA Ovnio M., Swank R.T., Fletcher C., Zhen L., Nowak E.K., Baumann H.,
RA Heintz N., Ganschow R.E.;
RT "Characterization and functional expression of a cDNA encoding eggsen

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RT (esterase-22): the endoplasmic reticulum-targeting protein of beta-
guanylidase."
RL Genomics 11:956-967(1992).
CC -1- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN
THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
carboxylic anion.
CC -1- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
reticulum.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC EMBL: S80291; AA821335.1; -.
DR PIR: A55281; A55281.
DR HSSP: P21836; IMAH.
DR MGD: MGI:95432; Es22.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolyase; Serine esterase; Endoplasmic reticulum;
KW signal; Multigene family.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 19 562 LIVER CARBOXYLESTERASE 22.
FT ACT_SITE 222 222 BY SIMILARITY.
FT ACT_SITE 467 467 BY SIMILARITY.
FT DISULFID 88 117 BY SIMILARITY.
FT DISULFID 274 285 BY SIMILARITY.
FT SITE 559 562 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 562 AA: 61581 MW: F81A4367A0CC82E3 C8G64;

Query Match 1.1%; Score 9; DB 1; Length 562;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCVLYNLY 133
DB 115 EDCVLYNLY 123

RESULT 25
EST1_CABR STANDARD: PRT; 562 AA.
ID EST1_CABR
AC 004456;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gut esterase 1 precursor (EC 3.1.1.1) (Non-specific carboxylesterase).
DE GRS-1.
OS Caenorhabditis briggsae.
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
CC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188021; Pubmed=8445654;
RA Kennedy B.P., Amodei E.O., Allen F.L., Chung M.A., Heschl M.F.P.,
RA McChes C.D.;
RT "The gut esterase gene (ges-1) from the nematodes Caenorhabditis
elegans and Caenorhabditis briggsae."
R. Mol. Biol. 229:890-908(1993).
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a

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CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC      or send an email to license@ebi.ac.uk).
CC
CC      EMBL; X63123; CAA44929.1; ..
CC
CC      DR PIR; S19307; S19307.
CC      DR HSSP; P21836; 1MAH.
CC      InterPro: IPR002019; CarboxesteraseB.
CC      InterPro: IPR000379; Ser_ests_site.
CC      Pfam: PF00135; Coesterase; 1.
CC      PROSITE; PS00422; CARBOXYL-ESTERASE_B_1.
CC      PROSITE; PS00941; CARBOXYL-ESTERASE_B_2.
CC      GlycoProtein; Hydroxylase; Serine esterase; Endoplasmic reticulum;
CC      KM Sgnal; Multigene family.
CC
CC      FT SGNAL 1 18
CC      FT CHAIN 1 566
CC      FT ACT_SITE 222 222
CC      FT ACT_SITE 457 467
CC      FT DISULFID 88 117
CC      FT DISULFID 274 285
CC      FT SITE 563 566
CC      FT CARBOHYD 90 80
CC      SEQUENCE 566 AA; 62016 MW; B046545307DEB5 CRC64;
CC
CC
CC      Query Match 1.1%; Score 9; DB 1; Length 566;
CC      Best Local Similarity 100.0%; P-Id. No. 0.8%;
CC      Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0.
CC
CC      QY 125 EDCLYLYNY 133
CC      115 EDCLYLYNY 123
CC
CC
CC      RESULT 27
CC      BEST HUMAN STANDARD; PRT; 567 AA.
CC      ID P3141; G0005; Q3657; Q1406; Q16737; Q16788; Q9JUY2.
CC      AC P3141; G0005; Q3657; Q1406; Q16737; Q16788; Q9JUY2.
CC      FT 01-NOV-1991 (Rel. 20; Created)
CC      FT 01-AUG-1992 (Rel. 23; Last sequence update)
CC      26-FEB-2003 (Rel. 41; Last annotation update)
CC      Diver carboxylacyltransferase precursor (EC 3.1.1.1) (acyl coenzyme
CC      A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine
CC      esterase) (HMBE) (Serine esterase 1) (Brain carboxyesterase h3x1).
CC      GN CSI; OR CSI; OR SESI.
CC      OS Homo sapiens (Human).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hemo.
CC      OX NCBI_TaxID=9606;
CC      RN 11
CC      RP SEQUENCE FROM N.A.
CC      RX MEDL:03=92201643; PubMed=1918003;
CC      RA Kanger J.S., Shi G.P., Marx E.A., Chin D.T., Gerard C.,
CC      Chapman H.A.;
CC      RT A serine esterase released by human alveolar macrophages is closely
CC      related to liver microsomal carboxylesterases."
CC      RL J. Biol. Chem. 266:18833-18838 (1991).
CC      [2]
CC      RP SEQUENCE FROM N.A.
CC      RC TISSUE=Liver;
CC      RX MEDLINE=9403283; PubMed=8218228;
CC      RA Kroeze D.L., McBride O.W., Gorzalez F.J.;
CC      RT "Glycosylation-dependent activity of baculovirus-expressed human
CC      liver carboxylesterases: cDNA cloning and characterization of two
CC      highly similar enzyme forms."
CC      RL Biochemistry 32:11606-11617 (1993).
CC      [3]
CC      RP SEQUENCE FROM N.A.
CC      RS TISSUE=Peripheral blood, and Placenta;

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AC P30122;
CT C1-AP3-1993 (Rel. 25, Last Created)
CT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (BAV)
DE (Bile-salt-stimulated lipase) (BSSL) (Carboxy ester lipase) (Ssterol
DE esterase) (Cholesterol esterase) (Pancreatic lysophospholipase)
DE (Fragment).
GN BSL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=90073663; PubMed=2590203;
RA Kyger E. N., Wiegand R. C., Lange L. G.;
RT "Cloning of the bovine pancreatic cholesterol
RT esterase/lysophospholipase."
RL Biochem. Biophys. Res. Commun. 164:1302-1309(1999).
RN [2]
RP SEQUENCE OF 19-40.
RC TISSUE=pancreas; PubMed=1020579;
RX MEDLINE=99238708; PubMed=99238708;
RA Tanaka H., Mierau I., Ito F.;
RT "Purification and characterization of bovine pancreatic bile salt-
RT activated lipase."
RL Biochem. 125:863-890(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 13-565, AND REVISION TO 45.
RX MEDLINE=97473004; PubMed=933420;
RA Wang X., Wang C. S., Tang C., Dyda F., Zhang X. C.;
RT "The crystal structure of bovine bile salt activated lipase: insights
RT into the bile salt activation mechanism."
RL Structure 5:1203-1218(1997).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 19-597.
RX MEDLINE=98215635; PubMed=9548741;
RA Chen C. H., Miercke L. J. W., Krucinski J., Stasz C. R., Saenz G.,
RA Wang X., Spilburg C. A., Lange L. G., Ellsworth J. L., Stroud R. N.;
RT "Structure of bovine pancreatic cholesterol esterase at 1.6 A: novel
RT structural features involved in lipase activation."
RL Biochemistry 37:5107-5117(1998).
CC -1- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONJUNCTION
CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION
CC OF DIETARY TRIGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = 1,3-diacylglycerol + a
CC fatty acid anion.
CC -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -1- ENZYME REGULATION: ACTIVATED BY BILE SALTS CONTAINING A 7-HYDROXYL
CC GROUP IN THE INFANTS INTESTINE WHERE IT AIDS TO DIGEST MILK FATS.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
CC EMBL; X28402; AAA56788.1;
CC
DR PIR; A33668; A33668.
DR PDB; 1AKN; 27-MAY-98.
DR PDB; 1AOL; 05-AUG-98.
DR PDB; 2BCE; 23-MAR-99.
DR InterPro; IPR002618; CarbesteraseB.
DR InterPro; IPR003379; Ser_ester_site.
DR Pfam; PF00135; Coesterase_1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

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KW Hydrolase; Serine esterase; Lipid degradation; Glycoprotein; Signal;
KW 3D-structure.
FT NON_TER 1
FT SIGNAL 18
FT CHAIN 19
FT ACT_SITE 212
FT ACT_SITE 338
FT ACT_SITE 338
FT ACT_SITE 455
FT ACT_SITE 455
FT DISULFID 82
FT DISULFID 264
FT CARBOHYD 205
FT CARBOHYD 379
FT CARBOHYD 379
FT CONFLICT 30
FT CONFLICT 45
FT CONFLICT 45
FT STRAND 24
FT TURN 27
FT STRAND 29
FT STRAND 32
FT STRAND 34
FT TURN 40
FT STRAND 44
FT TURN 59
FT STRAND 72
FT STRAND 72
FT STRAND 76
FT STRAND 76
FT STRAND 84
FT TURN 87
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FT TURN 129
FT TURN 139
FT TURN 140
FT TURN 141
FT HELIX 141
FT HELIX 143
FT TURN 146
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FT TURN 212
FT HELIX 213
FT HELIX 223
FT TURN 225
FT TURN 230
FT STRAND 233
FT TURN 237
FT HELIX 241
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FT HELIX 251
FT TURN 251
FT TURN 263
FT HELIX 269
FT HELIX 278
FT HELIX 281
FT TURN 287
FT HELIX 287
FT HELIX 299
FT HELIX 302
FT HELIX 318
FT HELIX 320
FT HELIX 322
FT TURN 326
FT STRAND 327
FT STRAND 329
FT TURN 335
FT TURN 336
FT STRAND 337
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FT TURN 338
FT HELIX 340
FT HELIX 346
FT HELIX 348
FT TURN 351
FT HELIX 351
FT HELIX 359
FT TURN 369
FT TURN 370
FT HELIX 371
FT HELIX 373
FT HELIX 374
FT HELIX 386
FT TURN 387
FT TURN 389
FT TURN 391
FT HELIX 395
FT TURN 410
FT TURN 411
FT HELIX 412
FT HELIX 425
FT STRAND 431
FT STRAND 436

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BILE-SALT-ACTIVATED LIPASE.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . )  
 N-LINKED (GLCNAC. . . )  
 F -> P (IN REF. 2).  
 I -> V (IN REF. 1).

FT TURN 447 448  
 FT STRAND 452 452  
 FT TURN 453 456  
 FT HELIX 457 460  
 FT TURN 461 462  
 FT HELIX 463 466  
 FT HELIX 468 470  
 FT HELIX 473 492  
 FT TURN 493 496  
 FT TURN 511 513  
 FT STRAND 515 519  
 FT TURN 525 526  
 FT STRAND 526 530  
 FT TURN 532 533  
 FT HELIX 534 541  
 FT TURN 542 542  
 FT HELIX 543 546  
 SQ SEQUENCE 597 AA; 65161 MW; 82357AED9CEBFD1 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 597;  
 Best Local Similarity 100.0%; Pred. No. 0.84;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 MEDCLINT 132  
 Db 95 MEDCLINT 103

## RESULT 29

ACBI\_CABER STANDARD; PRT; 620 AA.  
 ID ACBI\_CABER  
 AC Q27455;  
 DT 01-NOV-1997 (Rel. 35, Created);  
 DT 01-NOV-1997 (Rel. 35, Last sequence update);  
 DT 28-FEB-2003 (Rel. 41, Last annotation update);  
 DE Acetylcholinesterase 1 precursor (EC 3.1.1.7) (ACHe 1).  
 GN AChE-1.  
 OS Caenorhabditis briggsae.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6238;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9706944; PubMed=8912924;  
 RA Grauso M., Coleetto B., Berge J.B., Tourant J.-P., Arpagaus X.;  
 RT "Sequence comparison of AChE-1, the gene encoding acetylcholinesterase  
 of class A, in the two nematodes *Caenorhabditis elegans* and  
*Caenorhabditis briggsae*."  
 RT DNA Seq. 6:217-227(1996).  
 RL  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H<sub>2</sub>O = choline + acetate.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS (3;  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY).  
 CC -1- SUBCELLULAR LOCATION: MAY BE SECRETED OR MEMBRANE ASSOCIATED VIA  
 CC A NON-CATALYTIC SUBUNIT (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC  
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 CC  
 CC EXEM: U41846; A041269.1;  
 DR HSSP; P21936; WMA.  
 DR InterPro; IPR002018; Carboxylesterase3.  
 DR InterPro; IPR000997; Cholinesterase.  
 DR InterPro; IPR003379; Ser esters\_site.  
 DR Pfam; PF00135; Coesterase\_1.  
 DR PRINTS; PR00872; CHOLINESTERASE.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase; Serine esterase; Synapse; Membrane; Signal; Glycoprotein;  
 KW Neurotransmitter degradation; Multigene family.  
 FT SIGNAL 1 31  
 FT CHAIN 32 620  
 FT ACT\_SITE 216 216  
 FT ACT\_SITE 346 346  
 FT ACT\_SITE 468 468  
 FT DISULFID 82 109  
 FT DISULFID 270 286  
 FT DISULFID 430 558  
 FT DISULFID 618 618  
 FT CARBOHYD 74 74  
 FT CARBOHYD 272 272  
 FT CARBOHYD 486 486  
 FT CARBOHYD 536 536  
 SQ SEQUENCE 620 AA; 71501 MW; 69D73CD3996E11FC CRC64;

Query Match 1.1%; Score 9; DB 1; Length 620;  
 Best Local Similarity 100.0%; Pred. No. 0.87;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 529 NFAKTGDPN 537  
 Db 504 NFAKTGDPN 512

## RESULT 30

ACBI\_CABER  
 ID ACBI\_CABER  
 AC P38433;  
 DT 01-OCT-1994 (Rel. 30, Created);  
 DT 01-OCT-1994 (Rel. 30, Last sequence update);  
 DT 16-OCT-2001 (Rel. 40, Last annotation update);  
 DE Acetylcholinesterase 1 precursor (EC 3.1.1.7) (AChE 1).  
 GN AChE-1 OR W09812.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=94193691; PubMed=8144590;  
 RA Fournier D., Tourant J.-P., Chatonnet A., Berge J.-B.,  
 RT "CDNA sequence, gene structure, and in vitro expression of ace-1, the  
 gene encoding acetylcholinesterase of class A in the nematode  
*Caenorhabditis elegans*."  
 RT J. Biol. Chem. 269:9957-9965(1994).  
 RL [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Wu X., Le T.T.;  
 RT Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC IT CAN HYDROLYZE BUTYRYLTHIOCHOLINE.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H<sub>2</sub>O = choline + acetate.  
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: MAY BE SECRETED OR MEMBRANE ASSOCIATED VIA  
 CC A NON-CATALYTIC SUBUNIT.  
 CC -1- DEVELOPMENTAL STAGE: DETECTED AT ALL STAGES. FOUND TO BE MORE  
 CC ABUNDANT IN LARVAL STAGES THAN IN EMBRYOS OR ADULTS.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 CC  
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CC -----
DR EMBL: X75331; CA53062.1; -
DR EMBL: U56731; AAR00593.1; -
DR PIR: A54413; A54413.
DR HSPB: P21836; IMNA.
DR WormPep: M09512.1; CE07569.
DR InterPro: IPR02018; Carboxylesterase.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR00379; Ser_estrs_site.
DR Pfam: PF00335; Coesterase.1.
DR PRNTS: PRC0878; CHOLNSTRASE.
DR PROSITE: PS00122; CARBOXYL-ESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYL-ESTERASE_3_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Signal;
KW Neurotransmitter degradation; Multigene family.
FT SIGNAL 1
FT CHAIN 32
FT ACT_SITE 216 620
FT ACT_SITE 216 620
FT ACT_SITE 346 469
FT ACT_SITE 468 469
FT DISULFID 82 109
FT DISULFID 273 286
FT DISULFID 430 558
FT DISULFID 618 618
FT CARBOHYD 74 74
FT CARBOHYD 272 272
FT CARBOHYD 486 486
FT CARBOHYD 536 536
SQ SEQUENCE 620 AA; 71433 MW; 61D78C4839F55C65 CRC64;

Query Match 1.1%; Score 9; DB 1; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 529 NEAKTGDPM 537
Db 504 NFAKTIDPN 512

RESULT 31
GPI8_SCHPO STANDARD; PRT; 390 AA.
AC 09USFE
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GPI-anchored transamidase (EC 3.-.-.) (GPI transamidase).
SN GPI8 OR SPCCL1E10.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycotaceae;
OC Schizosaccharomycetes.
CX NCBI_TaxID=48961;
RN (1);
RS SEQUENCE FROM N.A.
RA Shams-Edin H.V.H.;
RT "The essential Schizosaccharomyces pombe gpi8+ gene complements a
bakers yeast GPI anchoring mutant.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=2848401; PubMed=11659360;
Wocd V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamilton N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jazels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Kungall K., Murphy L., Nibbel D., Odell C.,
Olliver K., O'Neill S., Pearson D., Quail X.A., Rabinowicz E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

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RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voiclaert G., Aert R., Robben J., Symonides B.,
RA Welljens J., Vansteels E., Rieger M., Schaefer M., Mueller-Nuer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Mambert R., Purcell R.,
RA Coffeau A., Cadieu E., Dreano S., Gloux S., Leleux V., Motter S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas R., Rochet M., Galliard C., Talada V.A., Garzon A., Thode G.,
RA Jada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Chmuguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombe W.R., Paulsen O., Potashkin J.,
RA Shpakovski G.V., Usey D., Barrett B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC - FUNCTION: Mediates GPI anchoring in the endoplasmic reticulum, by
replacing a protein's C-terminal GPI attachment signal peptide
with a pre-assembled GPI. During this transamidation reaction, the
GPI transamidase forms a carbonyl intermediate with the substrate
protein (By similarity).
CC - PATHWAY: GPI-anchored biosynthesis.
CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY C13.
CC -----
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CC -----
DR EMBL: AJ250428; CAC13970.1; -
DR EMBL: AL121783; CAB57644.1; -
DR SIF: T43953; T40853.
DR MEROPS: C13.005.-.
DR GeneDB_SPOB: SPCCL1E10.02C; -.
DR InterPro: IPR001096; Legumain.
DR Pfam: PF01650; Peptidase_C13; 1.
DR PRINTS: PRC0776; HEMOGLOBINASE.
KW Hydrolase; Thiol protease; GPI-anchored biosynthesis.
FT ACT_SITE 145 145
FT ACT_SITE 187 187
FT ACT_SITE 187 187
SQ SEQUENCE 380 AA; 43206 MW; D569E1F76330372 CRC64;

Query Match 1.3%; Score 9; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 764 LRSPDDI 771
Db 273 LRSPDDI 280

RESULT 32
CYSF_PLAYN STANDARD; PRT; 506 AA.
AC F46102;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine proteinase precursor (EC 3.4.22.-).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5860;
RN (1);
RS SEQUENCE FROM N.A.
RA MEDLINE=93250055; PubMed=8485161;
RX Rosenthal P.J.;
RA "A Plasmodium vivax cysteine proteinase shares unique features with
its Plasmodium falciparum analogue.";
RL Biochim. Biophys. Acta 1173:91-93(1993).
CC - FUNCTION: PROBABLY DEGRADES ERYTHROCYTE HEMOGLOBIN.

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CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC
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CC or send an email to license@ebi.ac.uk).
CC
CC -----
CC EMBL: J08500; NOT ANNOTATED_CDS.
CC PIR: S32561; S32561..
CC HSSP: P43235; IMEM.
CC MEROPS: C01.077; .
CC
CC InterPro: IPR000663; Peptidase_C1.
CC InterPro: IPR000169; SH3prot_acsite.
CC Pfam: PF00112; Peptidase_C1; 1.
CC PRINTS: PR00705; PAPAIN.
CC ProDom: PD000158; Peptidase_C1; 2.
CC SMART: SM00645; Pept_C1; 1.
CC PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
CC PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
CC PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
CC Hydrolase: Hydrolase; Nucleotidylase; Glycoprotein; Signal.
CC SIGNAL
CC FT PROPEP 262 262 ACTIVATION PEPTIDE (POTENTIAL).
CC FT CHAIN 263 506 CYSTEINE PROTEINASE.
CC FT ACT_SITE 287 287 BY SIMILARITY.
CC FT ACT_SITE 419 419 BY SIMILARITY.
CC FT ACT_SITE 470 470 BY SIMILARITY.
CC FT DISULFID 294 326 BY SIMILARITY.
CC FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC
CC QUERY MATCH 506 AA: 58255 MW: 74784944618617F: CR664;
CC
CC Query Match 1.0%; Score 8; DB 1; Length 506;
CC Best Local Similarity 100.0%; Pred. No. 8;
CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

RL Biochem. J. 269:279-280(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=91287805; PubMed=2062369;
RX Schrag J.D., Li Y., Wu S., Cyster M.;
RT "Ser-His-Glu triad forms the catalytic site of the lipase from
RL Geotrichum candidum."
RL Nature 351:761-765(1991).
CC -1- FUNCTION: THE EXTRACELLULAR LIPASE PRODUCED BY G. CANDIDUM
CC HYDROLYSES ALL ESTER BONDS IN TRIGLYCERIDE AND DISPLAYS A HIGH
CC AFFINITY FOR TRIOLEIN.
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H2O = diacylglycerol + a
CC fatty acid anion.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC PIR: P04992; AGU0QC.
CC PDB: 1THG; 3I-OC7-93.
CC InterPro: IPR002018; Carboxesterase.
CC InterPro: IPR000379; Ser_estr_site.
CC Pfam: PF00135; Coesterase; 1.
CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
CC Hydrolase: Lipid degradation; Glycoprotein; Signal; 3D-structure;
CC KW Pyrolicidone carboxylic acid.
CC FT SIGNAL 1 19
CC FT CHAIN 20 563 LIPASE.
CC FT MOD_RES 20 20 PYROLIDONE CARBOXYLIC ACID.
CC FT ACT_SITE 236 236
CC FT ACT_SITE 373 373
CC FT ACT_SITE 482 482
CC FT DISULFID 80 124
CC FT DISULFID 295 307
CC FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT STRAND 23 26
CC FT TURN 27 29
CC FT STRAND 30 33
CC FT STRAND 35 37
CC FT TURN 38 39
CC FT STRAND 40 47
CC FT STRAND 54 56
CC FT HELIX 57 58
CC FT TURN 69 72
CC FT STRAND 71 72
CC FT STRAND 74 74
CC FT STRAND 79 79
CC FT HELIX 85 96
CC FT HELIX 98 101
CC FT HELIX 104 113
CC FT TURN 114 114
CC FT STRAND 120 120
CC FT STRAND 126 132
CC FT TURN 133 134
CC FT TURN 137 138
CC FT STRAND 141 147
CC FT TURN 151 152
CC FT HELIX 156 159
CC FT HELIX 163 171
CC FT TURN 172 173
CC FT STRAND 177 181
CC FT STRAND 186 190
CC FT HELIX 194 199
CC FT TURN 200 200
CC FT TURN 202 203
CC FT HELIX 204 219
CC FT HELIX 220 223
CC FT TURN 224 224
CC FT STRAND 225 235
CC FT TURN 236 236
CC FT HELIX 237 247
CC FT HELIX 248 250
CC FT TURN 251 251
CC FT STRAND 254 255

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FT TURN 256 257
FT STRAND 258 259
FT STRAND 263 267
FT HELIX 285 293
FT TURN 294 294
FT TURN 297 298
FT HELIX 302 310
FT HELIX 313 327
FT TURN 329 332
FT HELIX 334 336
FT TURN 337 337
FT HELIX 351 356
FT TURN 357 358
FT STRAND 365 370
FT TURN 371 371
FT STRAND 372 372
FT TURN 373 377
FT HELIX 378 381
FT TURN 382 383
FT HELIX 387 397
FT TURN 398 400
FT HELIX 403 412
FT HELIX 417 419
FT TURN 423 424
FT TURN 426 429
FT HELIX 435 445
FT TURN 447 447
FT HELIX 448 457
FT TURN 459 460
FT STRAND 463 468
FT TURN 473 474
FT TURN 476 478
FT STRAND 481 481
FT TURN 482 485
FT HELIX 486 490
FT TURN 491 491
FT TURN 495 496
FT HELIX 497 510
FT TURN 513 514
FT TURN 527 529
FT STRAND 531 535
FT STRAND 540 544
FT TURN 547 548
FT HELIX 549 557
FT HELIX 559 561
SQ SEQUENCE 563 AA; 61230 MW; 38732767ACB7BA2A CRC64;

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Query Match 1.0%; Score 8; DB 1; Length 563;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 124 NEDCLYN 131
DB 121 NEDCLYN 128

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RESULT 34
LIP2 GEOCN

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ID LIP2 GEOCN STANDARD; PRT; 563 AA.
AC P22394;

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DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lipase 2 precursor (EC 3.1.1.3).
CN LIP2.

```

```

OS Geotrichum candidum (Oospora lactis).

```

```

OC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Galactomyces.

```

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OX NCBI_TaxID=27317;

```

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RN 1;

```

```

RE SEQUENCE FROM N.A.
RX MEDLINE=93380907; PubMed=8170674;
RA Nagao T., Shimada Y., Sugihara A., Tomimaga Y.;

```

```

RT "Cloning and sequencing of two chromosomal lipase genes from
Rt Geotrichum candidum."
Rt J. Biochem. 113:776-780(1993).
(2)
RP SEQUENCE OF 7-563 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=50375435; PubMed=2358037;
RA Shimada Y., Sugihara A., Iizumi T., Tomimaga Y.;
RT "cDNA cloning and characterization of Geotrichum candidum lipase II."
Rt J. Biochem. 107:703-707(1990).
(3)
RP SEQUENCE OF 20-26 AND 561-563.
RX MEDLINE=98256718; PubMed=2341377;
RA Sugihara A., Shimada Y., Tomimaga Y.;
RT "Separation and characterization of two molecular forms of Geotrichum
candidum lipase."
Rt J. Biochem. 107:426-430(1990).
CC -1- FUNCTION: THE EXTRACELLULAR LIPASE PRODUCED BY G. CANDIDUM
HYDROLYZES A.L. ESTER BONDS IN TRIGLYCERIDE AND DISPLAYS A HIGH
AFFINITY FOR TRIOLEIN.
CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
fatty acid anion.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
-----
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-----
CC EMBL: D00697; BAA0603.1; .
CC PIR: P04953; P04953.
CC PDB: 1THG; 3I-OCT-93.
CC InterPro: IPR002018; Carboxylesterase.
CC InterPro: IPR000379; Ser esters state.
CC Pfam: PF00135; Coesterase.
CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
CC Hydrolyase; Lipid degradation; Glycoprotein; Signal;
KW Pyroglutamate carboxylic acid; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 563 LIPASE 2.
FT WCD RES 20 20 PYROGLUTAMATE CARBOXYLIC ACID.
FT ACT_SITE 236 236
FT ACT_SITE 373 373
FT ACT_SITE 482 482
FT DISULFID 80 124
FT DISULFID 235 307
FT CARBOHYD 302 332
FT CARBOHYD 383 383
SQ SEQUENCE 563 AA; 61617 MW; 12FA134A258C52F CRC64;

```

```

Query Match 1.0%; Score 8; DB 1; Length 563;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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CY 124 NEDCLYN 131
DB 121 NEDCLYN 128

```

```

RESULT 35
ACES_BUNFA

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ID ACES_BUNFA STANDARD; PRT; 561 AA.
AC Q92035; Q10720;

```

```

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

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DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).

```

```

OS Bungarus fasciatus (Banded Krait).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Lepidodermata; Squamata; Sclerozoa; Serpentes; Colubridae;  
 CC Eupidae; Bursariae; Bursariae;  
 CC NCBI\_TaxID=8613;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom gland;  
 RA MEDLINE=9627907; PubMed=8662867;  
 RA Cousin X., Bon S., Duval N., Massoulié J., Bon C.;  
 RT "Cloning and expression of acetylcholinesterase from Bungarus  
 RT fasciatus venom. A new type of COOH-terminal domain: involvement of a  
 RT positively charged residue in the peripheral site.";  
 RL J. Biol. Chem. 271:15399-15108(1996).  
 RN [2]  
 RP SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.  
 RC TISSUE=Venom;  
 RA MEDLINE=96244524; PubMed=8674543;  
 RA Cousin X., Cremonesi C., Grassi J., Meliah K., Cerini G., Sallou B.,  
 RA Bon S., Massoulié J., Bon C.;  
 RL "Acetylcholinesterase from Bungarus venom: a monomeric species.";  
 RL FEBS Lett. 387:196-200(1996).  
 CC -1- FUNCTION: RAPIDLY HYDROLYSES CHOLINE REVERSED INTO THE SYNAPSE.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine - H<sub>2</sub>O = choline + acetate.  
 CC -1- SUBUNIT: Monomer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PFM: THE N-TERMINUS IS BLOCKED.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-9 IS THE INTACTOR.  
 CC -----  
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 CC -----  
 DR EMBL: U54591; AAC59905.1;  
 DR HSRP: P04058; ISGM;  
 DR InterPro: IPR002818; CarboxylesteraseB.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR000379; Ser\_ester\_site.  
 DR Pfam: PF00135; Coesterase\_1.  
 DR PRINTS: PR00878; CHOLINESTRASE.  
 DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1;  
 DR PROSITE: PS00941; CARBOXYLESTERASE\_2\_1;  
 KM Hydrolyse: Serine esterase; Synapse; Membrane; Signal; Glycoprotein;  
 KM Neurotransmitter degradation.  
 KW SIGNAL.  
 FT CHAIN 1 28  
 FT PROPEP 23 573 ACETYLCHOLINESTERASE.  
 FT ACT\_SITE 231 231 BY SIMILARITY.  
 FT ACT\_SITE 358 358 BY SIMILARITY.  
 FT ACT\_SITE 471 471 POTENTIAL.  
 FT DISULFID 98 125 BY SIMILARITY.  
 FT DISULFID 295 296 BY SIMILARITY.  
 FT DISULFID 433 552 BY SIMILARITY.  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 374 374 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 484 484 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 564 564 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT MUTAGEN 101 101 W-A-Y: INCREASES PERIPHERAL SITE BINDING.  
 FT MUTAGEN 316 316 K-D: INCREASES PERIPHERAL SITE BINDING.  
 FT CONFLICT 268 268 T -> S (IN REF. 2).  
 FT CONFLICT 350 350 V -> L (IN REF. 2).  
 SO SEQUENCE 582 AA; 64722 MW; 4360CB8457E399F CRC64;  
 Query Match 100%; Score 9; DB 1; Length 581;  
 Best Local Similarity 100.0%; Pred. No. 9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CY 125 EDCLYINI 132

DB 123 EDCLYINI 130  
 RESULT 36  
 ACES TORCA STANDARD; PRT; 586 AA.  
 AC P04058;  
 DT 01-NOV-1986 (Ref. 03, Created)  
 DT 21-JUN-1994 (Ref. 29, Last sequence update)  
 DT 15-SEP-2003 (Ref. 42, Last annotation update)  
 DE Acetylcholinesterase precursor (BC 3.1.1.7) (ACE1).  
 OS Torpedo californica (Pacific electric ray).  
 CC Euryptera; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 CC Etmobranchii; Squalea; Hynostomales; Pterichthyes; Batoidae;  
 CC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.  
 OK NCBI\_TaxID=7787;  
 RN [1]  
 RP SEQUENCE OF 10-586 FROM N.A.  
 RA MEDLINE=86118676; PubMed=3753747;  
 RA Schumacher M., Camp S., Maulet Y., Newton M., McPhee-Quigley K.,  
 RA Taylor S.S., Friedmann T., Taylor P.;  
 RT "Primary structure of Torpedo californica acetylcholinesterase  
 RT deduced from its cDNA sequence.";  
 RL Nature 319:407-409(1986).  
 RN [2]  
 RP SEQUENCE OF 1-9 FROM N.A.  
 RA MEDLINE=89066695; PubMed=3198606;  
 RA Schumacher M.;  
 RT "Multiple messenger RNA species give rise to the structural diversity  
 RT in acetylcholinesterase.";  
 RL J. Biol. Chem. 263:18979-18987(1988).  
 RN [3]  
 RP SEQUENCE OF 552-558.  
 RA MEDLINE=88087239; PubMed=3335534;  
 RA Glibney G., McPhee-Quigley K., Thompson B., Vedvick T., Low M.G.,  
 RA Taylor S.S., Taylor P., Thompson B., Vedvick T., Low M.G.,  
 RT "Divergence in primary structure between the molecular forms of  
 RT acetylcholinesterase.";  
 RL J. Biol. Chem. 263:1140-1145(1988).  
 RN [4]  
 RP ALTERNATIVE SPLICING.  
 RA MEDLINE=90166618; PubMed=2306366;  
 RA Maulet Y., Camp S., Glibney G., Rachinsky T.L., Ekstrom T.J.,  
 RA Taylor P.;  
 RT "S<sub>1</sub> gene encodes glycopospholipid-anchored and asymmetric  
 RT acetylcholinesterase forms: alternative coding exons contain inverted  
 RT repeat sequences.";  
 RL Neuron 4:289-301(1990).  
 RN [5]  
 RP DISULFIDE BONDS.  
 RA MEDLINE=87008586; PubMed=3759980;  
 RA McPhee-Quigley K., Vedvick T.S., Taylor P., Taylor S.S.;  
 RT "Profile of the disulfide bonds in acetylcholinesterase.";  
 RL J. Biol. Chem. 261:13565-13570(1986).  
 RN [6]  
 RP STRUCTURE OF THE GPI-ANCHOR.  
 RA MEDLINE=94079692; PubMed=8257440;  
 RA Mehler A., Vazou L., Silman I., Homans S.W., Ferguson M.A.;  
 RT "Structure of the glycosyl-phosphatidylinositol membrane anchor of  
 RT acetylcholinesterase from the electric organ of the electric fish,  
 RT Torpedo californica.";  
 RL Biochem. J. 296:473-479(1993).  
 RN [7]  
 RP GPI-ANCHOR.  
 RA MEDLINE=96176849; PubMed=8597567;  
 RA Buche G., Hjalmarsson K.;  
 RT "Residues in Torpedo californica acetylcholinesterase necessary for  
 RT processing to a glycosyl phosphatidylinositol-anchored form.";  
 RL Biochim. Biophys. Acta 1292:223-232(1996).  
 RN [8]  
 RP MUTAGENESIS.  
 RA MEDLINE=91017542; PubMed=2227195;

SA Glibrey G., Camp S., Dicane N., McPhee-Quigley K., Taylor P.;  
 RT "Mutagenesis of essential functional residues in  
 RL acetylcholinesterase.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 87:7546-7550(1990).  
 RA X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=9143928; PubMed=1678899;  
 RA Sussman J.L., Harel M., Frolow F., Oefner C., Goldman A., Toker L.,  
 RL Silman I.,  
 RT Atomic structure of acetylcholinesterase from Torpedo californica: a  
 RL prototypic acetylcholine-binding protein.";  
 RN Science 253:872-879(1991).  
 RA X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF COMPLEX WITH FASCICULIN.  
 RX MEDLINE=9636373; PubMed=8747462;  
 RA Harel M., Kleywegt G.J., Ravelli R.B., Silman I., Sussman J.L.,  
 RT Crystal structure of an acetylcholinesterase-fasciculin complex:  
 RT interaction of a three-fingered toxin from snake venom with its  
 RL target.";  
 RN Structure 3:1355-1366(1995).  
 RA X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=97143314; PubMed=8893325;  
 RA Harel M.L., Harel M., Pang Y.P., Silman I., Kozikowski A.P.,  
 RA Sussman J.L.,  
 RT "Structure of acetylcholinesterase complexed with the neurotoxic  
 RL alkaloid, (-)-tubocurarine A.";  
 RN Nat. Struct. Biol. 4:57-63(1997).  
 RA X-RAY CRYSTALLOGRAPHY (3.7 ANGSTROMS).  
 RX MEDLINE=99249780; PubMed=16231521;  
 RA Bartolucci C., Perola E., Celai L., Brufani M., Jamba D.,  
 RT "Back door" opening implied by the crystal structure of a  
 RL cardamylated acetylcholinesterase.";  
 RN Biochemistry 38:5714-5719(1999).  
 RA X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=9928267; PubMed=1635614;  
 RA Willard C.B., Kryger G., Gendelich A., Greenblatt H.M., Harel M.,  
 RA Harel M.L., Segal Y., Sarak D., Shafferman A., Silman I.,  
 RA Sussman J.L.,  
 RT "Crystal structures of aged phosphorylated acetylcholinesterase:  
 RT nerve agent reaction products at the atomic level.";  
 RN Biochemistry 39:7032-7039(1999).  
 RA X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=20074924; PubMed=1606746;  
 RA Greenblatt H.M., Kryger G., Lewis T., Silman I., Sussman J.L.,  
 RT "Structure of acetylcholinesterase complexed with (-)-galanthamine at  
 RL 2.3-A resolution.";  
 RN FEBS Lett. 463:321-326(1999).  
 RA X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=99197295; PubMed=16368293;  
 RA Kryger G., Silman I., Sussman J.L.,  
 RT "Structure of acetylcholinesterase complexed with E2020 (Arixcept®):  
 RL implications for the design of new anti-alzheimer drugs.";  
 RN Structure 7:297-307(1999).  
 RA FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE.  
 CC MAY BE INVOLVED IN CELL-CELL INTERACTIONS.  
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H2O = Choline + acetate.  
 CC -1- SUBUNIT: THE H FORM IS AN HOMODIMER; THE ASYMMETRIC FORM IS A  
 CC DISULFIDE-BONDED OLIGOMER COMPOSED OF A COLLAGENIC SUBUNIT (Q) AND  
 CC A VARIABLE NUMBER OF T CATALYTIC SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: THE H FORM IS ATTACHED TO THE MEMBRANE BY A  
 CC GPI-ANCHOR.  
 CC -1- ALTERNATIVE PRODUCTS.  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=H; Synonyms=Globular;  
 CC IsoId=P04058-1; Sequence=Displayed;  
 CC Name=T;  
 CC IsoId=P04058-2; Sequence=VSP\_001460;

CC -1- TISSUE SPECIFICITY: AChE IS FOUND IN THE SYNAPSES AND TO A LOWER  
 CC EXTENT IN EXTRASYNAPTIC AREAS OF MUSCLE AND NERVE, AND ON  
 CC ERYTHROCYTE MEMBRANES.  
 CC -1- PTM: An interchain disulfide bond is present in what becomes  
 CC position 593 of the T isoform.  
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lyase family.  
 CC -----  
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 CC -----  
 DR EMBL; X03439; CAA27169.1; -;  
 DR EMBL; X56516; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; X56517; -; NOT\_ANNOTATED\_CDS.  
 DR PDB; 2ACE; 08-NOV-96.  
 DR PDB; 1ACJ; 31-AUG-94.  
 DR PDB; 2ACK; 11-FEB-98.  
 DR PDB; 1ACL; 31-AUG-94.  
 DR PDB; 1AMN; 03-APR-96.  
 DR PDB; 1FSS; 03-SEP-97.  
 DR PDB; 1VOT; 16-JUN-97.  
 DR PDB; 1AX9; 11-FEB-98.  
 DR PDB; 1EVE; 22-MAR-99.  
 DR PDB; 1CFJ; 01-APR-99.  
 DR PDB; 1OCF; 18-MAY-99.  
 DR PDB; 2DFP; 28-JUN-99.  
 DR PDB; 1BOM; 25-JUN-99.  
 DR PDB; 1DX6; 02-JAN-00.  
 DR PDB; 1EQQ; 01-OCT-02.  
 DR PDB; 1E66; 08-MAR-02.  
 DR PDB; 1EAS; 08-NOV-00.  
 DR PDB; 1EAA; 12-JAN-00.  
 DR PDB; 1GPN; 29-AUG-02.  
 DR PDB; 1GCR; 15-MAR-02.  
 DR PDB; 1GOS; 15-MAR-02.  
 DR PDB; 1H23; 16-JAN-03.  
 DR PDB; 1H5J; 05-OCT-01.  
 DR PDB; 1JJB; 18-SEP-02.  
 DR PDB; 1C1D; 28-JAN-00.  
 DR PDB; 1O1E; 28-JAN-00.  
 DR PDB; 1O1F; 28-JAN-00.  
 DR PDB; 1O1G; 28-JAN-00.  
 DR PDB; 1O1H; 28-JAN-00.  
 DR PDB; 1O1I; 28-JAN-00.  
 DR PDB; 1O1J; 28-JAN-00.  
 DR PDB; 1O1K; 28-JAN-00.  
 DR PDB; 1O1M; 28-JAN-00.  
 DR PDB; 1O1N; 28-JAN-00.  
 DR PDB; 1O1P; 28-JAN-00.  
 DR PDB; 1VXO; 26-SEP-01.  
 DR PDB; 1VXR; 26-SEP-01.  
 DR InterPro: IPR002018; Carboxylesterase.  
 DR InterPro: IPR000997; Cholinesterase.  
 DR InterPro: IPR003379; Ser\_estr\_site.  
 DR Pfam: PF00135; Coesterase; 1.  
 DR PRINTS: PRO0378; CHOLINESTRASE.  
 DR -----  
 Query Match 1.3%; Score 8; DB 1; Length 586;  
 Best Local Similarity 100.0%; Pred. No. 9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 SDCLYNT 132  
 DB 133 SDCLYNT 120  
 RESULT 37  
 ACES\_TORMA  
 ID ACES\_TORMA STANDARD; PRT; 590 AA.





```

RT "Characterization of the mouse pancreatic/mammary gland cholesterol
RT esterase-encoding cDNA and gene."
RL Gene 155:255-259(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=lactating mammary gland;
RX MEDLINE=9607098; PubMed=8510260;
RA Lidner A.S., Kannus M., Jundberg L., Bjursell G., Nilsson G.;
RT "Molecular cloning and characterization of the mouse carboxyl ester
RT lipase gene and evidence for expression in the lactating mammary
RT gland."
RL Genomics 29:115-122(1995).
CC -1- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONJUNCTION
CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION
CC OF DIETARY TRIGLYCERIDES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL: U33169; AAA82088.1; -
DR EMBL: U37386; AAC52279.1; -
DR PIR: A57701; A57701.
DR HSSP: P30122; 2BCE.
DR SWISS-2DPAGE: 064285; MOUSE.
DR MGI: 88374; Cel.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE B.1; 1.
DR PROSITE: PS00341; CARBOXYLESTERASE B.2; 1.
DR K01 Hydrolyase; Serine esterase; Lipid degradation; Glycoprotein;
KM Repeat: Signal: 1.
FT SIGNAL: 20 BY SIMILARITY.
FT CHAIN: 22 BY SIMILARITY.
FT ACT_SITE: 214 BILE-SALT-ACTIVATED LIPASE.
FT ACT_SITE: 340 BY SIMILARITY.
FT ACT_SITE: 455 BY SIMILARITY.
FT ACT_SITE: 455 BY SIMILARITY.
FT DISULFID: 84 BY SIMILARITY.
FT DISULFID: 266 BY SIMILARITY.
FT DOMAIN: 553 563 4 X 1; AA TANDEN REPEATS. C-GLYCOSYLATED
FT FT REGION.
FT REPEAT: 553 563
FT REPEAT: 570 580 2.
FT REPEAT: 581 588 3.
FT CARBOHYD: 207 N-LINKED (GLCNAC: 1) (POTENTIAL).
FT CARBOHYD: 325 325 N-LINKED (GLCNAC: 1) (POTENTIAL).
SQ SEQUENCE 599 AA; 65813 MW; 9E4428FDFCA8602E CAC661;

Query Match: 1.0%; Score 8; DB 1; Length 593;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 125 EDCLYINI 132
DB 98 EDCLYINI 105

RESULT 39
BAL_RAT STANDARD; PRT; 612 AA.
AC PC7882; P14722;
AC 01-AUG-1988 (rel. 09. Created)
DT 01-APR-1990 (rel. 14, last sequence update)

01-OCT-1996 (Rel. 34, last annotation update)
DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (EC 3.1.1.13) (BAL)
DE [Bile-salt-stimulated lipase] (BSSL) (Carboxyl ester lipase) (Sero)
DE esterase) (Cholesterol esterase) (pancreatic lysophospholipase).
CN CEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB: Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=pancreas;
RX MEDLINE=96089378; PubMed=2688744;
RA Kassel J.B., Fontaine R.N., Turk C.W., Brockman H.L., Hui D.Y.;
RT "Molecular cloning and expression of cDNA for rat pancreatic
RT cholesterol esterase."
RL Biochim. Biophys. Acta 1006:227-237(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87242339; PubMed=3593682;
RA Han J.H., Strickova C., Rutter W.C.;
RT "Isolation of full-length putative rat lysophospholipase cDNA using
RT improved methods for mRNA isolation and cDNA cloning."
RL Biochemistry 26:1617-1625(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91299758; PubMed=2069957;
RA Fontaine R.N., Carter C.P., Hui D.Y.;
RT "Structure of the rat pancreatic cholesterol esterase gene."
RL Biochemistry 30:7008-7014(1991).
RN [4]
RP ACTIVE SITE SER-214.
RX MEDLINE=91009095; PubMed=2211595;
RA Dipersio L.P., Fontaine R.N., Hui D.Y.;
RT "Identification of the active site serine in pancreatic cholesterol
RT esterase by chemical modification and site-specific mutagenesis."
RL J. Biol. Chem. 265:16801-16806(1990).
RN [5]
RP ACTIVE SITE HIS-455.
RX MEDLINE=91154187; PubMed=1999399;
RA Dipersio L.P., Fontaine R.N., Hui D.Y.;
RT "Site-specific mutagenesis of an essential histidine residue in
RT pancreatic cholesterol esterase."
RL J. Biol. Chem. 266:4033-4036(1991).
CC -1- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONJUNCTION
CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION
CC OF DIETARY TRIGLYCERIDES.
CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -1- ENZYME REGULATION: ACTIVATED BY BILE SALTS CONTAINING A 7-HYDROXY
CC GROUP.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE PANCREAS AND THEN
CC TRANSPORTED TO THE INTESTINE.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL: X16054; CA34189.1; -
DR EMBL: M15893; AA41540.1; -
DR PIR: A34967; AA46376.1; -
DR HSSP: P30122; 2BCE.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.

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DR PROSITE: PS00122; CARBOXYLESTERASE_B_1;
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase; Serine esterase; Lipid degradation; Glycoprotein;
KW Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 612 BILE-SALT-ACTIVATED LIPASE.
FT ACT_SITE 214 214 BY SIMILARITY.
FT ACT_SITE 340 340 BY SIMILARITY.
FT ACT_SITE 455 455 BY SIMILARITY.
FT DISULFID 84 100 BY SIMILARITY.
FT DISULFID 256 277 N-LINKED (GLYCNAIC...) (POTENTIAL).
FT CARBOHYD 257 207 4 X 11 AA TANDEN REPEATS, O-GLYCOSYLATED
FT CARBOHYD 556 599 REGION.
FT REPEAT 556 566 1.
FT REPEAT 567 577 2.
FT REPEAT 578 588 3.
FT REPEAT 589 599 4.
FT MUTAGEN 440 440 H->Q, NO EFFECT ON ACTIVITY.
FT 455 455 H->Q,R,A,S,D: AROMATIS ACTIVITY.
FT CONFLICT 26 26 V->L (IN REF. 2).
FT CONFLICT 154 154 G->A (IN REF. 2).
FT CONFLICT 217 217 A->G (IN REF. 2).
FT CONFLICT 219 219 S->T (IN REF. 2).
FT CONFLICT 419 419 M->T (IN REF. 2) AND 31.
FT CONFLICT 513 513 T->N (IN REF. 3).
FT CONFLICT 576 577 GG->VV (IN REF. 3).
FT CONFLICT 608 609 GP->VA (IN REF. 3).
FT CONFLICT 611 611 G->A (IN REF. 3).
SQ SEQUENCE 612 AA; 67340 MW; 1569CEAE71E02A CRC64;

Query Match 1.0%; Score 8; DB 1; Length 612;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCCYLNI 132
Db 98 EDCCYLNI 105

RESULT 40
ACES_LERPDE STANDARD; PRT; 629 AA.
ID ACES_LERPDE
AC 027677;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
OS Lepitocrara decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
OC Physophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Lepitocrara.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SS; TISSUE=Larva, and Pupae;
RX MEDLINE=96337147; PubMed=8563913;
RA Zhu K.Y., Clark J.X.;
RT "Cloning and sequencing of a cDNA encoding acetylcholinesterase in
RT Colorado potato beetle, Lepitocrara decemlineata (Say).";
RJ Insect Biochem. Mol. Biol. 25:1129-1138(1995).
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBCELLULAR LOCATION: LINKED TO THE MEMBRANE OF THE NEURONAL
CC -1- CHOLINERGIC SYNAPSES BY A GPI-ANCHOR (BY SIMILARITY).
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC -----
DR EMBL: L41180; AAC0466.1; -.
DR HSSP: P21836; 1MAA.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser.estr._site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1;
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase; Serine esterase; Synapse; Membrane; Nerve; Signal;
KW Neurotransmitter degradation; Gpi-anchor; Glycoprotein.
FT SIGNAL 1 29 ACETYLCHOLINESTERASE.
FT CHAIN 30 629
FT ACT_SITE 253 253 BY SIMILARITY.
FT ACT_SITE 382 382 BY SIMILARITY.
FT ACT_SITE 496 496 BY SIMILARITY.
FT DISULFID 103 130 BY SIMILARITY.
FT DISULFID 307 322 BY SIMILARITY.
FT DISULFID 458 574 BY SIMILARITY.
FT DISULFID 585 595 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 125 125 N-LINKED (GLYCNAIC...) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLYCNAIC...) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLYCNAIC...) (POTENTIAL).
FT CARBOHYD 509 509 N-LINKED (GLYCNAIC...) (POTENTIAL).
SQ SEQUENCE 629 AA; 71142 MW; 06556F833EB16C72 CRC64;

Query Match 1.0%; Score 8; DB 1; Length 629;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCCYLNI 132
Db 128 EDCCYLNI 135

RESULT 41
ACES_ANOCT STANDARD; PRT; 664 AA.
ID ACES_ANOCT
AC P56161;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
OS Anopheles stephensi (Indo-Pakistani malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=30659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91191507; PubMed=1901515;
RA Hall L.M.C., Malcolm C.A.;
RT "The acetylcholinesterase gene of Anopheles stephensi.";
RJ Cell. Mol. Neurobiol. 11:131-141(1991).
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC IF CAN HYDOLYZE BUTYRYLTHIOCHOLINE.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: THE ACTIVE ENZYME SEEMS TO BE COMPOSED OF THE NON-
CC COVALENT ASSOCIATION OF A 55 kDa AND A 16 kDa POLYPEPTIDE. TWO
CC ACTIVE UNITS ARE LINKED TOGETHER BY A DISULFIDE BOND AT THE C-
CC TERMINUS OF THE 55 kDa PEPTIDE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: LINKED TO THE MEMBRANE OF THE NEURONAL
CC -1- CHOLINERGIC SYNAPSES BY A GPI-ANCHOR.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR HSSP: P21836; 1MAA.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser.estr._site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.

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AC 062101;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, mu type (EC 2.7.1.1) (PKC_mu); (protein kinase D).
GN PKCM OR PKCM OR PKD.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BAB/c; TISSUE=Lung;
RX MEDLINE=9435973; PubMed=8073925;
RA Valverde A.M., Simet-Smith J., Van Vint J., Rozengurt E.;
RT "Molecular cloning and characterization of protein kinase D: a target
RT for diacylglycerol and phorbol esters with a distinctive catalytic
RT domain."
RL Proc. Natl. Acad. Sci. U.S.A. 91:6576-6576(1994).
RN (2)
RP PHOSPHORYLATION OF SER-916.
RX MEDLINE=9940316; PubMed=104736-7;
RA Matthews S.A., Rozengurt E., Cantrell D.;
RT "Characterization of serine 916 as an in vivo autophosphorylation site
RT for protein kinase D/protein kinase Cmu."
RL J. Biol. Chem. 274:26543-26549(1999).
CC 1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHO-LIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC 1- ENZYME REGULATION: ACTIVATED BY DIACYLGLYCEROL AND PHORBOL ESTERS.
CC 1- PTM: Autophosphorylated.
CC 1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
DR EXBL: Z34524; CAA84283.1;
DR PIR: I48719; I48719.
DR HSSP: P28867; IPTQ.
DR MGD: MGI:99879; PKCM.
DR InterPro: IPR002219; DAG_FE-bind.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000719; PKC-kinase.
DR InterPro: IPR002230; Ser_thr_kinase.
DR Pfam: PF00133; DAG_PE-bind; 2.
DR Pfam: PF00163; PH; 1.
DR Pfam: PF00069; Kinase; 1.
DR PRINTS: PR00338; DAGPEDOMAIN.
DR PRODOM: PD00063; PKC_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SMC0233; PH; 1.
DR SMART: SMC0220; S_TKC; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2.
DR PROSITE: PS50093; PH_DOMAIN; 1.
DR PROSITE: PS00137; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50013; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat; Phosphorylation.
FT DOMAIN 145 194 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 277 326 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 428 547 PH.
FT DOMAIN 589 645 PROTEIN KINASE.
FT DOMAIN 16 26 POLY-ALA.

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FT DOMAIN 198 201 POLY-ARG.
FT NP_BIND 595 603 ATP (BY SIMILARITY).
FT BINDING 618 618 ATP (BY SIMILARITY).
FT ACT_SITE 712 712 BY SIMILARITY.
FT MOD_RES 916 916 PHOSPHORYLATION (ATTC-1).
SQ SEQUENCE 918 AA; 102067 MW; 234486186521BDDA CRC64;

Query Match 1.0%; Score 8; DB 1; Length 918;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDDDIDHQ 163
DB 791 EDDDIDHQ 798

RESULT 46
GUT1 YEAST STANDARD; PRT: 2:44 AA.
ID GUT1 YEAST
AC Q12680; Q12290;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 35, Last annotation update)
DE Glutamate synthase (NADPH precursor) (EC 1.4.1.13) (NADPH-GOGAT).
GN GUT1 OR YDL171C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN (1)
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC STRAIN=CN36;
RX MEDLINE=97082505; PubMed=892374;
RA Flierici P., Martegani M.P., Valenzuela L., Gonzalez A., Ballario P.;
RT "Sequence of the GUT1 gene from Saccharomyces cerevisiae reveals the
RT domain structure of yeast glutamate synthase."
RL Yeast 12:1359-1366(1996).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Pohl T.M.;
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC 1- CATALYTIC ACTIVITY: 2 L-glutamate + NADP(+) = L-glutamine + 2-
CC oxoglutarate + NADPH.
CC 1- COFACTOR: BINDS A 3Fe-4S CLUSTER; FAD AND FMN.
CC 1- SUBUNIT: Homotrimer.
CC 1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
CC -----
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CC -----
DR EXBL: X89221; CAA61505.1;
DR EMBL: Z67750; CAA91574.1;
DR EMBL: Z74219; CAA98745.1;
DR SCD: SC002330; GUT1.
DR GO: GO:0005623; C:cell; IDA.
DR GO: GO:0006537; P:glutamate biosynthesis; IEF.
DR InterPro: IPR000759; AGRdx_reductase.
DR InterPro: IPR002489; DCF11.
DR InterPro: IPR001327; FAD pyr_redox.
DR InterPro: IPR006982; Glu_syn_central.
DR InterPro: IPR006593; Glu_syn_NTN.
DR InterPro: IPR002932; Glu_synthase.
DR InterPro: IPR006005; Glu_synth_sub1.
DR InterPro: IPR000103; Pyridine_redox_2.
DR Pfam: PF04898; Glu_syn_central; 1.
DR Pfam: PF04897; Glu_syn_NTN; 1.
DR Pfam: PF01645; Glu_synthase; 1.

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DR Pfam: PF01433; GXXGX; 1.
DR Pfam: PF00370; Pyr_redox; 1.
DR PRINTS; PR00419; ADXRTASE.
DR PRINTS; PR00368; FADPR.
DR PRINTS; PR00469; PDRRTASE1.
DR TIGRfam: TIGR01317; GOGAT sm Gam; 1.
KW Oxidoreductase; iron-sulfur; fea-4S; Flavoprotein; FAD; FMN; NADP;
KW Glutamate biosynthesis; Zymogen.
FT PROPEP 1 53
FT CHAIN 54 2144
FT NP_BIND 1132 1163
FT METAL 1184 1184
FT METAL 1190 1190
FT METAL 1195 1195
FT CONFLICT 32 32
FT CONFLICT 168 172
FT CONFLICT 449 451
FT CONFLICT 1752 1752
SC SEQUENCE 2144 AA; 238200 MW; 5AA6948EF995149 CRC64;

Query Match 1.00; Score 8; DB 1; Length 2144;
Best Local Similarity 100.00; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0

CY 702 KRRETR 709
DB : 647 KRRETR 1654

RESULT 47
THYG_MOUSE STANDARD; PRT; 2766 AA.
ID THYG_MOUSE
AC 008710; O93590; Q90WY7;
ST 31-NOV-1997 (Ref. 35, Created)
DT 16-OCT-2001 (Ref. 40, Last sequence update)
DT 16-OCT-2001 (Ref. 40, Last annotation update)
DE Thyroglobulin precursor.
GN TG OR TGN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId:10091;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98008184; PubMed=9344706;
RA Caturegli P., Vidarain P.O., Vail M., Aguileta-Galaviz L.A.,
RA Rose N.R.
RT "Cloning and characterization of murine thyroglobulin cDNA."
RL Clin. Immunol. Immunopathol. 85:221-226(1997).
RN 12
RP SEQUENCE FROM N.A. AND VARIANT GOITER PRO-2283.
RC STRAIN=COG; TISSUE=Thyroid;
RX MEDLINE=98374279; PubMed=9707574;
RA Kim P.S., Hossain S.A., Park Y.-N., Lee I., Yoo S.-E., Arvan P.;
RT "A single amino acid change in the acetylcholinesterase-like domain of
thyroglobulin causes congenital goiter with hypothyroidism in the
cog/cog mouse: a model of human endoplasmic reticulum storage
diseases."
RT Proc. Natl. Acad. Sci. U.S.A. 95:9909-9913(1998).
RN 13
RP SEQUENCE FROM N.A.
RC STRAIN=AKR/J; TISSUE=Thyroid;
RA Hossain S.A., Yoo S.-E., Kim P.S.;
RT "Cloning, characterization, site-directed mutagenesis, and transient
expression of 8501-nucleotide AKR/J mouse thyroglobulin cDNA:
detection of a mutation in AKR/J mouse thyroglobulin cDNA."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PEPCOR OF THE IODINATED THYROID HORMONES THYROXINE
(74) AND TRIIODOTHYRONINE (73).
CC -1- SUBUNIT: Homodimer (by similarity).
CC -1- SUBCELLULAR LOCATION: secreted.
CC -1- TISSUE SPECIFICITY: THYROID GLAND SPECIFIC (BY SIMILARITY).
CC -1- PTM: SULFATED (BY SIMILARITY)

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[illegible]

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FT CARBOHYD 2294 2294 N-LINKED GLCNAC. (POTENTIAL).
FT CARBOHYD 2581 2581 N-LINKED GLCNAC. (POTENTIAL).
FT VARIANT 2283 2283 E -> P (IN GOITER).
FT CONFLICT 80 80 E -> K (IN REF. 2 AND 3).
FT CONFLICT 92 92 V -> I (IN REF. 2 AND 3).
FT CONFLICT 1327 1327 T -> A (IN REF. 2 AND 3).
FT CONFLICT 1427 1427 N -> S (IN REF. 1).
FT CONFLICT 1427 1427 N -> S (IN REF. 1).
FT CONFLICT 1436 1442 RTLOGM -> GLSLDY. (IN REF. 1).
FT CONFLICT 1721 1721 I -> T (IN REF. 2 AND 3).
FT CONFLICT 1813 1813 S -> T (IN REF. 1).
FT CONFLICT 1957 1957 RVK -> KVN (IN REF. 2 AND 3).
FT CONFLICT 2092 2092 S -> SS (IN REF. 2).
FT CONFLICT 2407 2407 R -> K (IN REF. 2 AND 3).
FT CONFLICT 2414 2414 G -> S (IN REF. 2 AND 3).
FT CONFLICT 2427 2427 R -> K (IN REF. 2 AND 3).
FT CONFLICT 2434 2434 A -> T (IN REF. 2 AND 3).
FT CONFLICT 2453 2453 TSSICEVVSCL -> NTHGSGTXYF (IN REF. 2 AND 3).
FT CONFLICT 2728 2728 D -> GN (IN REF. 1).
SQ SEQUENCE 2766 AA; 354512 MW; E195351DC5793A03 CRC64;

Query Match 1.0%; Score 8; DB 1; Length 2766;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYN 131
DB 2277 NEDCLYN 2284

RESULT 48
JHA_RHOMA STANDARD; PRT; 52 AA.
ID LHA_RHOMA
AC P80259;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Light-harvesting protein B-860, alpha chain (Antenna pigment protein, alpha chain).
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhodospirillum rubrum.
OX NCBI_TaxID=1080;
RN [1]
RP SEQUENCE.
RC STRAIN=DSV 2693;
RX MEDLINE=89351188; PubMed=2669779;
RA Brunschwig R.A., Bissig T., Wagner-Huber R., Frank G., Suter F.,
RA Niederer E., Zuber H.;
RT "The primary structures of the core antenna polypeptides from
RT Rhodospirillum rubrum."
RZ. Naturforsch. C 44:407-414 (1989).
CC -1- FUNCTION: ANTENNA COMPLEXES ARE LIGHT-HARVESTING SYSTEMS, WHICH
CC TRANSFER THE EXCITATION ENERGY TO THE REACTION CENTERS.
CC -1- SUBUNIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA
CC CHAINS. BINDING BACTERIOCHLOROPHYLL MOLECULES, AND ARRANGED
CC MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE
CC REACTION CENTER. THE NON-PIGMENTED GAMMA CHAINS MAY CONSTITUTE
CC ADDITIONAL COMPONENTS.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
CC InterPro: IPR000066; Antenna a/b.
DR InterPro: IPR002361; Antenna a/b.
DR Pfam: PF00556; LHC_1.
DR PRINTS: PR00673; LIGHTHARVSTA.
DR PROSITE: PS00968; ANTENNA_COMP_ALPHA.
KW Antenna complex; light-harvesting polypeptide; Transmembrane;
KW Macromolecular complex; Bacteriochlorophyll; Inner membrane.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 33 POTENTIAL.
FT DOMAIN 34 52 PERIPLASMIC (POTENTIAL).
FT METAL 29 29 MAGNESIUM (BACTERIOCHLOROPHYLL AXIAL
FT LIGAND) (POTENTIAL).
SQ SEQUENCE 52 AA; 6095 MW; 5DBE633E3010C6B9 CRC64;

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Query Match 0.9%; Score 7; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 440 TLVALFT 446
DB 13 TLVALFT 19

RESULT 49
Y55B MYCGE STANDARD; PRT; 127 AA.
ID Y55B MYCGE
AC Q92B81;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG055.2.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischman R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fritchman J.L.,
RA Nguyen D.T., Uterback T.R., Sauder D.M., Phillips C.A., Merrick J.W.,
RA Tomb J.-F., Dougherty B.A., Bitt K.F., Hu P.-C., Zuckers T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403 (1995).
RN [2]
RP IDENTIFICATION.
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischman R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fritchman J.L.,
RA Nguyen D.T., Uterback T.R., Sauder D.M., Phillips C.A., Merrick J.W.,
RA Tomb J.-F., Dougherty B.A., Bitt K.F., Hu P.-C., Zuckers T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
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CC -----
DR EMBL: U39685; AAC1281.1; -.
DR TIGR: MG055.2; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 13 35 POTENTIAL.
FT TRANSMEM 57 81 POTENTIAL.
SQ SEQUENCE 127 AA; 14631 MW; 4F0F3E6726D5ECF CRC64;

Query Match 0.9%; Score 7; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 LHNLEI 603
DB 7 LHNLEI 13

RESULT 50
REFA ANASP STANDARD; PRT; 133 AA.
ID REFA ANASP
AC Q820M8;
DT 28-FEB-2003 (Rel. 41, Created)

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EC 28-FEB-2003 (Rel. 41, Last sequence update)
LT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-binding factor A.
GN RBFA OR ABR0063.
CS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
ON NCBI_TaxID=103690.
RX MEDLINE=21595285; PubMed=1759840;
RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matsubara A., Itiguchi M., Shikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara Y., Matsumoto Y., Matsuro A., Kuraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT Cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
CC -!- FUNCTION: Associates with free 30S ribosomal subunits (but not
CC with 30S subunits that are part of 70S ribosomes or polysomes).
CC Essential for efficient processing of 16S rRNA. May interact with
CC the 5' terminal helix region of 16S rRNA (by similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: BELONGS TO THE RBFA FAMILY.
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CC EMBL: AP003581; BAB7587.1; -.
DR PIR: AGI814; AGI814.1.
DR HAMAP: MF_00003; -.
DR InterPro: IPR000239; Rib_bind_factA.
DR Pfam: PF02333; RBFA; 1.
DR ProDom: PD020327; Rib_bind_factA; 1.
DR TIGRfam: TIGR00062; Rbfa; 1.
DR PROSITE: PS01319; RBFA; 1.
KM rRNA processing; complete proteome
SQ SEQUENCE 133 AA; 14665 MW; 68994937547BFC54 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 RSPDIP 772
DB 118 RSPDIP 124

RESULT 51
CHLE_BOVIN STANDARD; PRT; 141 AA.
ID CHLE_BOVIN
AC P32749;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline
DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase)
DE (Fragment).
GN SCHE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Sutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=91201348; PubMed=2016308;

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RA Arpagaus M., Chatornet A., Masson P., Newton M., Vaughan T.A.,
RA Batteis C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates."
RL J. Biol. Chem. 266:6966-6974(1991).
CC -!- CATALYTIC ACTIVITY: An acetylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -!- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC -!- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -!- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC or send an email to license@isb-sib.ch).
CC EMBL: M62410; AAA51412.1; -.
DR PIR: F39768; F39768.
DR HSPB; P22303; 2CLD.
DR InterPro: IPR02018; Carbesterease.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR00379; Ser esters_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLNESTERASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_2; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KM Hydroxylase; Serine esterase; Glycoprotein.
FT NON_TER 1 1
FT ACCT_SITE 131 131 BY SIMILARITY.
FT CARBOHYD 33 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 141 141
SO SEQUENCE 141 AA; 15234 MW; 5FDFA11730564D3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLN 131
DB 23 EDCYLN 29

RESULT 52
CHLE_CANFA STANDARD; PRT; 141 AA.
ID CHLE_CANFA
AC P32750;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline
DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase)
DE (Fragment).
GN SCHE.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butleria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpagaus M., Chatornet A., Masson P., Newton M., Vaughan T.A.,
RA Batteis C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates."
RL J. Biol. Chem. 266:6966-6974(1991).
CC -!- CATALYTIC ACTIVITY: An acetylcholine + H(2)O = choline + a

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CC carboxylic acid anion.
CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M62411; AAA5145.1; -.
CC PIR: E39768; E39768.
CC HSSP: P22303; 2CLD.
CC InterPro: IPR002018; Carboxylesterase.
CC InterPro: IPR000937; Cholinesterase.
CC InterPro: IPR000379; Ser_estrs_site.
CC Pfam: PF00135; Coesterase_1.
CC PRINTS: PR00878; CHOLNESTRASE.
CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
CC KX Hydroxylase; Serine esterase; Glycoprotein.
CC FT ACT_SITE 131 131 BY SIMILARITY.
CC CARBOHYD 39 39 N-LINKED (GLCNAC... ) (POTENTIAL).
CC NON_TER 141 141
CC SEQUENCE 141 AA; 15086 MW; 9F81584590111FEB CRC64;

Query Match 0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 23 EDCLYLN 29

RESULT 53
CHLE_PIG STANDARD; PRT; 141 AA.
ID CHLE_PIG STANDARD; PRT; 141 AA.
AC P32751;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
DE esterase 1) (Butyrylcholine esterase) (Pseudocholinesterase)
DE (Fragment).
DE BCH2.
GN Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Carnivora; Canidae;
OC Canis lupus familiaris; Canis.
OC NCB1_TaxID=96823;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpaegus M., Chalmers A., Masson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polypeptide chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
```

```
CC ORGANOPHOSPHATE ESTERS.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M62777; AAA5636.1; -.
CC PIR: G39768; G39768.
CC HSSP: P22303; 2CLD.
CC InterPro: IPR002018; Carboxylesterase.
CC InterPro: IPR000937; Cholinesterase.
CC InterPro: IPR000379; Ser_estrs_site.
CC Pfam: PF00135; Coesterase_1.
CC PRINTS: PR00878; CHOLNESTRASE.
CC PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
CC KX Hydroxylase; Serine esterase; Glycoprotein.
CC FT ACT_SITE 131 131 BY SIMILARITY.
CC CARBOHYD 39 39 N-LINKED (GLCNAC... ) (POTENTIAL).
CC NON_TER 141 141
CC SEQUENCE 141 AA; 15224 MW; A3C1135E650D636 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 23 EDCLYLN 29

RESULT 54
CHLE_PIG STANDARD; PRT; 141 AA.
ID CHLE_PIG STANDARD; PRT; 141 AA.
AC P32752;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
DE esterase 1) (Butyrylcholine esterase) (Pseudocholinesterase)
DE (Fragment).
DE BCH2.
GN Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCB1_TaxID=96823;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Arpaegus M., Chalmers A., Masson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polypeptide chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M62778; AAA31005.1; -
DR PIR: D39768; D39768.
DR HSSP: P22303; ZCLJ.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PFC0135; Coesterase; 1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR KMe Hydrolase; Serine esterase; Glycoprotein.
FT ACT_SITE 131 133 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC...) (POTENTIAL).
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 15250 MW; 43D869C48D4164C CRC64;

Query Match 0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 23 EDCLYLN 29

RESULT 55
CHIEF_SHEEP
ID CHIEF_SHEEP STANDARD; PRT; 141 AA.
AC P32753;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-OCT-2001 (Rel. 43, Last annotation update)
DE Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
DE esterase II) (Butyrylcholine esterase) (Pseudocholinesterase)
DE [Fragment].
DE
OS Ovis aries (Sheep).
OS BCFE.
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Caprinae; Ovis.
CC NCBI_TaxID=9940;
CC
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91201348; PubMed=2016308;
RA Apagaus M., Chatornet A., Masson P., Newton M., Vaughan T.A.,
RA Barteis C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
RT butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC
CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE
CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
CC
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC
CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
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DR EMBL: M62780; AAA31509.1; -
DR PIR: B39768; B39768.
DR HSSP: P22303; ZCLJ.
DR InterPro: IPR002018; CarboxylesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PFC0135; Coesterase; 1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR KMe Hydrolase; Serine esterase; Glycoprotein.
FT ACT_SITE 131 131 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC...) (POTENTIAL).
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 15234 MW; 5FDFA11730564D3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 23 EDCLYLN 29

RESULT 56
CUS5_ARADI
ID CUS5_ARADI STANDARD; PRT; 156 AA.
AC P80519;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Adult-specific rigid cuticular protein 15.5 (ACP 15.5).
DE
OS Araneus diadematus (Spider).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
CC Araneomorphae; Eutelegynae; Araneoidae; Araneidae; Araneus.
CC NCBI_TaxID=45920;
CC
RN 11
RP SEQUENCE.
RC TISSUE=Cuticle;
RX MEDLINE=9716616; PubMed=9014336;
RA Norup T., Berg T., Stenholm H., Andersen S.O., Hoojrup P.;
RT "Purification and characterization of five cuticular proteins from
RT the spider Biochem. Mol. Biol. 26:907-915(1996).
CC
CC -1- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.
CC -1- MASS SPECTROMETRY: MM=15464.7; METHOD=Electrospray.
CC InterPro: IPR00618; Insect_cuticle.
CC Pfam: PF00379; Chitin bind_4; 1.
DR PROSITE: PS00233; CUTICLE_1.
DR Structural protein; Cuticle.
SQ SEQUENCE 156 AA; 15463 MW; 89C7AD3DBA5107D CRC64;

Query Match 0.9%; Score 7; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 VAPAVAA 457
DB 104 VAPAVAA 110

RESULT 57
CUS7_ARADI
ID CUS7_ARADI STANDARD; PRT; 159 AA.
AC P80519;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Adult-specific rigid cuticular protein 15.7 (ACP 15.7).
DE
OS Araneus diadematus (Spider).
CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
```

CC Araneomorphae; Entelegyidae; Araneidae; Araneidae; Araneus.  
CX NCBI\_TaxID=45920;  
RN (1)  
RP SEQUENCE.  
RC Tissue=Cuticle;  
RX MEDLINE=9716616; PubMed=90:4336;  
RA Nordt T., Berg T., Stenholm H., Andersen S.O., Hooprup P.;  
RT "Purification and characterization of five cuticular proteins from  
the spider Araneus diadematus";  
RL Insect Biochem. Mol. Biol. 26:907-915(1996).  
CC -1- FUNCTION: COMPONENT OF THE RIGID CUTICLE OF THE SPIDER.  
CC -1- MASS SPECTROMETRY: MW=15682.9; METHOD=Electrospray.  
DR InterPro: IPR000655; Insect-cuticle.  
DR Pfam: PF00373; Cutinase\_4; 1.  
DR PRINTS: PR03947; CUTICLE.  
DR PROSITE: PS00233; CUTICLE; 1.  
KW Structural protein; Cuticle.  
KW DOMAIN 92  
SQ SEQUENCE 159 AA; 15682 MW; 6FBA35E2299F598 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 159;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 451 VAPAVAA 457  
Db 109 VAPAVAA 115

RESULT 58  
EST1\_SCHGA

ID EST1\_SCHGA STANDARD; PRT; 198 AA.  
AC P81429;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Esterase SG1 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase)  
DE (Fragment).  
CK SGI

OS Schizaphis graminum (Aphid).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
OC Aphidoidea; Aphididae; Aphidini; Schizaphis.  
RN NCBI\_TaxID=13362;  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-41.  
RX MEDLINE=20078165; PubMed=10612041;  
RA Ono M., Swanson C.J., Field L.M., Devonshire A.L., Siegfried B.O.;  
RT "Amplification and methylation of an esterase gene associated with  
insecticide-resistance in greenbugs, Schizaphis graminum";  
RL Insect Biochem. Mol. Biol. 23:1065-1073(1998).  
CC -1- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON  
CC MECHANISM OF RESISTANCE TO ORGANOPHOSPHATE INSECTICIDES.  
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
CC carboxylic acid.  
CC -1- SIMILARITY: BELONGS TO THE type-B carboxylesterase/lipase family.  
CC -----  
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CC -----  
DR EMBL: Y17580; CAA75732.1; -  
DR HSSP: P37967; 1OE3.  
DR InterPro: IPR02018; Carboxesterase.  
DR Pfam: PF00135; Coesterase; 1.  
DR PROSITE: PS00122; CARBOXYLESTERASE\_B\_1; PARTIAL.  
DR PROSITE: PS00941; CARBOXYLESTERASE\_B\_2; 1.  
KW Hydrolase; Serine esterase; Glycoprotein; Signal.

FT SIGNAL 1 21  
FT CHAIN 22 >198  
FT DISULFID 87 104  
FT CARBOHYD 73 79  
FT CONFLICT 24 24  
FT CONFLICT 28 28  
FT NON\_TER 198 198  
SQ SEQUENCE 198 AA; 21897 MW; EFFE43E6A5D5987 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 198;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 125 EDCVLYN 131  
Db 102 EDCVLYN 108

RESULT 59

SC21\_RICCN  
ID SC21\_RICCN STANDARD; PRT; 199 AA.  
AC Q92JW5;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE SC02-like protein RCO042.  
GX RCO042.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
CX NCBI\_TaxID=781;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish N.;  
RX MEDLINE=21442074; PubMed=11557893;  
RA Oeata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
RA Raoult D.;  
RT Mechanisms of evolution in Rickettsia conorii and R. prowazekii;  
RL Science 293:2093-2098(2001).  
CC -1- SIMILARITY: BELONGS TO THE SC01/2 FAMILY.  
CC -----  
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CC -----  
DR EMBL: AE008572; AA02580.1; -  
DR PIR: B97705; B97705.  
DR InterPro: IPR03782; SC01\_Senc.  
DR Pfam: PF02610; SC01-Senc; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 199 AA; 23101 MW; 80CA08DD4DF0CB4 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 199;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 15 IKFTLID 21  
Db 53 IKFTLID 59

RESULT 60  
G1DA\_COXBU  
ID G1DA\_COXBU STANDARD; PRT; 204 AA.  
AC P94614;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Methyltransferase gids (EC 2.1.1.1) (Glucose inhibited division
DE protein 3).
GN GIDS OR G201925.
OS Coxella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_Taxid=777;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I;
RA Willems H., Jaeger C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN
(2)
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I / RSA 493;
RX MEDLINE=22608557; PubMed=12704232;
RA Sedlitz R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Davidson T.M., Beaman M.T.,
RA Debey R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.O.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzer R.A.,
RA Thompson H.A., Samuel U.E., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
RT burnetii."
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
CC -!- FUNCTION: Probable S-adenosyl-L-methionine dependent
CC methyltransferase specific for a sterol and/or lipid substrate (by
CC similarity). BELONGS TO THE GIDS FAMILY.
CC
CC -!- SIMILARITY: BELONGS TO THE GIDS FAMILY.
CC
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CC
DR EMBL: Y10436; CAA7146C.1;
DR EMBL: AEC6966; AAO94416.1;
DR TIGR: CB01925;
DR HAXAP: MF_00074;
DR InterPro: IPR003682; GIDB.
DR InterPro: IPR000051; SAM_bind.
DR Pfam: PF02527; GIDB; 1.
DR Pfam: PF004441; GIDB; 1.
DR TIGRfam: TIGR00308; gids; 1.
DR Transferase; Methyltransferase.
SQ SEQUENCE 204 AA; 22617 MW; EF70B016C18F445E CRC64;

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Query Match 0.9%; Score 7; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 16 KFTLIDS 22
Dh 91 KFTLIDS 97

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RASCUT 61
MAUD METEX STANDARD; PRT; 205 AA.
AC Q49126;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Methylamine utilization protease maud.
GN MAUD.
OS Methylbacterium extorquens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Methylbacteriaceae; Methylbacterium.
OX NCBI_Taxid=408;
RN
RP SEQUENCE FROM N.A.

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RC STRAIN=AT / NCIMB 9133;
RX MEDLINE=94292425; PubMed=8021167;
RA Chistoseedov A.Y., Chistoseedova L.V., McInliffe W.S., Lidstrom M.E.;
RT "Genetic organization of the mau gene cluster in Methylbacterium
RT extorquens AM1: complete nucleotide sequence and generation and
RT characteristics of mau mutants."
RL J. Bacteriol. 176:4052-4065(1994).
CC -!- FUNCTION: MAY BE SPECIFICALLY INVOLVED IN THE PROCESSING,
CC TRANSPORT, AND/OR MATURATION OF THE MAUD BETA-SUBUNIT.
CC -!- PATHWAY: Methylamine utilization.
CC
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CC
DR EMBL: J26406; AAB46935.1;
DR PIR: A38123; A38123.
DR InterPro: IPR006663; ThioRedox_dom2.
FM TRANSMEMBRANE.
FT TRANSMEM 5 25 POTENTIAL.
SQ SEQUENCE 205 AA; 22233 MW; 78364F5DA07C1104 CRC64;

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Query Match 0.9%; Score 7; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 SNVLMWL 10
Dh 9 SNVLMWL 15

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RESULT 62
YHVN_ECOLI.
ID YHVN_ECOLI. STANDARD; PRT; 208 AA.
AC P37676;
DT 01-OCT-1994 (rel. 30, Created)
DT 01-OCT-1994 (rel. 30, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Hypothetical protein yhnV.
GN YHVN OR B3468 OR C4261 OR Z4842 OR EC04317 OR SF3486.
CS Escherichia coli.
CS Escherichia coli O6.
CS Escherichia coli O157:H7. and
CS Shigella flexneri.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562, 217992, 83334, 623;
RN
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes."
RL Nucleic Acids Res. 22:2576-2586(1994).
RN
(2)
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=CG.H1 / CF7073 / ATCC 700928;
RX MEDLINE=2388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liu S.-R., Boutin A., Hackert J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN
(3)
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;

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RA MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Pankett G. III, Burling V., Mau R., Claesner J.C.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett C., Klink S., Boutin A., Shao Y., Miller B.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocostas K.,
RA Apodaca J., Aancharatan T.S., Lin T., Yen G., Schwartz D.C.,
RA Welch R.A., Baitner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0503952;
RX MEDLINE=2155623; PubMed=11258755;
RA Hayash T., Makino K., Chishiki M., Kirokawa K., Ishii K., Nishiyama K.,
RA Han C.-G., Otsubo E., Nakayama K., Murata T., Tanaka Y., Tobe T.,
RA Iida T., Takai H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kohara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 9:111-22(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu C., Wang Y., Lu M., Wang T., Du H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun Y., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang J., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157:H7."
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -----
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CC -----
DR EMBL; U00039; AAB18443.1; -
DR EMBL; AE000422; AAC76493.1; -
DR EMBL; AE015768; AAN82697.1; -
DR EMBL; AE005570; AAG58577.1; -
DR EMBL; AE002565; BAB37740.1; -
DR EMBL; AE015356; AAN44945.1; -
DR FTR; E86014; E86014; -
DR PIR; E86014; E86014; -
DR PIR; E91168; E91168; -
DR PIR; S47687; S47687; -
DR ECGene; E612214; yhmN; -
KM Hypothetical protein; Complete proteome.
FT CONFLICT 56 L -> Q (IN REF. 3).
SQ SEQUENCE 208 AA; 23790 MW; 9409944326CECB9E CRC64;

Query Match 0.9%; Score 7; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 681 VGASLLEF 687
DB 163 VGASLLEF 169

RESULT 63
TRAR AGRTV STANDARD; PRT; 234 AA.
AC P33959;
CT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Transcriptional activator protein trar.
GN TRAR.

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OS Agrobacterium vitis (Rhizobium vitis).
OC Bacteriia; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OC NCBI_TaxID=373;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2608;
RX MEDLINE=94281667; PubMed=8012036;
RA Fournier P., de Ruffray P., Otten L.;
RT "Natural instability of Agrobacterium vitis T1 plasmid due to unusual
RT duplication of a 2.3-kb DNA fragment."
RL Mol. Plant Microbe Interact. 7:164-172(1994).
CC -1- FUNCTION: POSITIVE REGULATION OF CONJUGAL TRANSFER OF T1
CC PLASMIDS.
CC -1- SIMILARITY: BELONGS TO THE LUXE/UMPA FAMILY OF TRANSCRIPTIONAL
CC REGULATORS. AUTOINDUCER REGULATED SUBSTRATE.
CC -----
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CC -----
DR EMBL; Z22732; CAAB0423.1; -
DR EMBL; Z22733; CAAB0425.1; -
DR EMBL; Z22734; CAAB0427.1; -
DR PIR; S37463; S37463; -
DR INTERPRO; IPR005143; Autoind. bind.
DR INTERPRO; IPR00792; HTH_LuxR.
DR Pfam; PF03472; Autoind. bind. 1.
DR Pfam; PF00196; GntR_1.
DR PRODOM; PD00307; HTH_LuxR; 1.
DR SMART; SM0042; HTH_LuxR; 1.
DR PROSITE; PS00622; HTH_LUXR_FAMILY; FALSE_NEG
KM Transcription regulation; DNA-binding; Activator; Quorum sensing;
KM Conjugation; Plasmid.
FT DNA BIND 191 210 H-T-H MOTIF (BY SIMILARITY).
FT VARIANT 230 230 K -> R.
SQ SEQUENCE 234 AA; 26528 MW; 33997F03B248B59 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 224 LTLALAK 16
DB 224 LTLALAK 230

RESULT 64
MSA2_PLAFC STANDARD; PRT; 262 AA.
AC 099317;
CT 01-OCT-1996 (Rel. 34, Created)
CT 01-OCT-1996 (Rel. 34, Last sequence update)
CT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface antigen 2 precursor (MSA-2) (Allelic form 1).
GN MSA2.
OS Plasmodium falciparum (Isolate Camp / Malaysia).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OC NCBI_TaxID=5835;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91218803; PubMed=2090943;
RA Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
RT "Sequence comparison of allelic forms of the Plasmodium falciparum
RT merozoite surface antigen MSA2."
RL Mol. Biochem. Parasitol. 43:211-220(1990).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
CC EPITHELIAL CELL.

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CC      -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC      (Potential) .
CC      -1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
CC      DR EMBL, M60186; AAA29587.1;
CC      DR InterPro: IPR00136; MSA 2;
CC      DR Pfam: PF00985; MSA 2;
CC      KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
CC      KW GPI-anchor; Mercaptoite;
CC      FT SIGNAL 1 20
CC      FT CHAIN 21 238
CC      FT PROPEP 239 262
CC      FT FT
CC      FT DOMAIN 44 188
CC      FT FT DOMAIN 91 98
CC      FT CARBOHYD 22 22
CC      FT CARBOHYD 36 36
CC      FT CARBOHYD 139 139
CC      FT CARBOHYD 211 211
CC      FT CARBOHYD 235 235
CC      FT CARBOHYD 236 236
CC      SO SEQUENCE 262 AA; 27374 MW; 720B32A335E9D154 CRC64;
CC
CC      Query Match 0.9%; Score 7; DB 1; Length 262;
CC      Best Local Similarity 100.0%; Pred. No. 49;
CC      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC      Oy 253 GSGAGAS 259
CC      |||||||
CC      Db 59 GSGAGAS 65
CC
CC      RESULT 65
CC      TRPA_MYCLE
CC      AC 09CC53;
CC      ID TRPA_MYCLE STANDARD; PRT; 270 AA.
CC      DT 28-FEB-2003 (Rel. 41, Created)
CC      DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC      DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC      DE Trypocphan synthase alpha chain (EC 4.2.1.20).
CC      GN TRPA OR M1273.
CC      OS Mycobacterium leprae.
CC      OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC      OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium...
CC      NCBI_TaxId:1769;
CC      RN (1)
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=TN;
CC      RA MEDLINE=21128732; PubMed=11234002;
CC      RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
CC      Wheeler P.R., Honore N., Garner H., Churcher C., Harris D.,
CC      Musgal K., Basham D., Brown D., Chillingworth T., Connor R.,
CC      Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
CC      Holtroyd S., Hornby T., Jagels K., Lacroix C., Maclean C., Meule S.,
CC      Murphy L., Oliver K., Quail M.A., Rajadurai M.A., Rutherford K.M.,
CC      Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
CC      Squires S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
CC      Barrall B.G.;
CC      RT "Massive gene decay in the leprosy bacillus.";
CC      RL Nature 409:1067-1071(2001).
CC      CC -1- FUNCTION: The alpha subunit is responsible for the adol cleavage
CC      of inoleglycerol phosphate to indole and glyceraldehyde 3-
CC      phosphate.
CC      CC -1- CATALYTIC ACTIVITY: L-serine + 1-(indol-3-yl)-glycerol 3-phosphate
CC      = L-tryptophan + glyceraldehyde 3-phosphate.

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CC -1- PATHWAY: Tyryptophan biosynthesis; fifth (last) step.
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE TRPA FAMILY.
-----
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CC
CC EMBL; AJ583921; CAC31654.1; -.
CC PIR; C87069; C87068.
CC Lepidoptera; ML1273; -.
CC HAMAP; MF_00133; -. 1.
CC InterPro; IPR003009; FMN_enzyme.
CC InterPro; IPR002028; Trp_synthaseA.
CC Pfam; PF00290; trp_synthA; 1.
CC ProDom; PD001535; Trp_synthaseA; 1.
CC TrpFAMS; TIGR00262; trpA; 1.
CC PROSITE; PS00167; TRP_SYNTHASE_ALPHA; 1.
CC Tyryptophan biosynthesis; Lyase; Complete proteome.
CC SEQUENCE 270 AA; 28330 MW; DSD3D9815D4CBXC CRC64;
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Oy Query Match 0.9%; Score 7; DB 1; Length 270;
Db Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 521 AYVMTYV 527
Oy |||||
Db 103 AYVMTYV 109
-----
RESULT: 66
TRPA_MYCTU STANDARD: PRT; 270 AA.
AC 006130;
DT 30-MAY-2000 (Rel. 39, Created:
DT 30-MAY-2000 (Rel. 39, Last sequence update:
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tyryptophan synthase alpha chain (EC 4.2.1.20).
CN TRPA OR EY1613 OR M1648 OR MTCY0132.05.
CS Mycobacterium tuberculosis.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_taxonomy:1773;
OY [1]
SF SEQUENCE FROM N.A.
SF STRAIN:H37RV.
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies K., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Horsley T., Jacobs K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream N.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RT Nature 393:537-544(1998).
RA [2]
RP SEQUENCE FROM N.A.
RC STRAIN:CDC 1551 / Oshkosh;
RA Petersen J.R.D., Allard D., Eisen J.A., Carpenter L., White C.,
RA Felsenstein J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam T.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman U., Khouri H., Gill C., Mikita A.,
RA Bishai W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";

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CC Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: The alpha subunit is responsible for the aldol cleavage
CC of indoleglycerol phosphate to indole and glyceraldehyde 3-
CC phosphate.
CC -!- CATALYTIC ACTIVITY: L-serine + L-(indol-3-yl)-glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (by
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE TRPA FAMILY.
CC -----
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CC -----
DR EMBL; Z55554; CAB68990.1; -
DR EMBL; AE307028; AAA45917.1; -
DR PIR; C70557; C70557.
DR TIGR; M1648; -
DR Truncullier; Rv1613; -
DR HAMAP; MF_C0331; -
DR InterPro; IPR003303; FMN enzyme.
DR InterPro; IPR002028; trp_synthaseA.
DR Pfam; PF00290; trp_synthA; 1.
DR ProDom; PD001535; trp_synthaseA; 1.
DR TIGRFAMs; TIGR00262; trpa; 1.
DR PROSITE; PS00167; TRP SYNTHASE ALPHA; 1.
DR Tryptophan biosynthesis; lyase; Complete proteome.
KW SEQUENCE 270 AA; 27727 MW; 9855994F704AC76 C6C64;

Query Match 0.9%; Score 7; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 521 AVMWTYW 527
Db 103 AVMWTYW 109

RESULT 67
TRPA_MYCIT STANDARD; PRT; 271 AA.
AC 068906;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tryptophan synthase alpha chain (EC 4.2.1.20).
OS TRPA.
SN Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=9atv;
RA Alavi M.R., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence and functional analysis of the tryptophan
RT synthase genes of Mycobacterium intracellulare."
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: The alpha subunit is responsible for the aldol cleavage
CC of indoleglycerol phosphate to indole and glyceraldehyde 3-
CC phosphate.
CC -!- CATALYTIC ACTIVITY: L-serine + L-(indol-3-yl)-glycerol 3-phosphate
CC = L-tryptophan + glyceraldehyde 3-phosphate.
CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (by
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE TRPA FAMILY.

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CC -----
DR EMBL; AF057042; AAC11735.1; -
DR HSSP; P00929; 2TYS.
DR HAMAP; MF_C0131; -
DR InterPro; IPR003009; FMN enzyme.
DR InterPro; IPR002028; Trp synthaseA.
DR Pfam; PF00290; trp_synthA; 1.
DR ProDom; PD001535; trp_synthaseA; 1.
DR TIGRFAMs; TIGR00262; trpa; 1.
DR PROSITE; PS00167; TRP SYNTHASE ALPHA; 1.
KW Tryptophan biosynthesis; lyase.
KW SEQUENCE 271 AA; 27804 MW; BA0E0C5C0786318 C6C64;

Query Match 0.9%; Score 7; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 521 AVMWTYW 527
Db 102 AVMWTYW 108

RESULT 68
ZUPT_XANAC STANDARD; PRT; 272 AA.
AC 086K05;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ZUPC transporter zupT.
SN ZUPC OR XAC2114.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaglio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Camarotte G., Camavar F., Cardozo J., Chambergro F., Chapina L.P.,
RA Cicarelli R.K.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro X.I.T.,
RA Fortighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.W., Lemos M.V.P.,
RA Locali E.C., Machado Y.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menez C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.X., Okera V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sera C.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Seculac J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nucleic Acids Res. 30(12):2002.
CC -!- FUNCTION: Mediates zinc uptake. May also transport other divalent
CC cations (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE ZIP FAMILY. ZUPC SUBFAMILY.
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 CC -----  
 DR EMBL: AE011847; AAM36967.1; -  
 DR HAMAP: MF\_00548; -  
 DR InterPro: IPR003689; Zn\_transp.zip.  
 DR Pfam: PF02335; Zip\_1.  
 KW Transport; Zinc transport; Transmembrane; Complete proteome.  
 FT TRANSMEM 10 32 POTENTIAL.  
 FT TRANSMEM 39 6 POTENTIAL.  
 FT TRANSMEM 76 35 POTENTIAL.  
 FT TRANSMEM 124 146 POTENTIAL.  
 FT TRANSMEM 136 178 POTENTIAL.  
 FT TRANSMEM 185 237 POTENTIAL.  
 FT TRANSMEM 211 233 POTENTIAL.  
 FT TRANSMEM 249 271 POTENTIAL.  
 SQ SEQUENCE 272 AA; 28664 MW; 69FC1117470BCE7 CRC64;  
 Query Match 0.9%; Score 7; DB 1; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 680 AVGASL 686  
 DB 166 AVGASL 192  
 RESULT 69  
 MS2 PLAF6 STANDARD; PRT; 274 AA.  
 AC P50497;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Merozoite surface antigen 2 precursor (MSA-2).  
 GN MSA2.  
 OS Plasmodium falciparum (isolate K1316).  
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodi-  
 OX NCBI\_TaxID=57269;  
 RN (1)  
 RX MEDLINE=92178285; PubMed=542312;  
 RA Marshall V.M., Coppel R.L., Anders R.F., Kemp D.J.;  
 RT "Two novel alleles within subfamilies of the merozoite surface  
 M01. Biochem. Parasitol. 50:181-184(1992).  
 RL M01. FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE  
 CC ERYTHROCYTE.  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor  
 CC (potential).  
 CC -1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.  
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 CC -----  
 DR EMBL: M73810; AAM29696.1; -  
 DR PIR: A45632; A45632.  
 DR InterPro: IPR001136; MSA\_2.  
 DR Pfam: PF00985; MSA\_2; 1.  
 KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;  
 KM GPI-anchor; Merozoite.  
 FT CHAIN 1 20 POTENTIAL.  
 FT CHAIN 21 250 HYDROPHOBIC REMOVED DURING MATURATION  
 FT PROPEP 251 274 POLYMORPHIC REGION.  
 FT DOMAIN 44 200 POLY-THR.  
 FT DOMAIN 97 110

FT CARBOHYD 22 22 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 36 36 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 223 223 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 248 248 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 274 AA; 28367 MW; 63C4CD1F07425D53 CRC64;  
 Query Match 0.9%; Score 7; DB 1; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 253 GSGAGAS 259  
 DB 59 GSGAGAS 65  
 RESULT 70  
 YCX6\_EUGER STANDARD; PRT; 274 AA.  
 ID YCX6\_EUGER  
 AC P48336;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 32.3 kDa protein in RECL-ATPE intergenic region (ORF274).  
 DE Euglena gracilis.  
 OS Euglenozoa; Euglenida; Euglenales; Euglena.  
 CC Chloroplast.  
 CC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.  
 OX NCBI\_TaxID=3039;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Z / UTEX 753;  
 RX MEDLINE=9347989; PubMed=8346031;  
 RA Hatlick R.B., Hong L., Dager R.G., Favreau M.R., Montfort A.,  
 RA Orsat B., Spielmann A., Stutz E.;  
 RT "Complete sequence of Euglena gracilis chloroplast DNA."  
 RL Nucleic Acids Res. 21:3537-3544(1993).  
 CC -----  
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 CC -----  
 DR EMBL: Z11874; -; NOT ANNOTATED; CDS.  
 DR PIR: X70810; CA50124.1; -  
 DR PIR: S34543; S34543.  
 KW Chloroplast; Hypothetical protein.  
 SQ SEQUENCE 274 AA; 32317 MW; 63C4CD1F07425D53 CRC64;  
 Query Match 0.9%; Score 7; DB 1; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 128 LYUNIV 134  
 DB 159 LYUNIV 165  
 RESULT 71  
 Y265\_MYCPN STANDARD; PRT; 282 AA.  
 ID Y265\_MYCPN  
 AC P75399;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein MG265 homolog (Al9\_orf282).  
 GN MP183 OR MP454.  
 OS Mycoplasma pneumoniae.  
 CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2104;  
 RN (1)



RP SEQUENCE FROM N.A.  
 SC STRAIN=ATCC 29342 / M129;  
 RX MEDLINE=97105885; PubMed=6948633;  
 RA Heremans R., Gilbert H., Plegans H., Pirkel E., Li B.-C.,  
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
 pneumoniae";  
 RL Nucleic Acids Res. 24:4420-4449 (1996).  
 CC -1- SIMILARITY: BELONGS TO THE COF/YHFA/YIDA/YIGL (E.COLI) / YGSE/YXEH  
 (B.SUBTILIS) FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AEC00044; AAB96132.1;  
 DR PIR: S73780; S73780.  
 DR InterPro: IPR006379; IAD\_SF\_11B.  
 DR InterPro: IPR005934; Hydrolase.  
 DR InterPro: IPR001350; Hydrolase.  
 DR Pfam: PF00702; Hydrolase; 1.  
 DR TIGRFAMs: TIGR00059; COF-subfamily; 1.  
 DR TIGRFAMs: TIGR01484; HAD-SF-11B; 1.  
 DR PROSITE: PS01228; COF 1; 1.  
 DR PROSITE: PS01229; COF 2; 1.  
 DR Hypothetical protein: Complete proteome.  
 KW SEQUENCE 282 AA; 3193 MW; 0095F9131B1B01AD CRC64;  
 SQ  
 Query Match 0.9%; Score 7; DB 1; Length 282;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 81 TRNTQCF 97  
 Db 52 -RNTQCF 58  
 RESULT 72  
 UPGA\_ECOLI  
 ID UPGA\_ECOLI STANDARD; PRT; 295 AA.  
 AC P10905;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE SN-glycerol-3-phosphate transport system permease protein upga.  
 GN UPGA OR B3452.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 CX NCBI\_TaxID=562;  
 RN (1)  
 RF SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=88996498; PubMed=3062313;  
 RA Overduin P., Boos W., Tomaszewski J.  
 RT "Nucleotide sequence of the upg genes of Escherichia coli K-12;  
 RT homology to the talose system";  
 RL Mol. Microbiol. 2:767-775 (1988).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=94316500; PubMed=8041620;  
 RA Solta H.J., Sorland V., Daniels D.L., Plunkett G. III, Blatter F.P.;  
 RT "Analysis of the Escherichia coli genome. V. DNA sequence of the  
 RT region from 76.0 to 81.5 minutes";  
 RL Nucleic Acids Res. 22:2576-2586 (1994).  
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM  
 CC FOR SN-GLYCEROL-3-PHOSPHATE; PROBABLY RESPONSIBLE FOR THE  
 CC TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (potential).  
 CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT  
 CC SYSTEM PERMEASE FAMILY, MALFG SUBFAMILY.  
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 CC -----  
 CC EMBL: X13141; CAA3532.1;  
 DR EMBL: U00039; AAB18427.1;  
 DR EMBL: AEC00421; AAC76477.1;  
 DR PIR: S03781; WMECCA.  
 DR EcoGene: EG-1046; UPGA.  
 DR InterPro: IPR000515; BPD\_transp.  
 DR Pfam: PF00528; BPD\_transp; 1.  
 DR PROSITE: PS00432; BPD\_TRANSF\_INN\_MEMBER; 1.  
 DR Transmembrane: Inner membrane; Transport; Complete proteome.  
 FT TRANSMEM 12  
 FT TRANSMEM 32  
 FT TRANSMEM 81 131 POTENTIAL.  
 FT TRANSMEM 110 130 POTENTIAL.  
 FT TRANSMEM 157 177 POTENTIAL.  
 FT TRANSMEM 208 228 POTENTIAL.  
 FT TRANSMEM 263 283 POTENTIAL.  
 KW SEQUENCE 295 AA; 33264 MW; C087650E0FB647A9 CRC64;  
 SQ  
 Query Match 0.9%; Score 7; DB 1; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 451 VAPAVAA 457  
 Db 117 VAPAVAA 123  
 RESULT 73  
 UPK2\_CLOAB  
 ID UPK2\_CLOAB STANDARD; PRT; 307 AA.  
 AC O97X66;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative undecaprenol kinase 2 (EC 2.7.1.66) (Bactitracin resistance  
 DE protein 2).  
 GN UPK2 OR BACAZ OR CAC0963.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 CX NCBI\_TaxID=1488;  
 RN (1)  
 RF SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=21359325; PubMed=11466286;  
 RA Noelling U., Breton G., Omelchenko M.V., Makarova K.S., Zeng C.,  
 RA Gibson R., Lee H.K., Dubois O., Qiu D., Hiltner A., Wolf Y.I.,  
 RA Tatusov R., Sabathe F., Doucette-Stamm L., Socacile P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum";  
 RL J. Bacteriol. 183:4823-4838 (2001).  
 CC -1- FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl  
 CC phosphate. Confers resistance to bacteriicin (by similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + undecaprenol = ADP + undecaprenyl  
 CC phosphate.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- MISCELLANEOUS: Bactitracin is thought to be involved in inhibition  
 CC of peptidoglycan synthesis by sequestering undecaprenyl  
 CC diphosphate reducing the pool of lipid carrier available.  
 CC -1- SIMILARITY: BELONGS TO THE UPK FAMILY.

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CC -----
DR EMBL: A500761.1; AAK78939.1; -
DR PIR: H97018; H97018.
DR HAVADP: MF_01006; -; 1.
DR InterPro: IPR003824; BACA.
DR Pfam: PF02673; BACA. 1.
DR TIGRfams: TIGR00753; under kin back: 1.
KW Transferase; Kinase; Antibiotic resistance; Transmembrane;
KW Complete proteome.
FT TRANSMEM 19 41 POTENTIAL.
FT TRANSMEM 36 75 POTENTIAL.
FT TRANSMEM 116 135 POTENTIAL.
FT TRANSMEM 145 164 POTENTIAL.
FT TRANSMEM 212 234 POTENTIAL.
FT TRANSMEM 249 271 POTENTIAL.
FT TRANSMEM 254 305 POTENTIAL.
SC SEQUENCE 307 AA; 33640 MW; 32FF21C78024F34D CRC64;

Query Match 0.9%; Score 7; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 GASLIF 688
Db 235 GASLIF 241

RESULT 74
Y011_RICPR STANDARD; PRT; 341 AA.
ID Y011_RICPR
AC GQZED;
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 16-OCT-2001 (Rel. 42, Last annotation update);
DE Hypothetical 37.5 kDa protein P011..
GN P011.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiinae; Rickettsia.
CX NCBI_TaxID=782;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid B;
RX MEDLINE=99019493; PubMed=9821893;
RA Andersson S.G.E., Zorrodipour A., Andersson C.O.,
RA Sichelric-Ponten T., Almark U.C.K., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF034 (NIFR3/SXM) FAMILY.
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CC -----
DR EMBL: A235270; CA14483.1; -
DR PIR: D71708; D71708.
DR InterPro: IPR003009; FMN enzyme.
DR InterPro: IPR004652; NIFR3 YhdG.
DR InterPro: IPR001269; UPF0034.
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DR Pfam: PF01207; Dns; 1.
DR TIGRfams: TIGR00737; NIFR3 YhdG; 1.
DR EPOSITE: P501136; UPF0034; 1.
KW Hypothetical protein; Complete proteome.
SC SEQUENCE 341 AA; 37519 MW; F7E8B77436C34D3 CRC64;

Query Match 0.9%; Score 7; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 LNYDML 370
Db 2 LNYDML 8

RESULT 75
A85C_MYCAV STANDARD; PRT; 352 AA.
ID A85C_MYCAV
AC 052972;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C) (Mycobyl)
DE transferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein C)
GN FBPC.
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriinae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1764;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15769;
RX MEDLINE=97427949; PubMed=9284137;
RA Ohara N., Ohara-Wada N., Kitaura H., Nishiyama T., Matsumoto S.,
RA Yamada T.;
RT "Analysis of the gene encoding the antigen 85 complex and MPT51 from
RT Mycobacterium avium."
RL Infect. Immun. 65:3680-3685(1997).
CC -1- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOBACTERIAL TRANSFERASE ACTIVITY REQUIRED FOR THE BICENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C.GLUTAMINUM PSI PROTEIN.
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CC -----
DR EMBL: D87323; BAA24161.1; -
DR HSSP: P31953; IDOY.
DR InterPro: IPR000801; Esterase_Put.
DR Pfam: PF00756; Esterase; 1.
KW Transferase; Acyltransferase; Antigen; Signal.
FT CHAIN 1 46 POTENTIAL.
FT ACT SITE 47 352 ANTIGEN 85-C.
FT ACT SITE 170 170 BY SIMILARITY.
FT ACT SITE 274 274 BY SIMILARITY.
FT ACT_SITE 306 306 BY SIMILARITY.
SC SEQUENCE 352 AA; 37756 MW; A29277C855006C4A CRC64;

Query Match 0.9%; Score 7; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 AVGASL 686
```

Db 25 AVGASLU 31

Search completed: November 5, 2003, 15:25:42  
Job time : 20 secs

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## OM protein - protein search, using SW model

Run on: November 5, 2003, 15:23:18 ; Search time 21 Seconds

(without alignments)

1644.079 Million cell updates/sec

File: US-09-978-423a-375

Perfect score: 816  
Sequence: 1 MINSNVLMLTAALIKFTL.....TSSGQNSITNLPKHSITRV 816Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 32877 seqs, 4230858 residues

Word size: 0

Total number of hits satisfying chosen parameters: 32877

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Listing first 100 summaries

Database:

1: /cgnt2\_6/ptodata/1/1aa/5A-COMB.pep.\*  
2: /cgnt2\_6/ptodata/1/1aa/5B-COMB.pep.\*  
3: /cgnt2\_6/ptodata/1/1aa/5A-COMB.pep.\*  
4: /cgnt2\_6/ptodata/1/1aa/5B-COMB.pep.\*  
5: /cgnt2\_6/ptodata/1/1aa/PCITUS-COMB.pep.\*  
6: /cgnt2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5.0	6.1	843	4	US-09-431-356C-20
2	4.8	5.3	836	4	US-09-491-356C-21
3	3.5	4.3	553	4	US-09-431-356C-24
4	3.2	3.9	823	4	US-09-431-356C-22
5	3.2	3.9	848	4	US-09-431-356C-22
6	1.2	1.5	535	1	US-08-445-050-4
7	1.2	1.5	535	2	US-08-204-691-4
8	1.2	1.5	546	1	US-08-445-050-5
9	1.2	1.5	546	2	US-08-204-691-5
10	1.2	1.5	568	1	US-03-445-050-6
11	1.2	1.5	568	1	US-08-204-691-6
12	1.2	1.5	571	6	5200183-17
13	1.2	1.5	668	1	US-08-445-050-9
14	1.2	1.5	668	2	US-06-204-691-9
15	1.2	1.5	722	1	US-08-347-718B-1
16	1.2	1.5	722	1	US-08-445-050-3
17	1.2	1.5	722	1	US-08-445-050-7
18	1.2	1.5	722	1	US-08-482-262-1
19	1.2	1.5	722	2	US-08-204-691-3
20	1.2	1.5	722	2	US-08-204-691-7
21	1.2	1.5	722	4	US-09-355-295B-4
22	1.2	1.5	722	6	5200183-3
23	1.2	1.5	742	1	US-08-347-718B-2
24	1.2	1.5	742	2	US-08-482-262-2
25	1.2	1.5	742	6	5200183-2
26	1.2	1.5	745	1	US-08-445-050-2
27	1.2	1.5	745	2	US-08-204-691-2

28	1.2	1.5	745	3	US-08-370-223-13	Sequence 13, Appl
29	1.2	1.5	745	4	US-09-355-295B-3	Sequence 32, Appl
30	1.2	1.5	747	4	US-09-347-878B-32	Sequence 1, Appl
31	9	1.1	539	3	US-09-264-737-1	Sequence 2, Appl
32	9	1.1	566	3	US-09-264-737-2	Sequence 2, Appl
33	9	1.1	584	2	US-08-845-295A-2	Sequence 2, Appl
34	9	1.1	584	3	US-09-140-931-2	Sequence 2, Appl
35	9	1.1	584	3	US-09-146-661-2	Sequence 2, Appl
36	9	1.1	584	3	US-09-150-515-2	Sequence 2, Appl
37	9	1.1	597	1	US-08-462-884A-1	Sequence 1, Appl
38	9	1.1	597	2	US-08-461-881B-1	Sequence 1, Appl
39	9	1.1	605	1	US-09-123-960-1	Sequence 1, Appl
40	9	1.1	605	1	US-08-462-884A-3	Sequence 3, Appl
41	9	1.1	605	1	US-08-461-881B-3	Sequence 3, Appl
42	9	1.1	605	2	US-09-123-960-3	Sequence 3, Appl
43	9	1.1	606	4	US-09-347-878B-34	Sequence 34, Appl
44	8	1.0	137	3	US-08-747-221B-11	Sequence 11, Appl
45	8	1.0	137	3	US-09-005-051-11	Sequence 11, Appl
46	8	1.0	244	3	US-08-827-171B-8	Sequence 8, Appl
47	8	1.0	528	3	US-08-747-221B-37	Sequence 37, Appl
48	8	1.0	528	3	US-09-005-051-37	Sequence 37, Appl
49	8	1.0	563	3	US-08-362-525-12	Sequence 12, Appl
50	8	1.0	570	3	US-08-747-221B-54	Sequence 54, Appl
51	8	1.0	570	3	US-08-747-221B-55	Sequence 55, Appl
52	8	1.0	570	3	US-09-005-051-54	Sequence 54, Appl
53	8	1.0	575	1	US-09-003-051-55	Sequence 55, Appl
54	8	1.0	575	1	US-08-348-920-1	Sequence 1, Appl
55	8	1.0	575	1	US-08-348-920-2	Sequence 2, Appl
56	8	1.0	595	3	US-08-747-221B-31	Sequence 31, Appl
57	8	1.0	595	3	US-09-005-051-31	Sequence 31, Appl
58	8	1.0	596	3	US-08-747-221B-25	Sequence 25, Appl
59	8	1.0	596	3	US-09-005-051-25	Sequence 25, Appl
60	8	1.0	723	6	5200183-4	Sequence 25, Appl
61	8	1.0	723	6	US-09-252-991A-28373	Sequence 28373, A
62	8	1.0	894	4	US-10-060-332-4	Sequence 4, Appl
63	8	1.0	894	4	US-08-308-086-8	Sequence 8, Appl
64	7	0.9	95	1	US-08-167-035-17	Sequence 17, Appl
65	7	0.9	96	1	US-08-208-887A-17	Sequence 17, Appl
66	7	0.9	96	2	US-08-479-078-20	Sequence 20, Appl
67	7	0.9	96	2	US-08-539-005-17	Sequence 17, Appl
68	7	0.9	96	4	US-09-280-598-19	Sequence 19, Appl
69	7	0.9	96	4	US-09-820-754-25	Sequence 25, Appl
70	7	0.9	99	3	US-08-956-652-25	Sequence 25, Appl
71	7	0.9	99	3	US-08-956-863-25	Sequence 25, Appl
72	7	0.9	99	3	US-08-948-547-25	Sequence 25, Appl
73	7	0.9	103	3	US-08-747-221B-8	Sequence 8, Appl
74	7	0.9	103	3	US-09-005-051-8	Sequence 8, Appl
75	7	0.9	117	4	US-08-976-063E-12	Sequence 12, Appl
76	7	0.9	147	4	US-09-482-273-209	Sequence 209, Appl
77	7	0.9	163	4	US-09-252-991A-22533	Sequence 22533, A
78	7	0.9	178	3	US-08-478-316-24	Sequence 24, Appl
79	7	0.9	178	4	US-09-019-793A-24	Sequence 24, Appl
80	7	0.9	178	4	PCR-US95-10904-71	Sequence 71, Appl
81	7	0.9	198	5	US-09-252-991A-19680	Sequence 19680, A
82	7	0.9	207	3	US-09-068-960-15	Sequence 15, Appl
83	7	0.9	207	3	52-5928-1	Sequence 15, Appl
84	7	0.9	255	6	US-09-252-991A-18795	Sequence 18795, A
85	7	0.9	334	4	US-09-328-352-7424	Sequence 7424, A
86	7	0.9	388	4	US-09-596-196-4	Sequence 10, Appl
87	7	0.9	418	1	US-08-176-427B-10	Sequence 10, Appl
88	7	0.9	418	1	US-08-356-060A-12	Sequence 12, Appl
89	7	0.9	418	3	US-08-946-329A-18	Sequence 18, Appl
90	7	0.9	418	3	US-08-967-357A-18	Sequence 18, Appl
91	7	0.9	418	3	US-08-460-900C-12	Sequence 12, Appl
92	7	0.9	418	3	US-08-729-743A-18	Sequence 18, Appl
93	7	0.9	418	3	US-08-757-230A-7	Sequence 7, Appl
94	7	0.9	418	3	US-08-674-509B-12	Sequence 12, Appl
95	7	0.9	418	3	US-08-654-698-12	Sequence 12, Appl
96	7	0.9	418	3	US-08-349-498-18	Sequence 18, Appl
97	7	0.9	418	4	US-08-557-874-12	Sequence 12, Appl
98	7	0.9	418	4	US-09-325-256-21	Sequence 21, Appl
99	7	0.9	418	4	US-08-700-393-7	Sequence 7, Appl
100	7	0.9	418	4		

## ALIGNMENTS

## RESULT 1

```

US-09-491-356C-20
: Sequence 22, Application US/09491356C
: Patent No. 6566061
: GENERAL INFORMATION:
: APPLICANT: Philibert, Robert A.
: APPLICANT: Gims, Edward I.
: APPLICANT: Delisi, Lynn
: TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
: FILE REFERENCE: 9465.6US11
: CURRENT APPLICATION NUMBER: US/09/491.356C
: PRIOR FILING DATE: 2000-01-26
: PRIOR APPLICATION NUMBER: PCT/US99/09365
: PRIOR FILING DATE: 1999-04-29
: PRIOR APPLICATION NUMBER: 60/083.465
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 23
: LENGTH: 943
: TYPE: PRT
: ORGANISM: Rattus norvegicus
US-09-491-356C-20

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## Query Match

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Best Local Similarity 5.1%; Score 50; DB 4; Length 843;
Best Local Similarity 100.0%; Pred. No. 5,5e-41;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## QY

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510 CNEKNDVMSAVVMTYNTWTFKATGDPNPVPODTKFIHMKNEFEFEVW 559
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546 CNEKNDVMSAVVMTYNTWTFKATGDPNPVPODTKFIHMKNEFEFEVW 555
|||||

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## DB

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RESULT 2
US-09-491-356C-21
: Sequence 21, Application US/09491356C
: Patent No. 6566061
: GENERAL INFORMATION:
: APPLICANT: Philibert, Robert A.
: APPLICANT: Gims, Edward I.
: APPLICANT: Delisi, Lynn
: TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
: FILE REFERENCE: 9465.6US11
: CURRENT APPLICATION NUMBER: US/09/491.356C
: PRIOR FILING DATE: 2000-01-26
: PRIOR APPLICATION NUMBER: PCT/US99/09365
: PRIOR FILING DATE: 1999-04-29
: PRIOR APPLICATION NUMBER: 60/083.465
: PRIOR FILING DATE: 1999-04-29
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 21
: LENGTH: 836
: TYPE: PRT
: ORGANISM: Rattus norvegicus
US-09-491-356C-21

```

## Query Match

```

Best Local Similarity 5.9%; Score 48; DB 4; Length 936;
Best Local Similarity 100.0%; Pred. No. 9e-39;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## QY

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510 CNEKNDVMSAVVMTYNTWTFKATGDPNPVPODTKFIHMKNEFEFEVW 557
|||||
521 CNEKNDVMSAVVMTYNTWTFKATGDPNPVPODTKFIHMKNEFEFEVW 565
|||||

```

## DB

```

RESULT 3
US-09-491-356C-24

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```

: Sequence 24, Application US/09491356C
: Patent No. 6566061
: GENERAL INFORMATION:
: APPLICANT: Philibert, Robert A.
: APPLICANT: Gims, Edward I.
: APPLICANT: Delisi, Lynn
: TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
: FILE REFERENCE: 9465.6US11
: CURRENT APPLICATION NUMBER: US/09/491.356C
: PRIOR FILING DATE: 2000-01-26
: PRIOR APPLICATION NUMBER: PCT/US99/09365
: PRIOR FILING DATE: 1999-04-29
: PRIOR APPLICATION NUMBER: 60/083.465
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 24
: LENGTH: 553
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-491-356C-24

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## Query Match

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Best Local Similarity 4.3%; Score 35; DB 4; Length 553;
Best Local Similarity 100.0%; Pred. No. 4.7e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## QY

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167 KPVVYIHGSGYMEGTGNMIDGSIASIGNVIVIT 201
|||||
200 KPVVYIHGSGYMEGTGNMIDGSIASIGNVIVIT 234
|||||

```

## DB

```

RESULT 4
US-09-491-356C-23
: Sequence 23, Application US/09491356C
: Patent No. 6566061
: GENERAL INFORMATION:
: APPLICANT: Philibert, Robert A.
: APPLICANT: Gims, Edward I.
: APPLICANT: Delisi, Lynn
: TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
: FILE REFERENCE: 9465.6US11
: CURRENT APPLICATION NUMBER: US/09/491.356C
: PRIOR FILING DATE: 2000-01-26
: PRIOR APPLICATION NUMBER: PCT/US99/09365
: PRIOR FILING DATE: 1999-04-29
: PRIOR APPLICATION NUMBER: 60/083.465
: PRIOR FILING DATE: 1999-04-29
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 23
: LENGTH: 823
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-491-356C-23

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## Query Match

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Best Local Similarity 3.9%; Score 32; DB 4; Length 823;
Best Local Similarity 100.0%; Pred. No. 6.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## QY

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399 SVSNFVDNLVGYPEGCKTJREFIKXYVTMD 410
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412 SVSNFVDNLVGYPEGCKTJREFIKXYVTMD 443
|||||

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## DB

## RESULT 5

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US-09-491-356C-22
: Sequence 22, Application US/09491356C
: Patent No. 6566061
: GENERAL INFORMATION:
: APPLICANT: Philibert, Robert A.
: APPLICANT: Gims, Edward I.
: APPLICANT: Delisi, Lynn
: TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13

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US-09-491-356C-24

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FILE REFERENCE: 9465.6US1;  
CURRENT APPLICATION NUMBER: US/09/491,356C  
CURRENT FILING DATE: 2000-01-26  
PRIOR APPLICATION NUMBER: PCT/US99/09365  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: 60/093,465  
PRIOR FILING DATE: 1998-04-29  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent version 3.1  
SEQ ID NO: 22  
LENGTH: 948  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-491-356C-22

Query Match 3.9%; Score 32; DB 4; Length 948;  
Best Local Similarity 100.0%; Pred. No. 6,56-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 399 SVSNFVDNLGYEPEKDTLRETIKRYTDMAD 430  
Db 432 SVSNFVDNLGYEPEKDTLRETIKRYTDMAD 463

RESULT 6  
US-08-445-050-4  
Sequence 4, Application US/08445050  
Patent No. 5763739  
GENERAL INFORMATION:  
APPLICANT: Blaeckberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Herneil, Olie  
APPLICANT: Lundberg, Lennart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toerneil, Jan  
TITLE OF INVENTION: No. 5763739el Polypept:dc5  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSER: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,050  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
APPLICATION NUMBER: SE 930686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Steerner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)354-813  
TELEFAX: (212)354-813  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary gland  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..535  
OTHER INFORMATION: /label= Variant\_A  
US-08-445-050-4

Query Match 1.5%; Score 12; DB 1; Length 535;  
Best Local Similarity 100.0%; Pred. No. 0,0028;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 526 YWTFNFAKTGDPN 537  
Db 467 YWTFNFAKTGDPN 478

RESULT 7  
US-08-204-691-4  
Sequence 4, Application US/08204691  
Patent No. 5827683  
GENERAL INFORMATION:  
APPLICANT: Blaeckberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Herneil, Olie  
APPLICANT: Lundberg, Lennart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toerneil, Jan  
TITLE OF INVENTION: No. 5827683el Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSER: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 930686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Steerner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)819-8783  
TELEFAX: (212)354-8113  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 535 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens

TISSUE TYPE: Mammary gland  
FEATURE: Peptide  
NAME/KEY: 1.546  
LOCATION: 1.546  
OTHER INFORMATION: /label= Variant\_A  
US-08-204-691-4  
Query Match 1.5%; Score 12; DB 2; Length 546;  
Best Local Similarity 100.0%; Pred. No. 3.0028;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 526 WWTNFAKTGDPN 537  
DB 467 WWTNFAKTGDPN 478  
RESULT 8  
US-08-445-050-5  
Sequence 5, Application US/08445050  
Patent No. 5763728  
GENERAL INFORMATION:  
APPLICANT: Blackeberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Herrrell, Olle  
APPLICANT: Lundberg, Lennart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toerrell, Jan  
TITLE OF INVENTION: No. 5763739el Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,050  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
APPLICATION NUMBER: SE 9300686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sterner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)819-8783  
TELEFAX: (212)354-8113  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 546 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary gland  
FEATURE:  
NAME/KEY: Peptide

LOCATION: 1.546  
OTHER INFORMATION: /label= Variant\_B  
US-08-445-050-5  
Query Match 1.5%; Score 12; DB 1; Length 546;  
Best Local Similarity 100.0%; Pred. No. 3.0028;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 526 WWTNFAKTGDPN 537  
DB 467 WWTNFAKTGDPN 478  
RESULT 9  
US-08-204-691-5  
Sequence 5, Application US/08204691  
Patent No. 5827683  
GENERAL INFORMATION:  
APPLICANT: Blackeberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Herrrell, Olle  
APPLICANT: Lundberg, Lennart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toerrell, Jan  
TITLE OF INVENTION: No. 5827683el Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sterner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)819-8783  
TELEFAX: (212)354-8113  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 546 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary gland  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1.546  
OTHER INFORMATION: /label= Variant\_B  
US-08-204-691-5  
Query Match 1.5%; Score 12; DB 2; Length 546;

Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 YWTFPAKTGDPN 537  
|||||  
DB 467 YWTFPAKTGDPN 478

## RESULT 10

US-08-445-050-6  
Sequence 6, Application US/08445056  
Patent No. 5763739  
GENERAL INFORMATION:  
APPLICANT: Blacberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Herneil, Oile  
APPLICANT: Lundberg, Jemart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toernell, Jan  
TITLE OF INVENTION: No. 5763739el Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/06/445,050  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
APPLICATION NUMBER: SE 9300686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Steiner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1:03326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)819-8783  
TELEFAX: (212)354-8113  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 568 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary gland  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..568  
OTHER INFORMATION: /label= Variant\_C  
US-08-445-050-6

Query Match 1.5%; Score 12; DB 1; Length 568;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 YWTFPAKTGDPN 537  
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DB 467 YWTFPAKTGDPN 478

## RESULT 11

US-08-204-691-6  
Sequence 6, Application US/08204691  
Patent No. 5827683  
GENERAL INFORMATION:  
APPLICANT: Blacberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Herneil, Oile  
APPLICANT: Lundberg, Jemart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toernell, Jan  
TITLE OF INVENTION: No. 5827683el Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Steiner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1:03326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)819-8783  
TELEFAX: (212)354-8113  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 568 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary gland  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..568  
OTHER INFORMATION: /label= Variant\_C  
US-08-204-691-6

Query Match 1.5%; Score 12; DB 2; Length 568;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 YWTFPAKTGDPN 537  
|||||  
DB 467 YWTFPAKTGDPN 478



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RESULT 12
52c0183-17
PATENT NO. 5200183
APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN
TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/537,426
FILING DATE: 12-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,635
FILING DATE: 04-MAR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO:17
LENGTH: 571
52c0183-17

Query Match          1.5%; Score 12; DB 6; Length 571;
Best Local Similarity 100.0%; Pred. No. 3,0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      526 YWTFNFAKTGDPN 537
DB      467 YWTFNFAKTGDPN 478

RESULT 13
US-08-445-050-9
Sequence 9, Application US/08445050
Patent No. 5763738
GENERAL INFORMATION:
APPLICANT: Blaeckberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Hernell, Oile
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5763739e1 Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/445,050
FILING DATE:
CLASSIFICATION: 83C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/03/204,691
FILING DATE:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
TELEPHONE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 9:
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SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-445-050-9

Query Match          1.5%; Score 12; DB 1; Length 668;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      526 YWTFNFAKTGDPN 537
DB      490 YWTFNFAKTGDPN 501

RESULT 14
US-08-204-691-9
Sequence 9, Application US/08204691
Patent No. 5827683
GENERAL INFORMATION:
APPLICANT: Blaeckberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lennart
APPLICANT: Hernell, Oile
APPLICANT: Lundberg, Lennart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5827683e1 Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
TELEPHONE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-204-691-9

Query Match          1.5%; Score 12; DB 2; Length 668;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      526 YWTFNFAKTGDPN 537
DB      467 YWTFNFAKTGDPN 478
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DB 493 WTNPAKTGDPN 501

RESULT 15  
US-08-347-718B-1  
Sequence 1, Application US/09347718B  
Patent No. 5696087  
GENERAL INFORMATION:  
APPLICANT: Wang, Chu-San  
APPLICANT: Tang, Jordan J.N  
TITLE OF INVENTION: METHOD FOR REDUCING INTESTINAL ABSORPTION OF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Fabsz  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/347,718B  
FILING DATE: December 1, 1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Patrec, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMR-F-50  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 722 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-347-718B-1

Query Match 1.5% Score 12; EB 1; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 WTNPAKTGDPN 537  
DB 467 WTNPAKTGDPN 478

RESULT 16  
US-08-445-050-3  
Sequence 3, Application US/08445050  
Patent No. 5763739  
GENERAL INFORMATION:  
APPLICANT: Blaeckberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Hernell, Olle  
APPLICANT: Lundberg, Lennart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toernell, Jan  
TITLE OF INVENTION: No. 5763739e1 Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,050  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
APPLICATION NUMBER: SE 9300686-4  
FILING DATE: 01-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9300722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Steiner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 954-8113  
TELEFAX: (212) 919-8783  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 722 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary gland  
US-08-445-050-3

Query Match 1.5% Score 12; DB 1; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 WTNPAKTGDPN 537  
DB 467 WTNPAKTGDPN 478

RESULT 17  
US-08-445-050-7  
Sequence 7, Application US/09445050  
Patent No. 5763739  
GENERAL INFORMATION:  
APPLICANT: Blaeckberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Lennart  
APPLICANT: Hernell, Olle  
APPLICANT: Lundberg, Lennart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toernell, Jan  
TITLE OF INVENTION: No. 5763739e1 Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,053
FILING DATE:
CLASSIFICATION: 80C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)8-9-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..722
OTHER INFORMATION: /label= Variant_N
US-08-445-053-7

Query Match 1.5%; Score 12; EB 1; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFKTGDPN 537
DB 467 YWTFNFKTGDPN 478

RESULT 18
US-08-482-262-1
Sequence 1, Application US/08482262
Patent No. 5821226
GENERAL INFORMATION:
APPLICANT: Wang, Chu-Sar
TITLE OF INVENTION: BAL C-TAIL DRUG DELIVERY MOLECULES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea T., Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,262
FILING DATE: June 7, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF:51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-05-482-262-1

Query Match 1.5%; Score 12; DB 2; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFKTGDPN 537
DB 467 YWTFNFKTGDPN 478

RESULT 19
US-08-204-691-3
Sequence 3, Application US/08204691
Patent No. 5827683
GENERAL INFORMATION:
APPLICANT: Blaeckberg, Lars
APPLICANT: Edlund, Michael
APPLICANT: Hansson, Lemnart
APPLICANT: Hennell, Oile
APPLICANT: Lundberg, Lemnart
APPLICANT: Stromqvist, Mats
APPLICANT: Toernell, Jan
TITLE OF INVENTION: No. 5827683el Polypeptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300686-4
FILING DATE: 01-MAR-1993
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Mammary Gland  
US-08-204-691-3

Query Match 1.5%; Score 12; DB 2; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537  
DB 467 YWTFNFAKTGDPN 478

RESULT 20  
US-08-204-691-7

Sequence 7, Application US/08204691  
Patent No. 5827683

GENERAL INFORMATION:  
APPLICANT: Backeberg, Lars  
APPLICANT: Edlund, Michael  
APPLICANT: Hansson, Dennis  
APPLICANT: Herzel, Oile  
APPLICANT: Lundberg, Lennart  
APPLICANT: Stromqvist, Mats  
APPLICANT: Toernell, Jan  
TITLE OF INVENTION: No. 5827683el Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/204,691  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 930686-4  
FILING DATE: 31-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9306722-7  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Steiner Ph.D., Richard J  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-850  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)819-8783  
TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 722 amino acids  
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

TISSUE TYPE: Mammary gland

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..722

OTHER INFORMATION: /label= Variant\_N

US-08-204-691-7

Query Match 1.5%; Score 12; DB 2; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537  
DB 467 YWTFNFAKTGDPN 478

RESULT 21  
US-09-355-295B-4

Sequence 4, Application US/09355295B  
Patent No. 6525241

GENERAL INFORMATION:  
APPLICANT: Dattipam, M.  
APPLICANT: Lundberg, L.  
APPLICANT: Stromqvist, M.  
TITLE OF INVENTION: Expression Methods  
FILE REFERENCE: 1754 SEQUENCE LISTING v2a.txt  
CURRENT APPLICATION NUMBER: US/09/355,295B  
CURRENT FILING DATE: 1999-07-18  
PRIOR APPLICATION NUMBER: PCT/SE99/00648  
PRIOR FILING DATE: 1999-04-21  
NUMBER OF SEQ ID NOS: 5  
SEQ ID NO 4  
LENGTH: 722  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-355-295B-4

Query Match 1.5%; Score 12; DB 4; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537  
DB 467 YWTFNFAKTGDPN 478

RESULT 22  
US-09-355-295B-4

Patent No. 5200183

APPLICANT: WANG, JORDAN J.N.; WANG, CHI-SUN

TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES

NUMBER OF SEQUENCES: 22

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/537,426

FILING DATE: 12-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 504,635

FILING DATE: 04-APR-1990

APPLICATION NUMBER: 122,410

FILING DATE: 19-NOV-1987

SEQ ID NO: 3

LENGTH: 722

US-09-355-295B-4

Query Match 1.5%; Score 12; DB 6; Length 722;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 526 YWTFNFAKTGDPN 537  
DB 467 YWTFNFAKTGDPN 478

RESULT 23  
US-08-347-718B-2

Sequence 2, Application US/08347718B  
Patent No. 5696087  
GENERAL INFORMATION:

APPLICANT: Wang, Chu-San  
APPLICANT: Tang, Jordan J.N  
TITLE OF INVENTION: METHOD FOR REDUCING INTESTINAL ABSORPTION OF  
TITLE OF INVENTION: CHOLESTERO.  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea U. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIC TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/347,7198  
FILING DATE: December 1, 1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea U.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP151  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 742 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 186..187  
OTHER INFORMATION: /note= "Position 187 represents a  
OTHER INFORMATION: potential N-linked glycosylation site."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 193..194  
OTHER INFORMATION: /note= "The serine at position 194  
OTHER INFORMATION: represents an active site serine."  
FEATURE:  
NAME/KEY: misc. feature  
LOCATION: 1..742  
OTHER INFORMATION: /Function = "Amino acid sequence for  
OTHER INFORMATION: the Human Milk Bile Salt-activated Lipase."  
US-09-347-7198-2  
Query Match 1.5%; Score 12; DB 1; Length 742;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 526 YWTFNFAKTGDPN 537  
DB 487 YWTFNFAKTGDPN 498  
RESULT 24  
US-08-482-262-2  
Patent No. 5821226  
GENERAL INFORMATION:  
APPLICANT: Wang, Chu-San  
APPLICANT: Tang, Jordan J.N  
TITLE OF INVENTION: BAL C-TAIL DRUG DELIVERY MOLECULES  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea U. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIC TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,262  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea U.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP151  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 742 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 186..187  
OTHER INFORMATION: /note= "Position 187 represents a  
OTHER INFORMATION: potential N-linked glycosylation site."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 193..194  
OTHER INFORMATION: /note= "The serine at position 194  
OTHER INFORMATION: represents an active site serine."  
FEATURE:  
NAME/KEY: misc. feature  
LOCATION: 1..742  
OTHER INFORMATION: /Function = "Amino acid sequence for  
OTHER INFORMATION: the Human Milk Bile Salt-activated Lipase."  
US-08-482-262-2  
Query Match 1.5%; Score 12; DB 2; Length 742;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 526 YWTFNFAKTGDPN 537  
DB 487 YWTFNFAKTGDPN 498  
RESULT 25  
5200183-2  
Patent No. 5200193  
APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN  
TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES  
NUMBER OF SEQUENCES: 22  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,426  
FILING DATE: 12-JUN-1990  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: 504,635  
FILING DATE: 04-APR-1990  
APPLICATION NUMBER: 122,410  
FILING DATE: 19-NOV-1987  
SEQ ID NO: 2  
LENGTH: 742

5200193-2

Query Match 1.5%; Score 12; DB 6; Length 742;

Best Local Similarity 100.0%; Pred. No. 0.0039; Mismatches 0; Indels 0; Caps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 526 YWTFNFAKTGDPN 537

DB 467 YWTFNFAKTGDPN 498

RESULT 26

US-08-445-050-2

Sequence 2, Application US/08445050

Patent No. 5763739

GENERAL INFORMATION:

APPLICANT: Blackberg, Lars

APPLICANT: Edlund, Michael

APPLICANT: Hansson, Lennart

APPLICANT: Herneil, Oile

APPLICANT: Lundberg, Lennart

APPLICANT: Stromqvist, Mats

APPLICANT: Toernell, Jan

TITLE OF INVENTION: No. 5763739el Polypeptides

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: White &amp; Case

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/06/445,050

FILING DATE:

CLASSIFICATION: 803

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/204,691

FILING DATE:

APPLICATION NUMBER: SE 930686-4

FILING DATE: 01-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9300722-7

FILING DATE: 04-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sterner Ph.D., Richard J

REGISTRATION NUMBER: 35,372

REFERENCE/DOCKET NUMBER: 1103326-850

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)819-8783

TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-445-050-2

Query Match 1.5%; Score 12; DB 1; Length 745;

Best Local Similarity 100.0%; Pred. No. 0.0038; Mismatches 0; Indels 0; Caps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 526 YWTFNFAKTGDPN 537

DB 490 YWTFNFAKTGDPN 501

RESULT 27

US-08-204-691-2

Sequence 2, Application US/08204691

Patent No. 5827683

GENERAL INFORMATION:

APPLICANT: Blackberg, Lars

APPLICANT: Edlund, Michael

APPLICANT: Hansson, Lennart

APPLICANT: Herneil, Oile

APPLICANT: Lundberg, Lennart

APPLICANT: Stromqvist, Mats

APPLICANT: Toernell, Jan

TITLE OF INVENTION: No. 5827683el Polypeptides

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: White &amp; Case

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,691

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9300686-4

FILING DATE: 01-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9300722-7

FILING DATE: 04-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sterner Ph.D., Richard J

REGISTRATION NUMBER: 35,372

REFERENCE/DOCKET NUMBER: 1103326-850

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)819-8783

TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-204-691-2

Query Match 1.5%; Score 12; DB 2; Length 745;

Best Local Similarity 100.0%; Pred. No. 0.0039; Mismatches 0; Indels 0; Caps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 526 YWTFNFAKTGDPN 537

DB 490 YWTFNFAKTGDPN 501

RESULT 28

US-08-370-223-13

Sequence 13, Application US/08370223

Patent No. 6,07026

GENERAL INFORMATION:

APPLICANT: Lange, I.I., Louis G.

APPLICANT: Kumar, B. Vijaya

TITLE OF INVENTION: Methods and Reagents for RFLP Analysis

TITLE OF INVENTION: of the Human Cholesterol Esterase Gene

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESS: Allegretti &amp; Witcoff, Ltd.

STREET: 10 South Wacker, Suite 3000

```

? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/370.223
? FILING DATE:
? CLASSIFICATION: 357
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/053.308
? FILING DATE:
? APPLICATION NUMBER: 07/730.224
? FILING DATE: July 15, 1991
? ATTORNEY/AGENT INFORMATION:
? NAME: McDonnell, John J.
? REGISTRATION NUMBER: 26,949
? REFERENCE/DOCKET NUMBER: 91,441
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-715-1000
? TELEFAX: 312-715-1234
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 745 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-370-223-13

Query Match: 1.5%; Score 12; DB 3; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNPAKTGDPN 537
DB 490 YWTFNPAKTGDPN 501

RESULT 29
US-09-355-295B-3
? Sequence 3, Application US/09355295B
? Patent No. 6525241
? GENERAL INFORMATION:
? APPLICANT: Calyptle, M.
? APPLICANT: Lundberg, L.
? APPLICANT: Stromqvist, M.
? TITLE OF INVENTION: Expression Methods
? FILE REFERENCE: 1754 SEQUENCE LISTING v2a.txt
? CURRENT APPLICATION NUMBER: US/09/355.295B
? CURRENT FILING DATE: 1999-07-18
? PRIOR APPLICATION NUMBER: PCT/SE99/00648
? PRIOR FILING DATE: 1999-04-21
? NUMBER OF SEQ ID NOS: 5
? SEQ ID NO 3
? LENGTH: 745
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-355-295B-3

Query Match: 1.5%; Score 12; DB 4; Length 745;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNPAKTGDPN 537
DB 490 YWTFNPAKTGDPN 501

RESULT 30
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US-09-347-878-32
? Sequence 32, Application US/09347878C
? Patent No. 6376213
? GENERAL INFORMATION:
? APPLICANT: Yuan, Chong
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
? FILE REFERENCE: 25885-1651
? CURRENT APPLICATION NUMBER: US/09/347.878C
? CURRENT FILING DATE: 1999-07-06
? NUMBER OF SEQ ID NOS: 75
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 32
? LENGTH: 747
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-347-878-32

Query Match: 1.5%; Score 12; DB 4; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNPAKTGDPN 537
DB 490 YWTFNPAKTGDPN 501

RESULT 31
US-09-264-737-1
? Sequence 1, Application US/09264737A
? Patent No. 6107549
? GENERAL INFORMATION:
? APPLICANT: Feng, Paul C.C.
? APPLICANT: Ruff, Thomas G.
? TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
? FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
? CURRENT APPLICATION NUMBER: US/09/264.737A
? CURRENT FILING DATE: 1999-03-09
? EARLIER APPLICATION NUMBER: 60/077.377
? EARLIER FILING DATE: 1998-03-10
? NUMBER OF SEQ ID NOS: 11
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 1
? LENGTH: 539
? TYPE: PRT
? ORGANISM: Rabbit
? US-09-264-737-1

Query Match: 1.1%; Score 9; DB 3; Length 539;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLYNY 133
DB 36 EDCYLYNY 104

RESULT 32
US-09-264-737-2
? Sequence 2, Application US/09264737A
? Patent No. 6107549
? GENERAL INFORMATION:
? APPLICANT: Feng, Paul C.C.
? APPLICANT: Ruff, Thomas G.
? TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
? FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
? CURRENT APPLICATION NUMBER: US/09/264.737A
? CURRENT FILING DATE: 1999-03-09
? EARLIER APPLICATION NUMBER: 60/077.377
? EARLIER FILING DATE: 1998-03-10
? NUMBER OF SEQ ID NOS: 11
? SOFTWARE: Patentin Ver. 2.0
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SEQ ID NO 2  
LENGTH: 566  
TYPE: PRT  
ORGANISM: Rabbit  
US-09-264-737-2

Query Match 1.1% Score 9; DB 3; Length 566;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNLY 133  
DB 115 EDCLYNLY 123

RESULT 33  
US-08-845-295A-2  
Sequence 2, Application US/08845295A  
Patent No. 58,7490  
GENERAL INFORMATION:  
APPLICANT: Hubbs, John C.  
TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of  
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eastman Chemical Company  
STREET: P.O. Box 511  
CITY: Kingsport  
STATE: Tennessee  
COUNTRY: USA  
ZIP: 37662-5075  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,295A  
FILING DATE: 25-April-97  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/017,879  
FILING DATE: 17-May-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Cheryl J. Tubach  
REGISTRATION NUMBER: 38,346  
REFERENCE/DOCKET NUMBER: 70432  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 423-229-6189  
TELEFAX: 423-229-1239  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 584 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: Protein  
US-08-845-295A-2

Query Match 1.1% Score 9; DB 2; Length 584;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNLY 133  
DB 119 EDCLYNLY 127

RESULT 34  
US-09-140-933-2  
Sequence 2, Application US/09140933  
Patent No. 6022719  
GENERAL INFORMATION:

APPLICANT: Hubbs, John C.  
TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of  
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eastman Chemical Company  
STREET: P.O. Box 511  
CITY: Kingsport  
STATE: Tennessee  
COUNTRY: USA  
ZIP: 37662-5075  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/140,933  
FILING DATE: 27-August-98  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/017,879; 08/845,295  
FILING DATE: 17-May-96; 25-April-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Cheryl J. Tubach  
REGISTRATION NUMBER: 38,346  
REFERENCE/DOCKET NUMBER: 70432  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 423-229-6189  
TELEFAX: 423-229-1239  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 584 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: Protein  
US-09-140-933-2

Query Match 1.1% Score 9; DB 3; Length 584;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYNLY 133  
DB 119 EDCLYNLY 127

RESULT 35  
US-09-146-661-2  
Sequence 2, Application US/09146661;  
Patent No. 6136575  
GENERAL INFORMATION:  
APPLICANT: Hubbs, John C.  
TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto  
TITLE OF INVENTION: Acid  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eastman Chemical Company  
STREET: P.O. Box 511  
CITY: Kingsport  
STATE: Tennessee  
COUNTRY: USA  
ZIP: 37662-5075  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,661  
FILING DATE: 03-September-98



CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/017,879; 08/845,295  
FILING DATE: 17-May-96; 25-April-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Cheryl J. Tubach  
REGISTRATION NUMBER: 38,346  
REFERENCE/DOCKET NUMBER: 70432  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 423-229-6189  
TELEFAX: 423-229-4239  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 584 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
US-09-146-661-2

Query Match: 1.1%; Score 9; CB 3; Length 584;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNI 133  
DB 119 EDCLYLNI 127

RESULT 36  
US-09-150-515-2  
Sequence 2, Application US/09150515  
Patent No. 6271006  
GENERAL INFORMATION:  
APPLICANT: Hubbs, John C.  
TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of  
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eastman Chemical Company  
STREET: P.O. Box 511  
CITY: Kingsport  
STATE: Tennessee  
COUNTRY: USA  
ZIP: 37662-5075  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/150,515  
FILING DATE: 09-SEP-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/017,879; 08/845,295  
FILING DATE: 17-May-96; 25-April-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Cheryl J. Tubach  
REGISTRATION NUMBER: 38,346  
REFERENCE/DOCKET NUMBER: 70432  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 423-229-6189  
TELEFAX: 423-229-4239  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 584 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
US-09-150-515-2

Query Match: 1.1%; Score 9; DB 3; Length 584;

Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNI 133  
DB 119 EDCLYLNI 127

RESULT 37  
US-08-462-884A-1  
Sequence 1, Application US/08462884A  
Patent No. 5624636  
GENERAL INFORMATION:  
APPLICANT: Lange III, Louis G  
TITLE OF INVENTION: Mammalian Pancreatic Cholesterol  
TITLE OF INVENTION: Esterase  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti  
STREET: 10 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60636  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,884A  
FILING DATE: Unknown  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: A. Blair Hughes  
REGISTRATION NUMBER: 32,901  
REFERENCE/DOCKET NUMBER: 89,852-J  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/715-1234  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 597 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURES:  
NAME/KEY: misc feature  
LOCATION: 1..597  
OTHER INFORMATION: /note= "Bovine pancreatic  
OTHER INFORMATION: cholesterol esterase"  
US-08-462-884A-1

Query Match: 1.1%; Score 9; DB 1; Length 597;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 EDCLYLNI 132  
DB 95 EDCLYLNI 103

RESULT 38  
US-08-451-881B-1  
Sequence 1, Application US/08461881B  
Patent No. 5792832  
GENERAL INFORMATION:  
APPLICANT: Lange III, Louis G  
TITLE OF INVENTION: Mammalian Pancreatic  
TITLE OF INVENTION: Cholesterol Esterase  
NUMBER OF SEQUENCES: 11

1 CORRESPONDENCE ADDRESS:  
2 ADDRESSER: McDermott, Roehren Hilbert & Bergroff  
3 STREET: 300 South Wacker Drive  
4 CITY: Chicago  
5 STATE: IL  
6 COUNTRY: USA  
7 ZIP: 60606  
8  
9 COMPUTER READABLE FORM:  
10 MEDIUM TYPE: 3.5" hard disc  
11 COMPUTER: IBM PC compatible  
12 OPERATING SYSTEM: PC-DOS/MS-DOS  
13 SOFTWARE: Patentin Release #1.0, Version #1.25  
14 CURRENT APPLICATION DATA:  
15 APPLICATION NUMBER: US/09/461,881B  
16 FILING DATE: June 5, 1995  
17 CLASSIFICATION: 435  
18 ATTORNEY/AGENT INFORMATION:  
19 NAME: A. Blair Hughes  
20 REGISTRATION NUMBER: 32,901  
21 REFERENCE/DOCKET NUMBER: 89,852-J  
22 TELECOMMUNICATION INFORMATION:  
23 TELEPHONE: 312/913-0001  
24 TELEFAX: 312/913-0002  
25 TELEX: 910/221-5317  
26 INFORMATION FOR SEQ ID NO: 1:  
27 SEQUENCE CHARACTERISTICS:  
28 LENGTH: 597 amino acids  
29 TYPE: amino acid  
30 TOPOLOGY: linear  
31 MOLECULE TYPE: protein  
32 FEATURE:  
33 NAME/KEY: misc feature  
34 LOCATION: 1..597  
35 OTHER INFORMATION: /note="Bovine pancreatic  
36 OTHER INFORMATION: cholesterol esterase"  
37  
38 US-08-461-881B-1  
39  
40 Query Match 1.1%; Score 9; DB 1; Length 597;  
41 Best Local Similarity 100.0%; Pred. No. 2.9;  
42 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
43  
44 QY 124 NEDCLYNI 132  
45 DB 95 NEDCLYNI 103  
46  
47 RESULT 39  
48 US-09-123-960-1  
49 Sequence 1, Application US/09133960  
50 Patent No. 5981293  
51 GENERAL INFORMATION:  
52 APPLICANT: Lange III, Louis G  
53 APPLICANT: Spilburg, Curtis A  
54 TITLE OF INVENTION: Mammalian Pancreatic  
55 NUMBER OF SEQUENCES: 11  
56 CORRESPONDENCE ADDRESS:  
57 ADDRESSEE: McDermott Roehren Hilbert & Bergroff  
58 STREET: 300 South Wacker Drive  
59 CITY: Chicago  
60 STATE: IL  
61 COUNTRY: USA  
62 ZIP: 60606  
63 COMPUTER READABLE FORM:  
64 MEDIUM TYPE: 3.5" hard disc  
65 COMPUTER: IBM PC compatible  
66 OPERATING SYSTEM: PC-DOS/MS-DOS  
67 SOFTWARE: Patentin Release #1.0, Version #1.25  
68 CURRENT APPLICATION DATA:  
69 APPLICATION NUMBER: US/09/123,960  
70 FILING DATE:  
71 CLASSIFICATION:  
72 PRIOR APPLICATION DATA:  
73 APPLICATION NUMBER: 08/461,881

1 FILING DATE: June 5, 1995  
2 ATTORNEY/AGENT INFORMATION:  
3 NAME: A. Blair Hughes  
4 REGISTRATION NUMBER: 32,901  
5 REFERENCE/DOCKET NUMBER: 89,852-K  
6 TELECOMMUNICATION INFORMATION:  
7 TELEPHONE: 312/913-0001  
8 TELEFAX: 312/913-0002  
9 TELEX: 910/221-5317  
10 INFORMATION FOR SEQ ID NO: 1:  
11 SEQUENCE CHARACTERISTICS:  
12 LENGTH: 597 amino acids  
13 TYPE: amino acid  
14 TOPOLOGY: linear  
15 MOLECULE TYPE: protein  
16 FEATURE:  
17 NAME/KEY: misc feature  
18 LOCATION: 1..597  
19 OTHER INFORMATION: /note="Bovine pancreatic  
20 OTHER INFORMATION: cholesterol esterase"  
21  
22 US-09-123-960-1  
23  
24 Query Match 1.1%; Score 9; DB 2; Length 597;  
25 Best Local Similarity 100.0%; Pred. No. 2.9;  
26 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
27  
28 QY 124 NEDCLYNI 132  
29 DB 95 NEDCLYNI 103  
30  
31 RESULT 40  
32 US-08-462-884A-3  
33 Sequence 3, Application US/08462884A  
34 Patent No. 5624836  
35 GENERAL INFORMATION:  
36 APPLICANT: Lange III, Louis G  
37 APPLICANT: Spilburg, Curtis A  
38 TITLE OF INVENTION: Mammalian Pancreatic Cholesterol  
39 NUMBER OF SEQUENCES: 11  
40 CORRESPONDENCE ADDRESS:  
41 ADDRESSEE: Banner & Allegretti  
42 STREET: 10 South Wacker Drive  
43 CITY: Chicago  
44 STATE: IL  
45 COUNTRY: USA  
46 ZIP: 60606  
47 COMPUTER READABLE FORM:  
48 MEDIUM TYPE: floppy disk  
49 COMPUTER: IBM PC compatible  
50 OPERATING SYSTEM: PC-DOS/MS-DOS  
51 SOFTWARE: Patentin Release #1.0, Version #1.25  
52 CURRENT APPLICATION DATA:  
53 APPLICATION NUMBER: US/08/462,884A  
54 FILING DATE: Unknown  
55 CLASSIFICATION: 435  
56 ATTORNEY/AGENT INFORMATION:  
57 NAME: A. Blair Hughes  
58 REGISTRATION NUMBER: 32,901  
59 REFERENCE/DOCKET NUMBER: 89,852-C  
60 TELECOMMUNICATION INFORMATION:  
61 TELEPHONE: 312/715-1000  
62 TELEFAX: 312/715-1234  
63 TELEX: 910/221-5317  
64 INFORMATION FOR SEQ ID NO: 3:  
65 SEQUENCE CHARACTERISTICS:  
66 LENGTH: 605 amino acids  
67 TYPE: amino acid  
68 TOPOLOGY: linear  
69 MOLECULE TYPE: protein  
70  
71 US-08-462-884A-3

Query Match 1.1%; Score 9; DB 1; Length 605;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 NEDCXYLNI 132  
Db 103 NEDCXYLNI 111

RESULT 41  
US-08-461-881B-3  
Sequence 3, Application US/08461881B  
Patent No. 5792832  
GENERAL INFORMATION:  
APPLICANT: Lange III, Louis G  
APPLICANT: Spilburg, Curtis A  
TITLE OF INVENTION: Mammalian Pancreatic  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDowell, Boehnen Hubert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" hard disc  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,881B  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: A. Blair Hughes  
REGISTRATION NUMBER: 32,901  
REFERENCE/DOCKET NUMBER: 89,852-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/913-0002  
TELEFAX: 312/913-0002  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 605 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-881B-3

Query Match 1.1%; Score 9; DB 1; Length 605;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 NEDCXYLNI 132  
Db 103 NEDCXYLNI 111

RESULT 42  
US-09-123-960-3  
Sequence 3, Application US/09123960  
Patent No. 5981299  
GENERAL INFORMATION:  
APPLICANT: Lange III, Louis G  
APPLICANT: Spilburg, Curtis A  
TITLE OF INVENTION: Mammalian Pancreatic  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDowell, Boehnen Hubert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: IL

COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" hard disc  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/123,960  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/461,881  
FILING DATE: June 5, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: A. Blair Hughes  
REGISTRATION NUMBER: 32,901  
REFERENCE/DOCKET NUMBER: 89,852-K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/913-0001  
TELEFAX: 312/913-0002  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 605 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-123-960-3

Query Match 1.1%; Score 9; DB 2; Length 605;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 NEDCXYLNI 132  
Db 103 NEDCXYLNI 111

RESULT 43  
US-09-347-878-34  
Sequence 34, Application US/09347878C  
Patent No. 6176210  
GENERAL INFORMATION:  
APPLICANT: Yvan, Chong  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES  
FILE REFERENCE: 25885-165.  
CURRENT APPLICATION NUMBER: US/09/347,878C  
CURRENT FILING DATE: 1999-07-06  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 34  
LENGTH: 606  
TYPE: PRT  
ORGANISM: Bos taurus  
OTHER INFORMATION: Bovine pancreatic cholesterol esterase protein sequence  
PUBLICATION INFORMATION:  
PATENT DOCUMENT NUMBER: 08/462,884  
PATENT FILING DATE: 1995-06-05  
PUBLICATION DATE: 1997-04-29  
US-09-347-878-34

Query Match 1.1%; Score 9; DB 4; Length 606;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 NEDCXYLNI 132  
Db 104 NEDCXYLNI 112

RESULT 44

US-08-747-221B-11  
Sequence 11, Application US/08747221B  
Patent No. 6063610  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary M.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6063610e) Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION NUMBER: US/08/747,221B  
APPLICATION NUMBER: US/08/747,221B  
FILING DATE: No. 6063610e) December 12, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: PC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-747-221B-11  
Query Match: 1.0%; Score 8; DB 3; Length 137;  
Best Local Similarity: 100.0%; Pred. No. 7.2;  
Matches: 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 125 EDCLYINI 132  
Db 112 EDCLYINI 119  
RESULT 45  
US-09-005-051-11  
Sequence 11, Application US/09005051  
Patent No. 6291222  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary M.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6291222e) Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,051  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/747,221  
FILING DATE: No. 6291222e) December 12, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: PC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-005-051-11  
Query Match: 1.0%; Score 8; DB 3; Length 137;  
Best Local Similarity: 100.0%; Pred. No. 7.2;  
Matches: 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 125 EDCLYINI 132  
Db 112 EDCLYINI 119  
RESULT 46  
US-09-827-171B-8  
Sequence 8, Application US/09827171B  
Patent No. 6254869  
GENERAL INFORMATION:  
APPLICANT: CAROLYN PETERSEN  
APPLICANT: JIN-KING HUNG  
TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,  
TITLE OF INVENTION: PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,  
TITLE OF INVENTION: TREATMENT, DIAGNOSIS AND  
TITLE OF INVENTION: DETECTION OF  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PETERS, VERNY, JONES & BIK A  
STREET: 385 Sherman Avenue, Suite 6  
CITY: Palo Alto  
STATE: California  
COUNTRY: United States of America  
ZIP: 94306-1940  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage  
COMPUTER: PC  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: WordPerfect 6.0a WINDOWS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,171B  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/014,233  
FILING DATE: March 27, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hana Verry  
REGISTRATION NUMBER: 30,518  
REFERENCE/DOCKET NUMBER: (HV)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-1677  
TELEFAX: (415) 324-1678  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids

TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Plasmodium vivax

Query Match 1.0%; Score 8; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 VTIAGAS 684  
DB 129 VTIAGAS 136

RESULT 47  
US-08-747-2218-37  
Sequence 37, Application US/087472218  
Patent No. 6063610

GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,2218  
FILING DATE: No. 6063610e1 December 12, 1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 528 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-747-2218-37

Query Match 1.0%; Score 8; DB 3; Length 528;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 527 WTNFAKTS 534  
DB 472 WTNFAKTS 479

RESULT 48  
US-03-005-051-37  
Sequence 37, Application US/0305051  
Patent No. 6231222  
GENERAL INFORMATION:

APPLICANT: Silver, Gary W.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,051  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/747,221  
FILING DATE: No. 6291222e1 December 12, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 528 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-005-051-37

Query Match 1.0%; Score 8; DB 3; Length 528;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 527 WTNFAKTS 534  
DB 472 WTNFAKTS 479

RESULT 49  
US-08-362-525-12  
Sequence 12, Application US/08362525  
Patent No. 6027910

GENERAL INFORMATION:  
APPLICANT: KIS, FRANCISCUS W.  
APPLICANT: SCHREUDER, MAARTEN P.  
APPLICANT: TOSCHKA, HOLGER Y.  
TITLE OF INVENTION: VERRIPS, CORNELIS T.  
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE  
TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-9918

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,525  
FILING DATE: 04-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92203080.5  
FILING DATE: 08-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92203089.7  
FILING DATE: 14-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/01763  
FILING DATE: 07-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16, 773  
REFERENCE/DOCKET NUMBER: 213289/T7020(V)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3003  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 563 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-362-525-12

Query Match 1.0%; Score 8; DB 3; Length 563;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NEDCLYLN 131  
DB 121 NEDCLYLN 128

RESULT 5C  
US-08-747-221B-54  
Sequence 54, Application US/08747221B  
Patent No. 60636-0  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
ATTORNEY/AGENT INFORMATION:  
NAME: Wisniewski, Nancy  
REGISTRATION NUMBER: No. 6063610e1 Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Carol Talkington Verser, Ph.D.  
STREET: 1925 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,221B  
FILING DATE: No. 6063610e1 December 12, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: PC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 570 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-747-221B-54

Query Match 1.0%; Score 8; DB 3; Length 570;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 132  
DB 86 EDCLYLN 93

RESULT 51  
US-08-747-221B-55  
Sequence 55, Application US/08747221B  
Patent No. 6063610  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
ATTORNEY/AGENT INFORMATION:  
NAME: Wisniewski, Nancy  
REGISTRATION NUMBER: No. 6063610e1 Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Carol Talkington Verser, Ph.D.  
STREET: 1925 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,221B  
FILING DATE: No. 6063610e1 December 12, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: PC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 570 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-747-221B-55

Query Match 1.0%; Score 8; DB 3; Length 570;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 132  
DB 86 EDCLYLN 93

RESULT 52  
US-09-005-051-54  
Sequence 54, Application US/09005051  
Patent No. 629122  
GENERAL INFORMATION:

```

? APPLICANT: Silver, Gary M.
? APPLICANT: Wisniewski, Nancy
? TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nuclic Acid
? NUMBER OF SEQUENCES: 66
? CORRESPONDENCE ADDRESS:
? ADDRESS: Carol Talkington Verser, Ph.D.
? ADDRESS: Heska Corporation
? STREET: 1825 Sharp Point Drive
? CITY: Fort Collins
? STATE: Colorado
? COUNTRY: USA
? ZIP: 80525
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: Windows 95
? SOFTWARE: WordPerfect for Windows, Version 7.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/005,051
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/747,221
? FILING DATE: No. 6291222e1 December 12, 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Verser, Carol Talkington
? REGISTRATION NUMBER: 37,459
? REFERENCE/DOCKET NUMBER: PC-1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 970/493-7272
? TELEFAX: 970/484-9505
? INFORMATION FOR SEQ ID NO: 54:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 570 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
? US-09-005-051-54
?
? Query Match 1.0%; Score 8; DB 3; Length 570;
? Best Local Similarity 100.0%; Pred. No. 27;
? Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
?
? QY 125 EDCLYINI 132
? Db 96 EDCCLYINI 93
?
? RESULT 53
? US-09-005-051-55
? Sequence 55, Application US/09005051
? Patent No. 6291222
? GENERAL INFORMATION:
? APPLICANT: Silver, Gary M.
? APPLICANT: Wisniewski, Nancy
? TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nuclic Acid
? NUMBER OF SEQUENCES: 66
? CORRESPONDENCE ADDRESS:
? ADDRESS: Carol Talkington Verser, Ph.D.
? ADDRESS: Heska Corporation
? STREET: 1825 Sharp Point Drive
? CITY: Fort Collins
? STATE: Colorado
? COUNTRY: USA
? ZIP: 80525
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: Windows 95
? SOFTWARE: WordPerfect for Windows, Version 7.0
? CURRENT APPLICATION DATA:

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? APPLICATION NUMBER: US/09/005,051
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/747,221
? FILING DATE: No. 6291222e1 December 12, 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Verser, Carol Talkington
? REGISTRATION NUMBER: 37,459
? REFERENCE/DOCKET NUMBER: PC-1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 970/493-7272
? TELEFAX: 970/484-9505
? INFORMATION FOR SEQ ID NO: 55:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 570 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
? US-09-005-051-55
?
? Query Match 1.0%; Score 8; DB 3; Length 570;
? Best Local Similarity 100.0%; Pred. No. 27;
? Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
?
? QY 125 EDCLYINI 132
? Db 86 EDCCLYINI 93
?
? RESULT 54
? US-08-348-920-1
? Sequence 1, Application US/08348920
? Patent No. 5695750
? GENERAL INFORMATION:
? APPLICANT: Doctor, Bhupendra P.
? APPLICANT: Maxwell, Donald
? APPLICANT: Saxena, Ashima
? APPLICANT: Radic, Zoran
? APPLICANT: Taylor, Palmer
? TITLE OF INVENTION: Compositions for Use to Deactivate
? NUMBER OF SEQUENCES: 2
? CORRESPONDENCE ADDRESS:
? ADDRESS: John F. Moran
? STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
? STREET: Detrick
? CITY: Frederick
? STATE: MD
? COUNTRY: US
? ZIP: 21702-5012
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentia Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/348,920
? FILING DATE: 25-NOV-1994
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Herdicks, Gienaa
? REGISTRATION NUMBER: 32,535
? REFERENCE/DOCKET NUMBER: doc348,920
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (302) 619-7807
? TELEFAX: 301-619-7714
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 575 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: unknown

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MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-348-920-1

Query Match 1.0%; Score 8; DB 1; Length 575;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132  
Db 92 EDCLYLNI 99

RESULT 55  
US-08-348-920-2  
Sequence 2, Application US/08348920  
Patent No. 5695750  
GENERAL INFORMATION:  
APPLICANT: Doctor, Bhupendra P.  
APPLICANT: Maxwell, Donald  
APPLICANT: Saxena, Ashima  
APPLICANT: Ragic, Zoran  
APPLICANT: Taylor, Palmer  
TITLE OF INVENTION: Compositions for Use to Deactivate  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John F. Moran  
STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort  
STREET: Detrick  
CITY: Frederick  
STATE: MD  
COUNTRY: US  
ZIP: 21702-5012  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent-in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,920  
FILING DATE: 25-Nov-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: ddc348,920  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 619-7807  
TELEFAX: 301-619-7714  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 575 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-348-920-2

Query Match 1.0%; Score 8; DB 1; Length 575;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132  
Db 92 EDCLYLNI 99

RESULT 56  
US-08-747-221B-31  
Sequence 31, Application US/08747221B  
Patent No. 6063610  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Miszewski, Nancy  
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,221B  
FILING DATE: No. 6063610ember 12, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 595 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-747-221B-31

Query Match 1.0%; Score 8; DB 3; Length 595;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132  
Db 111 EDCLYLNI 118

RESULT 57  
US-09-005-051-31  
Sequence 31, Application US/09005051  
Patent No. 6291222  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Miszewski, Nancy  
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95



SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,051  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/747,221  
FILING DATE: No. 6291222ember 12, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 595 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-005-051-31

Query Match 1.0%; Score 8; DB 3; Length 595;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132  
Db 111 EDCLYLNI 118

RESULT 58  
US-08-747-221B-25  
Sequence 25, Application US/08747221B  
Patent No. 6063610  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,221B  
FILING DATE: No. 6063610ember 12, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-747-221B-25

Query Match 1.0%; Score 8; DB 3; Length 596;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132  
Db 112 EDCLYLNI 119

RESULT 59  
US-09-005-051-25  
Sequence 25, Application US/09005051  
Patent No. 6291222  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary W.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid  
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,051  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/747,221  
FILING DATE: No. 6291222ember 12, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: FC-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-005-051-25

Query Match 1.0%; Score 8; DB 3; Length 596;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 EDCLYLNI 132  
Db 112 EDCLYLNI 119

RESULT 60  
5200183-4  
Patent No. 5290183  
APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN  
TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES  
NUMBER OF SEQUENCES: 22  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,426  
FILING DATE: 12-JUN-1990

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 504,635  
FILING DATE: 04-APR-1990  
APPLICATION NUMBER: 122,410  
FILING DATE: 19-NOV-1987  
SEQ ID NO:4:  
LENGTH: 723  
5200183-4

Query Match 1.0%; Score 8; DB 6; Length 723;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCYLYNI 132  
DB 79 EDCYLYNI 86

RESULT 61  
US-09-252-991A-29373  
Sequence 28373, Application US/03252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,789  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/034,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 28373  
LENGTH: 767  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29373

Query Match 1.0%; Score 8; DB 4; Length 767;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 PAVAADLH 460  
DB 309 PAVAADLH 316

RESULT 62  
US-09-735-934A-4  
Sequence 4, Application US/09735934A  
Patent No. 6372468  
GENERAL INFORMATION:  
APPLICANT: Li, Jia-Yin et al  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: C1000851  
CURRENT APPLICATION NUMBER: US/09/735,934A  
CURRENT FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 894  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-735-934A-4

Query Match 1.0%; Score 8; DB 4; Length 894;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDEDIHQ 163  
DB 767 EDEDIHQ 774

RESULT 63  
US-10-060-332-4  
Sequence 4, Application US/10060332  
Patent No. 6528294  
GENERAL INFORMATION:  
APPLICANT: Li, Jia-Yin et al  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: C1000851DIV  
CURRENT APPLICATION NUMBER: US/10/060,332  
CURRENT FILING DATE: 2002-02-01  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 894  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-060-332-4

Query Match 1.0%; Score 8; DB 4; Length 894;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 EDEDIHQ 163  
DB 767 EDEDIHQ 774

RESULT 64  
US-08-308-086-8  
Sequence 8, Application US/08308086  
Patent No. 5786454  
GENERAL INFORMATION:  
APPLICANT: Gabriel Waksman and Andrey Shaw  
TITLE OF INVENTION: Modified SH2 Domains and Methods of Use  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,086  
FILING DATE: 09-16-97  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patricia L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 95 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-308-086-8

Query Match: 0.9%; Score 7; DB 1; Length 96;  
Best Local Similarity: 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTLLR 765  
|||||  
DB 35 DYTLLR 41

## RESULT 65

US-08-167-035-17  
Sequence 17, Application US/08167035  
Patent No. 5618691  
GENERAL INFORMATION:  
APPLICANT: Schllessinger, Joseph  
APPLICANT: Skolnick, Edward Y.  
APPLICANT: Margolis, Benjamin J.  
TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR  
IDENTIFYING TARGET PROTEINS FOR ENZYMOLOGIC PURPOSES  
TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: 10036-2711  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08167035  
FILING DATE: 16-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-062  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 793-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-167-035-17

Query Match: 0.9%; Score 7; DB 1; Length 96;  
Best Local Similarity: 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTLLR 765  
|||||  
DB 34 DYTLLR 40

## RESULT 66

US-08-208-887A-17  
Sequence 17, Application US/08208887A  
Patent No. 5677421  
GENERAL INFORMATION:  
APPLICANT: Schllessinger, Joseph  
APPLICANT: Skolnick, Edward Y.  
APPLICANT: Margolis, Benjamin J.  
TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR  
IDENTIFYING TARGET PROTEINS FOR ENZYMOLOGIC PURPOSES  
TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: 10036-2711  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08208887A  
FILING DATE: 11-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 793-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-208-887A-17

TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: 10036-2711  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08208887A  
FILING DATE: 11-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-063  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 793-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-208-887A-17

Query Match: 0.9%; Score 7; DB 1; Length 96;  
Best Local Similarity: 100.0%; Pred. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTLLR 765  
|||||  
DB 34 DYTLLR 40

## RESULT 67

US-08-479-078-20  
Sequence 20, Application US/08479078  
Patent No. 5814466  
GENERAL INFORMATION:  
APPLICANT: Rawson, Anthony  
TITLE OF INVENTION: Method for Assaying for a Substance that  
Affects an SH2-Phosphorylated Ligand Regulatory System  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bereskin & Parr  
STREET: 40 King Street, West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 3Y2  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08479078  
FILING DATE: June 6, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Linda V. Kurdadyk  
REGISTRATION NUMBER: 34,971  
REFERENCE/DOCKET NUMBER: 3153-154  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 364-7311  
TELEFAX: (416) 361-1398  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-479-078-20

Query Match 0.9%; Score 7; DB 2; Length 96;  
Best Local Similarity 100.0%; Preg. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTTLR 765  
|||||  
DB 35 DYTTLR 41

RESULT 68  
US-08-539-005-17  
Sequence 17, Application US/08539005  
Patent No. 5858686  
GENERAL INFORMATION:  
APPLICANT: Schlessinger, Joseph  
APPLICANT: Skolnick, Edward Y.  
APPLICANT: Margolis, Benjamin L.  
TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR  
IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE  
KINASES AND NOVEL TARGET PROTEINS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: 10036-2711  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/539.005  
FILING DATE: 4-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/167,035  
FILING DATE: 16-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-062  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-539-005-17

Query Match 0.9%; Score 7; DB 2; Length 96;  
Best Local Similarity 100.0%; Preg. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTTLR 765

|||||  
DB 34 DYTTLR 40

RESULT 69  
US-09-280-598-19  
Sequence 19, Application US/09280598  
Patent No. 6391584  
GENERAL INFORMATION:  
APPLICANT: Schlessinger, Joseph  
APPLICANT: Skolnick, Edward Y.  
APPLICANT: Margolis, Benjamin L.  
APPLICANT: App, Harold  
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR  
IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE  
KINASES AND NOVEL TARGET PROTEINS  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280,598  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/252,820  
FILING DATE: 02-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 96 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-280-598-19

Query Match 0.9%; Score 7; DB 4; Length 96;  
Best Local Similarity 100.0%; Preg. No. 50;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 DYTTLR 765  
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DB 34 DYTTLR 40

RESULT 70  
US-08-820-754-25  
Sequence 25, Application US/08820754  
Patent No. 5976835  
GENERAL INFORMATION:  
APPLICANT: Darnell Jr., James E.  
APPLICANT: Schindler, Christian W.  
APPLICANT: Fu, Xian-Yuan  
APPLICANT: Wen, Xian-Yuan  
APPLICANT: Zhong, Zhong  
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN  
SEQUENCES AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/820,754  
FILING DATE: 19-MAR-1997  
CLASSIFICATION: 53C  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,185  
FILING DATE: 11-MAR-1994  
APPLICATION NUMBER: US 07/980,498  
FILING DATE: 21-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/854,296  
FILING DATE: 19-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO US93/02569  
FILING DATE: 19-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,588  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-073 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
IMMEDIATE SOURCE:  
CLONE: p85(alpha)N  
US-08-820-754-25

Query Match 0.9%; Score 7; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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39 DYTLLR 45

Db 39 DYTLLR 45

RESULT 71  
US-08-956-652-25  
Sequence 25, Application US/08956652  
Patent No. 6033475  
GENERAL INFORMATION:  
APPLICANT: Darnell Jr., James E.  
APPLICANT: Schindler, Christian W.  
APPLICANT: Fu, Xian-Yuan  
APPLICANT: Wen, Zilong  
APPLICANT: Zhong, Zhong  
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,652  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,185  
FILING DATE: 11-MAR-1994  
APPLICATION NUMBER: US 07/980,498  
FILING DATE: 23-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/854,296  
FILING DATE: 19-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO US93/02569  
FILING DATE: 19-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,588  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-073 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
IMMEDIATE SOURCE:  
CLONE: p85(alpha)N  
US-08-956-652-25

Query Match 0.9%; Score 7; DB 3; Length 99;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 759 DYTLLR 765  
|||  
39 DYTLLR 45

Db 39 DYTLLR 45

RESULT 72  
US-08-956-869-25  
Sequence 25, Application US/08956869  
Patent No. 6030808  
GENERAL INFORMATION:  
APPLICANT: Darnell Jr., James E.  
APPLICANT: Schindler, Christian W.  
APPLICANT: Fu, Xian-Yuan  
APPLICANT: Wen, Zilong  
APPLICANT: Zhong, Zhong

TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,869  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/212,185  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/854,296  
FILING DATE: 19-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO US93/02569  
FILING DATE: 19-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,586  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-073 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
IMMEDIATE SOURCE:  
CLONE: p85.alpha1N  
US-08-956-869-25  
Query Match 0.9%; Score 7; DB 3; Length 99;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 759 DYLTLR 765  
DB 39 DYLTLR 45  
RESULT 73  
US-08-948-547-25  
Sequence 25, Application US/08948547  
Patent No. 6124118  
GENERAL INFORMATION:  
APPLICANT: Darrell Jr., James E.  
APPLICANT: Schindler, Christian W.  
APPLICANT: Fu, Xian-Yuan  
APPLICANT: Wen, Zilong  
APPLICANT: Zhong, Zhong  
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN

TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/948,547  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/212,185  
FILING DATE: 11-MAR-1994  
APPLICATION NUMBER: US 07/980,498  
FILING DATE: 23-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/854,296  
FILING DATE: 19-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO US93/02569  
FILING DATE: 19-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,586  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-073 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
IMMEDIATE SOURCE:  
CLONE: p85.alpha1N  
US-08-948-547-25  
Query Match 0.9%; Score 7; DB 3; Length 99;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 759 DYLTLR 765  
DB 39 DYLTLR 45  
RESULT 74  
US-08-747-221B-8  
Sequence 8, Application US/08747221B  
Patent No. 6063610  
GENERAL INFORMATION:  
APPLICANT: Silver, Gary M.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: No. 6063610e1 Carboxylesterase Nucleic Acid  
NUMBER OF SEQUENCES: 66

```

CORRESPONDENCE ADDRESS:
ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 606361 December 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-747-221B-8

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 103;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 80 EDCLYLN 86

RESULT 75
US-09-005-051-8
Sequence 2, Application US/09005051
GENERAL INFORMATION:
PATENT NO. 6291222
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222e1 Carboxylesterase Nucleic Acid
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222e2 December 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington

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REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-051-8

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 103;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLN 131
DB 80 EDCLYLN 86

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Search completed: November 5, 2003, 15:26:50  
 Job time : 24 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: November 5, 2003, 15:18:43 ; Search time 47 Seconds

(without alignments)

2755.763 Million cell updates/sec

Title: US-09-978-423a-375

Perfect score: 816

Sequence: 1 MLNSNVLLMLTLALIKETLI.....TFSGGQNSTYLPHGHSTTRV 816

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	816	100.0	816	20	AAV4174C Human PRO701 prote
2	816	100.0	816	21	AAAB4296 Human PRO701 (CMQ3
3	816	100.0	816	21	AAAB3427 Human PRO701 prote
4	816	100.0	816	24	ABU61126 Human PRO701 polyp
5	538	65.9	817	24	ABP82852 Human protein sequ
6	388	47.5	509	22	AAAB94127 CES2 related polyp
7	388	47.5	509	23	ABAB82853 CES2 related polyp
8	326	40.0	816	23	AAAB49308 Human neurotrophin
9	208	25.5	396	22	AAU87273 Novel central nerv

10	76	9.3	1.55	22	ABP17862 Human nervous syst
11	50	6.1	509	22	AAV93705 Human polypeptide,
12	48	5.9	271	22	ABG10266 Novel human diago
13	48	5.9	308	21	AAAB0734 Human CRFX ORF498
14	48	5.9	801	23	ABP07524 Human drug metabo
15	48	5.9	835	23	AAE25020 Human drug metabo
16	48	5.9	835	23	ABP97215 Novel human prote
17	48	5.9	835	23	ABP07675 Human carboxyleste
18	48	5.9	837	22	AAAB6240 Human MBSP4 polype
19	46	5.6	49	22	ABG51838 Human liver peptid
20	43	4.3	1434	22	ABG10270 Novel human diago
21	35	4.3	828	23	ABP43803 3 isoform protein
22	32	3.9	229	21	AAAB4913 Human secreted pro
23	32	3.9	229	21	AAAB4914 Human secreted pro
24	32	3.8	726	22	ABG10264 Human polypeptide
25	31	3.8	144	22	AAO07845 Novel central nerv
26	28	3.4	81	22	AAU23324 Novel human enzyme
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28	28	3.4	335	22	AAAB93845 Human polypeptide,
29	28	3.4	419	22	ABG16824 Novel human diago
30	26	3.2	165	22	ABG10269 Novel human diago
31	26	3.2	134	22	AAO04336 Human albumin fusi
32	21	2.6	228	23	ABG64991 Human albumin fusi
33	18	2.2	228	23	AAE21452 Human gene 1 encod
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35	15	1.8	162	23	ABG64990 Human albumin fusi
36	15	1.8	162	23	ABE21473 Human gene 1 encod
37	12	1.5	359	21	AAAB5426 Human pancreatic c
38	12	1.5	535	15	AAAB58985 Bile salt-stimulat
39	12	1.5	538	16	AAAB75098 Recombinant bile s
40	12	1.5	538	17	AAAB10058 Human wild-type b:
41	12	1.5	566	15	AAAB58981 Bile salt-stimulat
42	12	1.5	568	15	AAAB58982 Bile salt-stimulat
43	12	1.5	568	17	AAAB9258 Human bile salt-st
44	12	1.5	668	15	AAAB58983 Bile salt-stimulat
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46	12	1.5	722	15	AAAB58984 Bile salt-stimulat
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48	12	1.5	722	16	AAAB75107 Bile salt-activate
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51	12	1.5	722	23	ABE004576 Human milk bile sa
52	12	1.5	725	23	AAU098994 Bile salt-stimulat
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56	12	1.5	744	15	AAAB45189 BSS/L/CBL Homo sa
57	12	1.5	745	13	AAAB20098 Bile salt-stimulat
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64	11	1.3	537	22	ABAB68593 Drosophila melanog
65	9	1.1	92	23	AAO17545 Human carboxyleste
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67	9	1.1	507	22	ABAB61993 Drosophila melanog
68	9	1.1	541	22	ABAB57789 Drosophila melanog
69	9	1.1	543	20	AAAB33146 Rabbit liver carbo
70	9	1.1	544	23	AAO188372 Human acyl coenzym
71	9	1.1	562	24	ABP97364 Mouse acyl coenzym
72	9	1.1	564	22	ABAB60215 Drosophila melanog
73	9	1.1	565	20	AAAB33145 Rabbit liver carbo
74	9	1.1	566	21	AAAB08202 Amino acid sequenc
75	9	1.1	567	22	AAAB73263 Human triacylglyce
76	9	1.1	567	23	AAO17544 Human liver carbox
77	9	1.1	568	24	ABP97363 Human acyl coenzym
78	9	1.1	568	23	ABG31485 D. melanogaster ju
79	9	1.1	575	23	ABP61004 Novel human protei
80	9	1.1	581	23	ABAB79537 Human carboxyleste
81	9	1.1	581	23	ABP61005 Novel human protei
82	9	1.1	581	24	ABAB54639 Human NOVX polypep





XX The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AA333861 to  
 CC AA233338, and AA14685 to AA14774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.

XX Sequence 816 AA:

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Best Local Similarity 100.0%; P-Val. No. 0;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 121 QCNEDCLYNTIYVPEDGANTKKNADGTSNDGEGEDDHDONSKKRWYVYIGSSYME 180  
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 241 AFGGPKRYTIFGSGAGSCVSLTSHSSEGLFQKALICSTALSSKAWYQYQAKYTR 300  
 DB 241 AFGGPKRYTIFGSGAGSCVSLTSHSSEGLFQKALICSTALSSKAWYQYQAKYTR 300  
 241 AFGGPKRYTIFGSGAGSCVSLTSHSSEGLFQKALICSTALSSKAWYQYQAKYTR 300  
 QY 301 LADKVGCMNLDITDMVECLRNKVELIQDTTPATVHAFSPVIGDGVIDDFQILMEQ 360  
 301 LADKVGCMNLDITDMVECLRNKVELIQDTTPATVHAFSPVIGDGVIDDFQILMEQ 360  
 DB 301 LADKVGCMNLDITDMVECLRNKVELIQDTTPATVHAFSPVIGDGVIDDFQILMEQ 360  
 301 LADKVGCMNLDITDMVECLRNKVELIQDTTPATVHAFSPVIGDGVIDDFQILMEQ 360  
 QY 361 GEELNDIMLVNCGEGCKFNGGIVDNEGVTPNPDPSYSFVNNLYGYESGCTPET 420  
 361 GEELNDIMLVNCGEGCKFNGGIVDNEGVTPNPDPSYSFVNNLYGYESGCTPET 420  
 DB 361 GEELNDIMLVNCGEGCKFNGGIVDNEGVTPNPDPSYSFVNNLYGYESGCTPET 420  
 361 GEELNDIMLVNCGEGCKFNGGIVDNEGVTPNPDPSYSFVNNLYGYESGCTPET 420  
 QY 421 KFMVYMAKDNKPNETRRKTLVALFTDQWVAPAVADLHAQYGSPTFFVAFYHCGSEM 480  
 421 KFMVYMAKDNKPNETRRKTLVALFTDQWVAPAVADLHAQYGSPTFFVAFYHCGSEM 480  
 DB 421 KFMVYMAKDNKPNETRRKTLVALFTDQWVAPAVADLHAQYGSPTFFVAFYHCGSEM 480  
 421 KFMVYMAKDNKPNETRRKTLVALFTDQWVAPAVADLHAQYGSPTFFVAFYHCGSEM 480  
 QY 481 KESNADSAHGEVYVFGIPMIGFELPSGNSKQDMLSAVMTYNTNFAKTCDEQPV 540  
 481 KESNADSAHGEVYVFGIPMIGFELPSGNSKQDMLSAVMTYNTNFAKTCDEQPV 540  
 DB 481 KESNADSAHGEVYVFGIPMIGFELPSGNSKQDMLSAVMTYNTNFAKTCDEQPV 540  
 481 KESNADSAHGEVYVFGIPMIGFELPSGNSKQDMLSAVMTYNTNFAKTCDEQPV 540  
 QY 541 PCPTKFIHTKPRFEEVWASXVNPDOYTHGKPRYGVHQAQVAVWFLTSHLHNT 600  
 541 PCPTKFIHTKPRFEEVWASXVNPDOYTHGKPRYGVHQAQVAVWFLTSHLHNT 600  
 DB 541 PCPTKFIHTKPRFEEVWASXVNPDOYTHGKPRYGVHQAQVAVWFLTSHLHNT 600  
 541 PCPTKFIHTKPRFEEVWASXVNPDOYTHGKPRYGVHQAQVAVWFLTSHLHNT 600  
 QY 601 NEIFQVYSTTKVPEDMTSPFYGTRRSFAKIMPTTKPAIPANPNPGRSXPHTGED 660  
 601 NEIFQVYSTTKVPEDMTSPFYGTRRSFAKIMPTTKPAIPANPNPGRSXPHTGED 660  
 DB 601 NEIFQVYSTTKVPEDMTSPFYGTRRSFAKIMPTTKPAIPANPNPGRSXPHTGED 660  
 601 NEIFQVYSTTKVPEDMTSPFYGTRRSFAKIMPTTKPAIPANPNPGRSXPHTGED 660  
 QY 661 TTVLLETKQYSTELSVTAAGASLLFNILAFALVYKCKRRETHRRSPQRNTND 720  
 661 TTVLLETKQYSTELSVTAAGASLLFNILAFALVYKCKRRETHRRSPQRNTND 720  
 DB 661 TTVLLETKQYSTELSVTAAGASLLFNILAFALVYKCKRRETHRRSPQRNTND 720  
 661 TTVLLETKQYSTELSVTAAGASLLFNILAFALVYKCKRRETHRRSPQRNTND 720  
 QY 721 IAHQNEEISLSQKOLEHDEGCESLQAAHDLTLTCCPDYTTLRSDDPLPLTPWTIT 780  
 721 IAHQNEEISLSQKOLEHDEGCESLQAAHDLTLTCCPDYTTLRSDDPLPLTPWTIT 780  
 DB 721 IAHQNEEISLSQKOLEHDEGCESLQAAHDLTLTCCPDYTTLRSDDPLPLTPWTIT 780  
 721 IAHQNEEISLSQKOLEHDEGCESLQAAHDLTLTCCPDYTTLRSDDPLPLTPWTIT 780  
 QY 781 MIPNTLGGWQPLHTNTFGGQNSTNLPHGSTTRV 816  
 781 MIPNTLGGWQPLHTNTFGGQNSTNLPHGSTTRV 816

DB 781 MIPNTLGGWQPLHTNTFGGQNSTNLPHGSTTRV 816

RESULT 2

ID AA344296 standard; Protein: 8:6 AA.

AA344296;

08-FEB-2001 (first entry)

Human PRO701 (UNQ365) protein sequence SEQ ID NO:375.

Human: secreted protein, transmembrane protein, PRO; EST: cytosolic;

expressed sequence tag; detection: cancer.

Hom sapiens.

WO200053756-A2.

14-SEP-2000.

18-FEB-2000; 2000WO-US04341.

08-MAR-1999; 99WO-US05028.

12-MAR-1999; 99US-0123957.

29-MAR-1999; 99US-0126773.

21-APR-1999; 99US-0130232.

28-APR-1999; 99US-0131445.

14-MAY-1999; 99US-0134287.

23-JUN-1999; 99US-0141037.

26-JUL-1999; 99US-0145698.

29-OCT-1999; 99US-0162506.

30-NOV-1999; 99WO-US28313.

02-DEC-1999; 99WO-US28551.

16-DEC-1999; 99WO-US28565.

30-DEC-1999; 99WO-US30095.

30-DEC-1999; 99WO-US31243.

05-JAN-2000; 2000WO-US30219.

06-JAN-2000; 2000WO-US30277.

06-JAN-2000; 2000WO-US30376.

(GENTH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers J, Eaton DL,

Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME,

Coddard A, Godowski PJ, Grimaldi CC, Gurney AL, Hillan MJ,

Klavan TJ, Kuo SS, Napier MA, Pan J, Paori RF, Roy NA,

Shelton DL, Stewart TA, Tumas D, Williams PM, Wood W.;

WFI: 2000-611443/58.

N-FSDB: AAC78552.

Novel PRO polypeptides and polynucleotides used in detection methods,

to target bioactive molecules to specific cells, and to modulate

cellular activities -

Claim 12; Fig 151; 636p; English.

AAC78458 to AAC78599 represent polynucleotide and EST (expressed

sequence tag) sequences which encode secreted or transmembrane PRO

polypeptides. The PRO polynucleotides and polypeptides have cytostatic

activity. The polynucleotides and polypeptides can be used for detecting

the presence of PRO polypeptides in samples, for linking bioactive

molecules to cells and for modulating biological activities of cells,

using the polypeptides for specific targeting. The polypeptide targeting

can be used to kill the target cells, e.g. for the treatment of cancers.

The polypeptide pairs provide specific targeting of bioactive molecules

to cells. AAC78600 to AAC78987 represent PCR primers and probes used in

the isolation of the PRO polynucleotide sequences.

Sequence 816 AA:

Query Match 100.0%; Score 816; DB 21; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNSNVLLVLTALAIKFTLIDSOAQPVNVNNGKIRGLTLPNELIGPVQYGVYPA 60
DB 1 MNSNVLLVLTALAIKFTLIDSOAQPVNVNNGKIRGLTLPNELIGPVQYGVYPA 60
QY 61 SPPTGRRFCPPPEPSMTGINTTQFAVCPQHLDEEELTCKNPIWETALDITMTYV 120
DB 61 SPPTGRRFCPPPEPSMTGIRKRTTQFAVCPQHLDEEELTCKNPIWETALDITMTYV 120
QY 121 QCNEDCYLNIYVPEEDGANTKQADDTSNDRCEDEDIDQNSKKPPVYVINGSYVE 190
DB 121 QCNEDCYLNIYVPEEDGANTKQADDTSNDRCEDEDIDQNSKKPPVYVINGSYVE 180
QY 181 GTGNMIDGILSLXGVYVITITNYSGLIGFSTGQQAANKVGLDQCALRMKEENYG 240
DB 181 GTGNMIDGILSLXGVYVITITNYSGLIGFSTGQQAANKVGLDQCALRMKEENYG 240
QY 241 AFGGPKRYTIFSGAGACVSLTLSHYSEGFOKATQSGETALSNNVNCFAKXTRI 300
DB 241 AFGGPKRYTIFSGAGACVSLTLSHYSEGFOKATQSGETALSNNVNCFAKXTRI 300
QY 301 LADKVGCMNLDCTDMWECGRNKNYKELIQITTPATYHIAFGFVIGDVIIPDQGLMEQ 360
DB 301 LADKVGCMNLDCTDMWECGRNKNYKELIQITTPATYHIAFGFVIGDVIIPDQGLMEQ 360
QY 361 GEFINDIMLVNCGEGKFEVDGIYNEEGVTPNPDPSVSKFVNLYGPEGKTLRET 420
DB 361 GEFINDIMLVNCGEGKFEVDGIYNEEGVTPNPDPSVSKFVNLYGPEGKTLRET 420
QY 421 IKFMYTMDAKENPETRRKTLVALFTDQWVAPAVACDLHAGYSGFTFYAFYHQCSEY 480
DB 421 IKFMYTMDAKENPETRRKTLVALFTDQWVAPAVACDLHAGYSGFTFYAFYHQCSEY 480
QY 481 KQSMADSAHGDEVYVFGPMIGTELESCNFSKCDWLSAVMTYWTNFAKTGDPNQP 540
DB 481 KQSMADSAHGDEVYVFGPMIGTELESCNFSKCDWLSAVMTYWTNFAKTGDPNQP 540
QY 541 PODEKFIHKRPFEEVAAKSNKPDQVLTGKRRVSDHRAKVAFWELVPHLNL 600
DB 541 PODEKFIHKRPFEEVAAKSNKPDQVLTGKRRVSDHRAKVAFWELVPHLNL 600
QY 601 NEIFQVYSTTKVPPDMTSFVYGRSPAKIMPTKRPATIPANNPKSKDPKHTGED 660
DB 601 NEIFQVYSTTKVPPDMTSFVYGRSPAKIMPTKRPATIPANNPKSKDPKHTGED 660
QY 661 TVLLIETKRDYSELSTVTAAGASLLFNLILAPALYKGRKRHETRRRSPQKNTND 720
DB 661 TVLLIETKRDYSELSTVTAAGASLLFNLILAPALYKGRKRHETRRRSPQKNTND 720
QY 721 IAHIOEEIMSLQKLEIDHECESQADITRLTLPCEYTLTLRRSPDIPMLPNTT 780
DB 721 IAHIOEEIMSLQKLEIDHECESQADITRLTLPCEYTLTLRRSPDIPMLPNTT 780
QY 781 MIPNTLTGMQPLHTEFTFSGGQNSINLPHGSHTRY 816
DB 781 MIPNTLTGMQPLHTEFTFSGGQNSINLPHGSHTRY 816

```

RESULT 3  
 AAB33427  
 ID AAB33427 standard; Protein; 816 AA.

XX AAB33427;

XX 29-JAN-2001 (first entry)

DE Human PRO701 protein UNQ365 SEQ ID NO:67.

XX Human; immune related disease; diagnosis; arthritis; inflammatory; cardiac;

KM dermatological; antirheumatic; antihypertensive; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; neurotropic; neuroprotective;  
 KW antinaemic; hepatotropic; vituridic; antipsoriatic; antiallergic;  
 KW antinaemic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease.  
 XX Homo sapiens.  
 PD W0200053758-A2.  
 PD 14-SEP-2000.  
 XX  
 PF 02-MAR-2000; 2000MO-US05841.  
 XX  
 PR 08-MAR-1999; 99MO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 22-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99MO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99MO-US12252.  
 PR 23-JUN-1999; 99US-0144037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146282.  
 PR 01-SEP-1999; 99MO-US20111.  
 PR 08-SEP-1999; 99MO-US20594.  
 PR 13-SEP-1999; 99MO-US20944.  
 PR 15-SEP-1999; 99MO-US21090.  
 PR 15-SEP-1999; 99MO-US21547.  
 PR 05-OCT-1999; 99MO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99MO-US28214.  
 PR 30-NOV-1999; 99MO-US28413.  
 PR 30-NOV-1999; 99MO-US28439.  
 PR 01-DEC-1999; 99MO-US28301.  
 PR 01-DEC-1999; 99MO-US28634.  
 PR 02-DEC-1999; 99MO-US28551.  
 PR 02-DEC-1999; 99MO-US28564.  
 PR 02-DEC-1999; 99MO-US28565.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30999.  
 PR 30-DEC-1999; 99MO-US31274.  
 PR 05-JAN-2000; 2000MO-US00219.  
 PR 06-JAN-2000; 2000MO-US00277.  
 PR 06-JAN-2000; 2000MO-US00376.  
 PR 11-FEB-2000; 2000MO-US03565.  
 PR 18-FEB-2000; 2000MO-US04341.  
 PR 18-FEB-2000; 2000MO-US04342.  
 PR 22-FEB-2000; 2000MO-US04414.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi A<sup>1</sup>, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W,  
 XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V,  
 XX Stewart TA, Tumas D, Watanabe CX, Wood WI, Yan M;  
 XX WPI; 2000-572271/53.  
 DR N-PSDB; AAC58592.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

20 arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 PS Claim 33; Fig 29; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, glucose-sensitive enteropathy and Whipple's disease.  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX

SO Sequence 816 AA;

Query Match 100.0%; Score 816; DB 21; Length 816;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLNSNVLLMLTALA...KFLILDSQCYPVNNTYK...TGLTPLNELSGVEQLGTPYA 60  
 DB 1 MLNSNVLLMLTALA...KFLILDSQCYPVNNTYK...TGLTPLNELSGVEQLGTPYA 60  
 QY 61 SPTGERRFQPPSPSSWTS...RNTQFAVCPHLPDRSLHDM...LPWFANDTXTTYV 120  
 DB 61 SPTGERRFQPPSPSSWTS...RNTQFAVCPHLPDRSLHDM...LPWFANDTXTTYV 120  
 QY 121 QDCNECCLYNIVYPTEDGAT...TKNADITSDNDEDED...HDONSRRPVVYIHGSGYME 180  
 DB 121 QDCNECCLYNIVYPTEDGAT...TKNADITSDNDEDED...HDONSRRPVVYIHGSGYME 180  
 QY 122 QDCNECCLYNIVYPTEDGAT...TKNADITSDNDEDED...HDONSRRPVVYIHGSGYME 180  
 DB 122 QDCNECCLYNIVYPTEDGAT...TKNADITSDNDEDED...HDONSRRPVVYIHGSGYME 180  
 QY 181 GTGNMIDGSLASGNVIVITN...RGLGFLSGDGAAGNVECLD...OIALEWTEENNG 240  
 DB 181 GTGNMIDGSLASGNVIVITN...RGLGFLSGDGAAGNVECLD...OIALEWTEENNG 240  
 QY 241 AFGGDPKRVTFISGAGAGS...CVSLTLTSHYSEGLFCKA...ISAGTALSSMAVYQPAKTR 300  
 DB 241 AFGGDPKRVTFISGAGAGS...CVSLTLTSHYSEGLFCKA...ISAGTALSSMAVYQPAKTR 300  
 QY 301 LADRVGCKMLDTTMEVCE...LKNKKEJ...CQTTTATYH...AFGPVIDGV...PDPFQIMEQ 360  
 DB 301 LADRVGCKMLDTTMEVCE...LKNKKEJ...CQTTTATYH...AFGPVIDGV...PDPFQIMEQ 360  
 QY 361 GEFNVYD...MVGNGEGIK...EYDGVINDKEDG...TDPDPSSVSPF...CNYGPEGCTLRRT 420  
 DB 361 GEFNVYD...MVGNGEGIK...EYDGVINDKEDG...TDPDPSSVSPF...CNYGPEGCTLRRT 420  
 QY 421 IKFMYTDADKENETRAKTL...VALFTDQWAPAVAAD...LNAQVSPITYFAFYHHCSEY 480  
 DB 421 IKFMYTDADKENETRAKTL...VALFTDQWAPAVAAD...LNAQVSPITYFAFYHHCSEY 480  
 QY 481 KPSWADSNAGDEVYVFGI...PVIAGPTLEFSCNFSKQDVC...LSAVVQTYWTFNAKTDPRQV 540  
 DB 481 KPSWADSNAGDEVYVFGI...PVIAGPTLEFSCNFSKQDVC...LSAVVQTYWTFNAKTDPRQV 540  
 QY 541 PODTKFHTKPRREEVAKS...KYNPKDQYLH...GLKPRVRDVR...TKVAFMLEVPEHNL 600  
 DB 541 PODTKFHTKPRREEVAKS...KYNPKDQYLH...GLKPRVRDVR...TKVAFMLEVPEHNL 600  
 QY 601 NEIFQVSTTKVFPDMTSP...PYGTRSPAKI...MPTTKRPAITPANNKSHSDPKRTGED 660  
 DB 601 NEIFQVSTTKVFPDMTSP...PYGTRSPAKI...MPTTKRPAITPANNKSHSDPKRTGED 660

QY 56: ITVLIETRYDYSTEHSVTIANVASTLFLNK...IAFAALYYKKQKPRHETRRRPSQANTND 720  
 DB 66: ITVLIETRYDYSTEHSVTIANVASTLFLNK...IAFAALYYKKQKPRHETRRRPSQANTND 720  
 QY 72: IAHQNEIRMSQKQLEHDECESLQAHDLRLTLPEDYTLT...RRSPDIP...LTPNTIT 780  
 DB 72: IAHQNEIRMSQKQLEHDECESLQAHDLRLTLPEDYTLT...RRSPDIP...LTPNTIT 780  
 QY 781 MIPNTLTGQAPLHETFPSSGQSNLPHGSTRV 816  
 DB 781 MIPNTLTGQAPLHETFPSSGQSNLPHGSTRV 816  
 RESULT 4  
 ABU61126  
 ID ABU61126 standard; Protein; 816 AA.  
 XX  
 AC ABU61126;  
 XX  
 XX 08-MAY-2003 (first entry)  
 XX  
 DE Human PRO701 polypeptide.  
 XX  
 KM Human; PRO polypeptide; secreted and transmembrane protein;  
 KM immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;  
 KM cardiac insufficiency; nervous system disorder; kidney disorder;  
 KM bone disorder; cartilage disorder; arthritis; tumor; wound healing;  
 KM genetic disorder; cytostatic; antidiabetic; antiinflammatory;  
 KM antiarthritic; anti-tumor; vulnerary; antianaemic; dermatological;  
 KM cardiant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002:69284-A1.  
 XX  
 PD 14-NOV-2002.  
 XX  
 FE 16-OCT-2001; 2001US-0978697.  
 XX  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 20-NOV-1998; 98WO-US24855.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 06-MAR-1999; 99WO-US05028.  
 PR 10-FEB-1999; 99WO-US05190.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 01-DEC-2000; 2000WO-US31678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 22-MAR-2001; 2001WO-US09552.

PR 25-MAY-2001; 2001MO-US17092.  
 PR 01-JUN-2001; 2001MO-US17800.  
 PR 20-JUN-2001; 2001MO-US19692.  
 PR 29-JUN-2001; 2001MO-US21066.  
 PR 09-JUL-2001; 2001MO-US21735.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 03-NOV-1997; 97US-064449P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 21-NOV-1997; 97US-066364P.  
 PR 10-MAR-1998; 98US-077450P.  
 PR 11-MAR-1998; 98US-077643P.  
 PR 11-MAR-1998; 98US-077649P.  
 PR 13-MAR-1998; 98US-078004P.  
 PR 20-MAR-1998; 98US-078886P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 20-MAR-1998; 98US-079535P.  
 PR 20-MAR-1998; 98US-079539P.  
 PR 25-MAR-1998; 98US-079294P.  
 PR 26-MAR-1998; 98US-079656P.  
 PR 27-MAR-1998; 98US-079663P.  
 PR 27-MAR-1998; 98US-079664P.  
 PR 27-MAR-1998; 98US-079689P.  
 PR 27-MAR-1998; 98US-079728P.  
 PR 27-MAR-1998; 98US-079786P.  
 PR 30-MAR-1998; 98US-079920P.  
 PR 30-MAR-1998; 98US-079923P.  
 PR 26-MAY-1981; 81US-026721P.  
 PR 17-MAR-1998; 98US-0340220.  
 PR 26-JUN-1998; 98US-0105413.  
 PR 07-OCT-1998; 98US-0166978.  
 PR 02-NOV-1998; 98US-0184216.  
 PR 06-NOV-1998; 98US-0187368.  
 PR 07-DEC-1998; 98US-0202054.  
 PR 22-DEC-1998; 98US-0218517.  
 PR 05-MAR-1999; 99US-0254465.  
 PR 10-MAR-1999; 99US-0265686.  
 PR 12-APR-1999; 99US-0284291.  
 PR 14-MAY-1999; 99US-0311832.  
 PR 14-MAY-1999; 99US-0380137.  
 PR 25-AUG-1999; 99US-0380138.  
 PR 25-AUG-1999; 99US-0380142.  
 PR 08-NOV-2000; 2000US-C709238.  
 PR 27-NOV-2000; 2000US-C727249.  
 PR 20-DEC-2000; 2000US-C747253.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 22-MAR-2001; 2001US-0816920.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 03-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 30-JUL-2001; 2001US-0918585.  
 PR (GENE) GENENTECH INC.  
 XX  
 XX Askenazi A, Baker KP, Botstein J, Desnoyers I, Eaton D;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gelber H, Gerltsen YE;  
 PI Godard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Kljavin LJ, Kuo SS, Napier MA, Pan Z, Pooni NF, Roy MA;  
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;  
 XX  
 DR WPI: 2003-286163/28.  
 DR N-PSDB: ABX92581.  
 XX  
 XX Novel secreted and transmembrane polypeptides and polynucleotides  
 PT encoding them useful for treating cancer, kidney diseases, bone,  
 XX cartilage disorders and immune deficiencies  
 XX  
 XX Claim 12; Fig 151; 459pp; English.

CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists. The  
 CC bioactive molecule maybe a toxin, radiolabel or antibody, and causes  
 CC apoptosis or death of the cell. The PRO polypeptides are useful for  
 CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,  
 CC cardiac insufficiency, nervous system disorders, kidney disorders,  
 CC bone and cartilage disorders or arthritis, tumours, and wound healing.  
 CC The polynucleotide sequences encoding PRO polypeptides are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation  
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
 CC generating transgenic animals or knockout animals, for the genetic  
 CC analysis of individuals with genetic disorders, and in gene therapy.  
 CC AB061071-AB061164 represent the human PRO polypeptides of the  
 CC invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdtdentry.html.  
 XX  
 SQ Sequence 816 AA:  
 Query Match 100.0%; Score 816; DB 24; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNSNVLLMTALA-KFTLIDSOAQYPPVNTGVKIRGRTPLMEILGPVQYIGVPPA 60  
 DB 1 MNSNVLLMTALA-KFTLIDSOAQYPPVNTGVKIRGRTPLMEILGPVQYIGVPPA 60  
 QY 61 SPTGERRFPQPEPSSWGTINTQFAVCCQCHDERSLTMDM-PIMTAN-DE-XTYV 120  
 DB 61 SPTGERRFPQPEPSSWGTINTQFAVCCQCHDERSLTMDM-PIMTAN-DE-XTYV 120  
 QY 121 QQNEDELYLNTVPTEDGANTKKADDTITSEKSEDEDIDQNSKKPVMVYIHGGSYME 180  
 DB 121 QQNEDELYLNTVPTEDGANTKKADDTITSEKSEDEDIDQNSKKPVMVYIHGGSYME 180  
 QY 121 QQNEDELYLNTVPTEDGANTKKADDTITSEKSEDEDIDQNSKKPVMVYIHGGSYME 180  
 DB 121 QQNEDELYLNTVPTEDGANTKKADDTITSEKSEDEDIDQNSKKPVMVYIHGGSYME 180  
 QY 181 GTCNMIDGSIISYGVVYITINRYGLTGFSTDDQAKKVCYLLDQOALRM-EEVNG 240  
 DB 181 GTCNMIDGSIISYGVVYITINRYGLTGFSTDDQAKKVCYLLDQOALRM-EEVNG 240  
 QY 181 GTCNMIDGSIISYGVVYITINRYGLTGFSTDDQAKKVCYLLDQOALRM-EEVNG 240  
 DB 181 GTCNMIDGSIISYGVVYITINRYGLTGFSTDDQAKKVCYLLDQOALRM-EEVNG 240  
 QY 241 AFGGDPKRYTIFGSGAGASCVSULTLSHSEGLFQKALIQSSTA-SMAVNYQPAKYTRI 300  
 DB 241 AFGGDPKRYTIFGSGAGASCVSULTLSHSEGLFQKALIQSSTA-SMAVNYQPAKYTRI 300  
 QY 301 LADKVGCMMLDITDMWECLRNKRYKELLQOITTPATYHIAFSPV-IDGVIPDDPOLMEQ 360  
 DB 301 LADKVGCMMLDITDMWECLRNKRYKELLQOITTPATYHIAFSPV-IDGVIPDDPOLMEQ 360  
 QY 361 GEFLLNYDIMEGVNOGEGLFKFDGVIDNEDEGVTPNPFDFSVFNVLXYGPRGXOTLRET 420  
 DB 361 GEFLLNYDIMEGVNOGEGLFKFDGVIDNEDEGVTPNPFDFSVFNVLXYGPRGXOTLRET 420  
 QY 421 IKFMVTDMAKKNPETRRKTYALFTDHWAPAAVADILAQYSPTYFAFHRQSEY 480  
 DB 421 IKFMVTDMAKKNPETRRKTYALFTDHWAPAAVADILAQYSPTYFAFHRQSEY 480  
 QY 481 KPSWASAGDEVPYFGIPMGPELFCFNSCKDDVM-SAVVMYWKCFATGSPNCPV 540  
 DB 481 KPSWASAGDEVPYFGIPMGPELFCFNSCKDDVM-SAVVMYWKCFATGSPNCPV 540  
 QY 541 PDDTKFHTKPNRFEVWASKYNPQDYLH-GLKPRVVDHYRATKVAFLMLVPHLNL 600  
 DB 541 PDDTKFHTKPNRFEVWASKYNPQDYLH-GLKPRVVDHYRATKVAFLMLVPHLNL 600  
 QY 601 NEIFQVSTTKVPPDMSPFYGRNRSAKTIWPTTKPAIIPANNPKSKCPHTKGPED 660  
 DB 601 NEIFQVSTTKVPPDMSPFYGRNRSAKTIWPTTKPAIIPANNPKSKCPHTKGPED 660

QY 661 TTVLIERKREYSTELESTAVASLLFLNLAFALVYKKDKRKHETRRSPQNTND 720  
DB 662 TTVLIERKREYSTELESTAVASLLFLNLAFALVYKKDKRKHETRRSPQNTND 720  
QY 721 IAHQNEIMSLQKQEHQHECESLQAHPTLRCTCPDQTLTLRRSPDCPLKNTTTC 780  
DB 721 IAHQNEIMSLQKQEHQHECESLQAHPTLRCTCPDQTLTLRRSPDCPLKNTTTC 780  
QY 781 MIPNTLTGQPLHTFNTFFSGQNSTNLPHGSTRPV 816  
DB 781 MIPNTLTGQPLHTFNTFFSGQNSTNLPHGSTRPV 816

## RESULT 5

AB882852  
ID AB882852 standard; Protein: 817 AA.

AC AB882852;

XX 31-MAR-2003 (first entry)

DE C852 related polypeptide (Genbank identifier number GI# 6330941).

XX C852; p53; cytostatic; gene therapy; human; angiogenic; cancer;

KM carboxylesterase.

XX Homo sapiens.

PN M02029041-A2.

XX 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US17314.

XX 05-JUN-2001; 2001US-2960762.

XX 10-OCT-2001; 2001US-328605P.

XX 15-FEB-2002; 2002US-357253P.

XX (EXEL-) EXELIXIS INC.

XX Friedman L, Plozman GD, Bevilin M, Francis-Lang H;

XX WPI; 2003-156848/15.

XX identifying a candidate p53 pathway-modulating agent as therapeutic  
PT targets for disorders associated with defective p53 function e.g.  
PT cancer by contacting an assay system with a test agent where the system  
PT provides reference activity.

XX Claim 13; Page 55-58; 60pp; English.

XX The invention relates to identifying a candidate p53 pathway modulating  
CC agent. The method involves contacting an assay system comprising purified  
CC C852 polypeptide or nucleic acid, or their functionally active fragment  
CC or derivative, with a test agent under conditions where, but for the  
CC presence of the test agent, the system provides a reference activity.  
CC The methods are useful for identifying modulators of the p53 pathway as  
CC therapeutic targets for disorders associated with defective p53 function,  
CC such as angiogenic, apoptotic or cell proliferative disorders, e.g.  
CC cancer. The modulators are useful as research reagents, diagnostics and  
CC therapeutics. Sequences AB882851-53 represent C852 (carboxylesterase);  
CC related polypeptide sequences.

XX Sequence 817 AA;

Query Match 658; Score 538; DB 24; Length 817;  
Best Local Similarity 59.8%; Pred. No. 0;  
Matches 658; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 159 DHHQNSKKPYVYTHGGSTWEGTGMIDGSLASGNYVYTNVNLGLIGLSTGDA 218  
DB 159 DHHQNSKKPYVYTHGGSTWEGTGMIDGSLASGNYVYTNVNLGLIGLSTGDA 218

QY 219 AKGNVGLDQCALPRLTEENNGARGGDPKRTTIGSGAGACVSLTLSSHSEGLPQAI 278  
DB 219 AKGNVGLDQCALPRLTEENNGARGGDPKRTTIGSGAGACVSLTLSSHSEGLPQAI 278  
QY 279 TOSGTLSSKAVNYPAPAYRTILADKGCNNLCTTMCWECILRNKXVYELLQCTTAPAYH 338  
DB 279 TOSGTLSSKAVNYPAPAYRTILADKGCNNLCTTMCWECILRNKXVYELLQCTTAPAYH 338  
QY 339 IAFGEVIGDVIYPPDQQLMEQGEFFLNDIMLVNQGEGKLFVGVGIVDNEGVTPNDFE 398  
DB 339 IAFGEVIGDVIYPPDQQLMEQGEFFLNDIMLVNQGEGKLFVGVGIVDNEGVTPNDFE 398  
QY 399 SVSNFVNDLXGYPESKDTLRRTIKFMYTDADKSNPETRRKTLVALFDHQVAPAVATA 457  
DB 399 SVSNFVNDLXGYPESKDTLRRTIKFMYTDADKSNPETRRKTLVALFDHQVAPAVATA 457  
QY 458 DLHAQYGSPTFYAFYHHCQSEKPSMADSAHGDVYVFGIPMGFTELSGNSKQDV 517  
DB 458 DLHAQYGSPTFYAFYHHCQSEKPSMADSAHGDVYVFGIPMGFTELSGNSKQDV 517  
QY 459 DLHAQYGSPTFYAFYHHCQSEKPSMADSAHGDVYVFGIPMGFTELSGNSKQDV 518  
DB 459 DLHAQYGSPTFYAFYHHCQSEKPSMADSAHGDVYVFGIPMGFTELSGNSKQDV 518  
QY 519 MLSAVVMTYMTNFAKTGDPNPQVDPDTKFIHTKRNRPBEVAMSKYNPKDQLYJHGLXPR 577  
DB 519 MLSAVVMTYMTNFAKTGDPNPQVDPDTKFIHTKRNRPBEVAMSKYNPKDQLYJHGLXPR 577  
QY 578 VADHYRATKVAFWLELVHLNLNLNLEIPQYVSTTTKVPPDMTSPFYGYRSGPAKIWPPTK 637  
DB 578 VADHYRATKVAFWLELVHLNLNLNLEIPQYVSTTTKVPPDMTSPFYGYRSGPAKIWPPTK 637  
QY 638 RPAITPANNPKSKDPKHTGPEDTVLLETREDYSTELESTAVASLLFLNLIAFALY 697  
DB 638 RPAITPANNPKSKDPKHTGPEDTVLLETREDYSTELESTAVASLLFLNLIAFALY 697  
QY 698 YKDKRRHETRRSPQNTNDIAHIGNEIMSLQKQEHQHECESLQAHPTLRCTCP 757  
DB 698 YKDKRRHETRRSPQNTNDIAHIGNEIMSLQKQEHQHECESLQAHPTLRCTCP 757  
QY 758 PDYTLTLRRSPDDIPLMTPNTITMLPNTLTGQPLHTFNTFFSGQNSTNLPHGSTRPV 816  
DB 758 PDYTLTLRRSPDDIPLMTPNTITMLPNTLTGQPLHTFNTFFSGQNSTNLPHGSTRPV 816

## RESULT 6

AAE94127

ID AAB94127 standard; Protein: 509 AA.

XX AAB94127;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:14381.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-01:6126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99CP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-0183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Oca T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto O;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -

XX Claim 8; SEQ ID 14381; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide which comprises a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full length  
 CC cDNAs easily without any specialised methods. AAH3156 to AAH3528 and  
 CC AAH3633 to AAH3742 represent human cDNA sequences; AAH92446 to  
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.

XX Sequence 509 AA;

Query Match 47.5%; Score 388; DB 22; Length 509;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 508; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 309 MLDTTDMVECLRNKKYKELIQCTTPATYHIAFGVITDGVIPDDPOLMEGGEFLNYDI 368  
 DB 1 MLDTTDMVECLRNKKYKELIQCTTPATYHIAFGVITDGVIPDDPOLMEGGEFLNYDI 60  
 QY MGVNCGEGAKFVDGIVNEDGVTPNDFPSVSNFVNDLYGPEGKDLRETIKMYTDM 428  
 DB 61 MGVNCGEGAKFVDGIVNEDGVTPNDFPSVSNFVNDLYGPEGKDLRETIKMYTDM 120  
 QY 429 ADKENPETERKTLVALFTDQWVAPAVA-ADLHAQYGSPTFYAFYHHQOSEMKPSWADS 487  
 DB 121 ADKENPETERKTLVALFTDQWVAPAVATLHAQYGSPTFYAFYHHQOSEMKPSWADS 180  
 QY 488 AHGDEVVYVFGIPIGPTFLFSCNSKQDVMLSAVMTYWTNFAKTGDPNPVQDTRFI 547  
 DB 181 AHGDEVVYVFGIPIGPTFLFSCNSKQDVMLSAVMTYWTNFAKTGDPNPVQDTRFI 240  
 QY 546 HTKPRFEVAMSKNPXKQDLYLH-GLKPRVDEVRATKVAFWMLZVHLNINLEFOYV 607  
 DB 241 HTKPRFEVAMSKNPXKQDLYLH-GLKPRVDEVRATKVAFWMLZVHLNINLEFOYV 300  
 QY 608 STTKVPPPDXTSPFYGRRSAPAKIMPTTKRPAITPANNPCHSDPHKTSGETTVLLET 667  
 DB 301 STTKVPPPDXTSPFYGRRSAPAKIMPTTKRPAITPANNPCHSDPHKTSGETTVLLET 360  
 QY 668 KRDYSTEILSVTAAGASLFLNIALAFALYKPKDRBETHRRSPQNTNDLAHONE 727  
 DB 361 KRDYSTEILSVTAAGASLFLNIALAFALYKPKDRBETHRRSPQNTNDLAHONE 420  
 QY 728 EIMSQQMKOLEHHECESICADTALITCPDPTVTLERSSDDIPLMTPTNTITPTVLT 787  
 DB 421 EIMSQQMKOLEHHECESICADTALITCPDPTVTLERSSDDIPLMTPTNTITPTVLT 480  
 QY 788 GNOPLATNTESGGGNSINLPHGSHITV 816  
 DB 481 GNOPLATNTESGGGNSINLPHGSHITV 509

RESULT 7  
 ID ABB82853  
 AC ABB82853 standard; Protein; 509 AA.

XX ABB82853;  
 CC 31-MAR-2003 (first entry)  
 CC CES2 related polypeptide (GenBank identifier number GI# 18595051).

XX CES2, p53; cytosolic; gene therapy; human; angiogenic; cancer;  
 XX carboxylesterase.

XX Homo sapiens.

XX MO203295041-A2.

XX 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US17314.

XX 05-JUN-2001; 2001US-296576P.

XX 10-OCT-2001; 2001US-129605P.

XX 15-FEB-2002; 2002US-157253P.

XX (EXCEL-) EXELIXIS INC.

XX Friedman L, Plowman GD, Belvin M, Francis-Lang H;

XX WPI; 2003-156848/15.

XX identifying a candidate p53 pathway-modulating agent as therapeutic  
 PT targets for disorders associated with defective p53 function e.g.  
 PT cancer by contacting an assay system with a test agent where the system  
 PT provides reference activity -

XX Claim 13; Page 58-60; 60pp; English.

XX The invention relates to identifying a candidate p53 pathway modulating  
 CC agent. The method involves contacting an assay system comprising purified  
 CC CES2 polypeptide or nucleic acid, or their functionally active fragment  
 CC or derivative, with a test agent under conditions where, but for the  
 CC presence of the test agent, the system provides a reference activity.  
 CC The methods are useful for identifying modulators of the p53 pathway as  
 CC therapeutic targets for disorders associated with defective p53 function,  
 CC such as angiogenic, apoptotic or cell proliferative disorders, e.g.  
 CC cancer. The modulators are useful as research reagents, diagnostics and  
 CC therapeutics. Sequences ABB82851-53 represent CES2 (carboxylesterase)  
 CC related polypeptide sequences.

XX Sequence 509 AA;

Query Match 47.5%; Score 388; DB 24; Length 509;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 508; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 309 MLDTTDMVECLRNKKYKELIQCTTPATYHIAFGVITDGVIPDDPOLMEGGEFLNYDI 368  
 DB 1 MLDTTDMVECLRNKKYKELIQCTTPATYHIAFGVITDGVIPDDPOLMEGGEFLNYDI 60  
 QY 369 MGVNCGEGAKFVDGIVNEDGVTPNDFPSVSNFVNDLYGPEGKDLRETIKMYTDM 428  
 DB 61 MGVNCGEGAKFVDGIVNEDGVTPNDFPSVSNFVNDLYGPEGKDLRETIKMYTDM 120  
 QY 429 ADKENPETERKTLVALFTDQWVAPAVA-ADLHAQYGSPTFYAFYHHQOSEMKPSWADS 487  
 DB 121 ADKENPETERKTLVALFTDQWVAPAVATADLHAQYGSPTFYAFYHHQOSEMKPSWADS 180  
 QY 488 AHGDEVVYVFGIPIGPTFLFSCNSKQDVMLSAVMTYWTNFAKTGDPNPVQDTRFI 547  
 DB 181 AHGDEVVYVFGIPIGPTFLFSCNSKQDVMLSAVMTYWTNFAKTGDPNPVQDTRFI 240

QY 548 HTXNRFEEVAMSKYNPKQQLYHLGKXERYCHRYATKVAFWELVPHLHNLNLEIFQV 607  
 DB 241 HCKENREEVAMSKYNPKQQLYHLGKPRVRDHYATKVAFWELVPHLHNLNLEIFQV 300  
 QY 608 STTKKVPDMTSPFYGRSPFAKIWPTEKSPATTPANPNSKDPKXGPEDTYET 667  
 DB 301 STTKKVPDMTSPFYGRSPFAKIWPTEKSPATTPANPNSKDPKXGPEDTYET 360  
 QY 668 KRDTSTELSVTAVGASLLPLNIYAFALVYKCKRRHETHRSPQNTNDAHIONE 727  
 DB 361 KRDTSTELSVTAVGASLLPLNIYAFALVYKCKRRHETHRSPQNTNDAHIONE 420  
 QY 728 EIKSLQMKOLEHREHCECJQHADTLRLTCPPDYTLTBRSPDLPVLTPTNTTINLT 787  
 DB 421 EIKSLQMKOLEHREHCECJQHADTLRLTCPPDYTLTBRSPDLPVLTPTNTTINLT 480  
 QY 788 GMOPHTENTFGSGONSTNLPHGSTRV 816  
 DB 481 GMOPHTENTFGSGONSTNLPHGSTRV 509

RESULT 8  
 AAM48908  
 ID AAM48908 standard; Protein: 916 AA.  
 AC AAM48908;  
 XX  
 CT 05-APR-2002 (first entry)  
 DE Human neurotrophin family member 46980 protein.  
 KW Human neurotrophin family; 46980; analgesic; neuroprotective; cytoskeletal;  
 KW pain disorder; complex regional pain syndrome; causalgia; neuralgia;  
 KW central pain; dysesthesia syndrome; carotidynia; neuronal disorder;  
 KW cancer; gene therapy.  
 OS Homo sapiens.  
 FN WO2001:94563-A2.  
 PD 13-DEC-2001.  
 XX  
 PE 06-JUN-2001; 2001WO-US-9335.  
 XX  
 PR 06-JUN-2000; 2000US-209949P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Curtis RAD;  
 XX  
 DR W21: 2002-147671/19.  
 DR N-PSDB: ABA97533.  
 PT New 46980 polypeptides and polynucleotides encoding them, useful for as  
 PT diagnostic targets and therapeutic agents for controlling pain, pain  
 PT disorders (e.g. complex regional pain syndrome, causalgia), neuronal  
 PT disorders or cancer.  
 XX  
 ES Claim 3; Page 139; 12pp; English.  
 CC The present invention provides the protein and coding sequences of a  
 CC novel member of the human neurotrophin family, designated 46980. The  
 CC sequences can be used in the control of pain, to treat pain disorders  
 CC such as complex regional pain syndrome, causalgia, neuralgia, central  
 CC pain and dysesthesia syndrome and carotidynia, neuronal disorders, and  
 CC cancer. The present sequence is the protein of the invention.

Sequence 916 AA:  
 Query Match 40.0%; Score 326; DB 23; Length 916;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 546; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 163 QNSKRPVWYTHGSSYMECTGMIDGSLVAGNIVTNYRLDCTGFLSTGDAKGN 222  
 DB 162 QNSKRPVWYTHGSSYMECTGMIDGSLVAGNIVTNYRLDCTGFLSTGDAKGN 221  
 QY 223 YGLDLCIQALRWTEENNVAFGGQPKRYVTFSGAASGVSLTISHYEGGFQKAI 105G 282  
 DB 222 YGLDLCIQALRWTEENNVAFGGQPKRYVTFSGAASGVSLTISHYEGGFQKAI 105G 281  
 QY 283 TALSSANVYQPAKXTRILADKVGCMVLDITVYECLEANKVKELIQCTTPATYHAFG 342  
 DB 282 TALSSANVYQPAKXTRILADKVGCMVLDITVYECLEANKVKELIQCTTPATYHAFG 341  
 QY 343 PVLDGQVPEDDPQILMEQGEFLNVDIMGVNGBGLKRVNVDGVNEDGVTPNDFSVSN 402  
 DB 342 PVLDGQVPEDDPQILMEQGEFLNVDIMGVNGBGLKRVNVDGVNEDGVTPNDFSVSN 401  
 QY 403 FVDNLYGYPEGKDTRETIKEMVYTMARKENPETERKTLVALFTDHWVAPVAADLHA 461  
 DB 402 FVDNLYGYPEGKDTRETIKEMVYTMARKENPETERKTLVALFTDHWVAPVAADLHA 461  
 QY 462 QYGSPTFYFAFYHHQSEKPSMADSAH3DEVYVFGIPLISPTLEFSCNFSKNDVLSA 521  
 DB 462 QYGSPTFYFAFYHHQSEKPSMADSAH3DEVYVFGIPLISPTLEFSCNFSKNDVLSA 521  
 QY 522 VMTYVYTNPAKTGDRQVPQDTKTLHFKPNRFEVAMSKYNPKQQLYHLGKPRVRD 581  
 DB 522 VMTYVYTNPAKTGDRQVPQDTKTLHFKPNRFEVAMSKYNPKQQLYHLGKPRVRD 581  
 QY 582 YRATKVAFWLELVPHLHNLNLEIFQVSTTKVPPDMTSPFYGRSPFAKIWPTEKSPA 641  
 DB 582 YRATKVAFWLELVPHLHNLNLEIFQVSTTKVPPDMTSPFYGRSPFAKIWPTEKSPA 641  
 QY 642 TPANPKSKDPRHKTGPEDTLYLIEKRDYSTLSVTIAVGSLLFLNLIAFAAYKKD 701  
 DB 642 TPANPKSKDPRHKTGPEDTLYLIEKRDYSTLSVTIAVGSLLFLNLIAFAAYKKD 701  
 QY 702 KRRHETHR 709  
 DB 702 KRRHETHR 709

RESULT 9  
 AAC87273  
 ID AAC87273 standard; Protein: 396 AA.  
 AC AAC87273;  
 XX  
 CT 05-JUN-2002 (first entry)  
 DE Novel central nervous system protein #183.  
 KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
 KW hyperproliferative disorder; neoplasia; cardiovascular disorder;  
 KW cardiac arrest; cerebrovascular disorder; schizophrenia; angiodystrophy;  
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
 KW adenocarcinoma; reproductive system disorder; cancer; leukemia; neovascularization;  
 KW endocrine disorder; diabetes; cancer; leukemia; neovascularization;  
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
 KW myocardial infarction; wound healing; cell proliferation; skin aging;  
 KW food additive; food preservative; gene therapy.  
 OS Homo sapiens.  
 FN WO2001:55318-A2.  
 PD 02-AUG-2001.  
 XX  
 PE 17-JAN-2001; 2001WO-US01332.  
 XX  
 PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.





XX The invention describes an isolated nucleic acid molecule (i) encoding a  
CC novel central nervous system protein. (ii) and polypeptides (iii) encoded  
CC by (i), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angioneurotic nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastroenteritis disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardia,  
CC infection. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 25.5%; Score 208; DB 22; Length 396;  
Best Local Similarity 100.0%; Pred. No. 6,1e-209;  
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 DHDNSKRPVWYTHGGSYMEGTGNTDGSILASVGNVVTINRFGIGLSTGSDA 218  
DB 128 DHDNSKRPVWYTHGGSYMEGTGNTDGSILASVGNVVTINRFGIGLSTGSDA 187  
QY 219 AKGNVGLDIOIALRWIENVGAFGSDPKRVTIFGSGAGSCVSLTSHVSEGLPOKA 278  
DB 188 AKGNVGLDIOIALRWIENVGAFGSDPKRVTIFGSGAGSCVSLTSHVSEGLPOKA 247  
QY 279 IGGTALSSWAWVQPAKYTRILADKVGCMEDTTNMFELRNKRYELIQCTTPATYH 338  
DB 248 IGGTALSSWAWVQPAKYTRILADKVGCMEDTTNMFELRNKRYELIQCTTPATYH 307  
QY 339 IAFSPVIDGVIPDDPOLMEGGFENY 366  
DB 308 IAFSPVIDGVIPDDPOLMEGGFENY 335

RESULT 1C  
ABBI7862  
ID ABBI7862 standard; Protein; 165 AA.

AC ABBI7862;  
CT 23-JAN-2002 (first entry);

DE Human nervous system related polypeptide SEQ ID NO 6519.

Human; nociceptive; neuroprotective; cytoskeletal; dermatological; viroinhibitor;  
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulvovaginal;  
antiparkinsonian; antispasmodic; antihypertensive; antidiabetic; cancer;  
antipneumonia; hepatoprotective; cerebroprotective; antiinflammatory;  
antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
neurological disease; infection; nephrotoxic; gene therapy; vaccine.

OS Homo sapiens.

XX WO200159063-A2.

XX 16-AUG-2001.

XX 17-JAN-2001; 2001WO-US01334.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226272.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226686.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 06-SEP-2000; 2000US-0231242.  
PR 09-SEP-2000; 2000US-0231243.  
PR 09-SEP-2000; 2000US-0231244.  
PR 09-SEP-2000; 2000US-0231413.  
PR 09-SEP-2000; 2000US-0231414.  
PR 09-SEP-2000; 2000US-0232063.  
PR 09-SEP-2000; 2000US-0232064.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0233397.  
PR 14-SEP-2000; 2000US-0233398.  
PR 14-SEP-2000; 2000US-0233399.  
PR 14-SEP-2000; 2000US-0233400.  
PR 14-SEP-2000; 2000US-0233401.  
PR 14-SEP-2000; 2000US-0233402.  
PR 14-SEP-2000; 2000US-0233403.  
PR 14-SEP-2000; 2000US-0233404.  
PR 14-SEP-2000; 2000US-0233405.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.



XX The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been  
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
CC molecules have been determined. Primers for synthesizing the full length  
CC cDNA are useful for clarifying the function of the protein encoded by  
CC the cDNA. The full length clones were obtained by construction of full  
CC length enriched cDNA libraries that were synthesized by the oligo-capping  
CC method. The primers enable the production of the full length cDNA easily  
CC without any special methods. The present sequence is a polypeptide  
CC encoded by a full length human cDNA of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in CD-ROM format directly from EPO.  
XX  
SQ Sequence 509 AA;  
XX  
Query Match 5.1%; Score 50; DB 22; Length 509;  
Best Local Similarity 100.0%; Pred. No. 4,3e-43;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 510 CNFSKNDVMSAVVMTWTNTNPAKTGDPNQVPQDTKFIHTKPNFESEV 559  
DB 212 CNFSKNDVMSAVVMTWTNTNPAKTGDPNQVPQDTKFIHTKPNFESEV 261  
RESULT 12  
ABG10266  
ID ABG10266 standard; Protein; 271 AA.  
XX  
AC ABG10266;  
XX  
CT 13-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #10257.  
XX  
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder;  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2301WO-US8631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HSE-) HSEFQ INC.  
XX  
PE Drmanac RT, Liu C, Tang Y;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS74453.  
XX  
PT New isolated polynucleotide and encoded polypeptides useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
NS Claim 20; SEQ ID No 40625; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG010-ABG0377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 271 AA;  
XX  
Query Match 5.9%; Score 48; DB 22; Length 271;  
Best Local Similarity 100.0%; Pred. No. 3e-41;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 510 CNFSKNDVMSAVVMTWTNTNPAKTGDPNQVPQDTKFIHTKPNFESEV 557  
DB 184 CNFSKNDVMSAVVMTWTNTNPAKTGDPNQVPQDTKFIHTKPNFESEV 231  
RESULT 13  
AAB40734  
ID AAB40734 standard; Protein; 308 AA.  
XX  
AC AAB40734;  
XX  
CT 08-FEB-2001 (first entry)  
XX  
DE Human ORF498 polypeptide sequence SEQ ID NO:996.  
XX  
KM Human; open reading frame; ORF; detection; cytosolic; hepatotropic;  
KM vulnereity; antiparasitic; antiparkinsonian; neurotropic; neuroprotective;  
KM anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiac;  
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidabetic;  
KM hypotensive; dermatologic; immunosuppressive; antiinflammatory;  
KM antiviral; antibacterial; antifungal; antineumatic; antihydro;  
KM antihaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KM cholesterol ester storage; systemic lupus erythematosus; infection;  
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KM thrombosis; contraceptive.  
XX  
OS Homo sapiens.  
XX  
PN WO200056473-A2.  
XX  
PD 05-OCT-2000.  
XX  
PF 31-MAR-2000; 2000WO-US8621.  
XX  
PR 31-MAR-1999; 99US-0127607.  
PR 02-APR-1999; 99US-0127636.  
PR 05-APR-1999; 99US-0127728.  
PR 30-MAR-2000; 2000US-0540763.  
XX  
PA (CJRA-) CUNAGEN CORP.  
XX  
PE Shinketsu RA, Teach M;  
XX  
DR WPI; 2000-602362/57.  
DR N-PSDB; AAC74943.  
XX  
PT Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease -  
XX  
NS Claim 11; Page 970-971; 5507pp; English.

XX AAC74446 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORF open reading frames 1 to 316. The ORF  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;  
 CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;  
 CC osteoprotic; anticonvulsant; antiallergic; immunosuppressant;  
 CC immunostimulant; cadant; thrombolytic; coagulant; vasodilator;  
 CC antidiabetic; hypotensive; dermatologic; immunosuppressive;  
 CC antiinflammatory; antibacterial; antiviral; antifungal; antithyroid;  
 CC antihypertensive; antianemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORF-associated disorder. The  
 CC nucleic acids can be used to express ORF proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, ap-astic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

CC Sequence 309 AA;

Query Match 5.9%; Score 48; DB 21; Length 308;  
 Best Local Similarity 100.0%; Pred. No. 3,4e-4;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 510 CNFSKNVWLSAVWMTWTFNFAKTGDPNPVQCTKFTKPNREEV 557  
 Db 587 CNFSKNVWLSAVWMTWTFNFAKTGDPNPVQCTKFTKPNREEV 214

RESULT 14

AAB07524

XX ID ABB07524 standard; Protein: 801 AA.

XX AC ABB07524;

XX DT 23-APR-2002 (first entry)

XX DE Human drug metabolizing enzyme (DME) (ID: 7473875C01).

XX XX Drug metabolizing enzyme; DME; antiallergic; antineurotic; antiasthmatic;  
 KW osteopathic; antirheumatic; antiallergic; dermatologic; nephrotoxic;  
 KW antiinflammatory; vulnerary; antibacterial; virucide; antiparasitic;  
 KW procoagulant; fungicide; antihelminthic; cytostatic; ophthalmological;  
 KW antiatherosclerotic; hepatotropic; antidiabetic; anorectic; human;  
 KW thrombolytic; metabolic; anticoagulant; antihypertensive; gynecological;  
 KW antianimal; antileptic; antididiabetic; laxative; enzyme.

XX OS Homo sapiens.

XX PN MO280204612-A2.

XX PD 17-JAN-2002.

XX PF 05-JUL-2001; 2001MO-US21324.

XX PR 07-JUL-2003; 2000US-216804P.

XX PR 14-JUL-2003; 2000US-218948P.

XX PR 21-JUL-2000; 2000US-220037P.

XX PR 28-JUL-2003; 2000US-221837P.

XX PA (INCYTE) INCYTE GENOMICS INC.

XX PI Baughn MR, Bruns CM, Das D, Ding L, Elliott VS, Gandhi AR;

PI Hafalia AKA, Keatney L, Khan FA, Lal P, Lee EA, Lu DM, Lu Y;

PI Nguyen DE, Patterson C, Ramkumar C, Rang HZ, Santhakala MS;

PI Yang YJ, Thangavelu K, Thornton M, Trisoley CM, Walla NK, Xu Y;

PI Yang J, Yao MG, Yue H;

DR MPI; 2002-164641/21.

DR N-PSDB; ABA94727.

XX Novel drug metabolizing enzymes and polynucleotides encoding the

PT enzymes, useful for treating, diagnosing or preventing

PT autoimmune/inflammatory, cell proliferative, developmental and

PT endocrine disorders

XX Claim 1; Page 148-149; 167pp; English.

XX The invention provides human drug metabolizing enzyme (DME) polypeptides

CC and polynucleotides. DMEs can be expressed by standard recombinant

CC methods. The DME polypeptides, polynucleotides, modulators and

CC antibodies are useful from diagnosing, treating and preventing autoimmune

CC inflammatory (e.g. allergies, anemia, asthma, osteoporosis, rheumatoid

CC arthritis, atopic dermatitis, glomerulonephritis and irritable bowel

CC syndrome, trauma and bacterial, viral, parasitic, protozoal, fungal or

CC hematologic infections), cell proliferative (e.g. cancer, atherosclerosis,

CC and hepatitis), developmental (e.g. cerebral palsy and cataract),

CC endocrine (e.g. diabetes, goiter, hyperplasia, amenorrhea and

CC gynecostasia), eye (e.g. iritis and glaucoma, metabolic (e.g. Addison's

CC disease, diabetes and obesity), and gastrointestinal disorders (e.g.

CC anorexia, nausea, abdominal angina, ulcerative colitis, diarrhea and

CC constipation). The DME polypeptides are useful in drug screening

CC techniques and to analyze the proteome of a tissue or cell type. The DME

CC polynucleotides are useful for creating knock-in humanized animals or

CC transgenic animals to model human diseases, and in somatic or germline

CC gene therapy. The present sequence represents a human DME polypeptide

CC sequence.

XX Sequence 801 AA;

Query Match 5.9%; Score 48; DB 23; Length 801;

Best Local Similarity 100.0%; Pred. No. 8.1e-41;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 510 CNFSKNVWLSAVWMTWTFNFAKTGDPNPVQCTKFTKPNREEV 557  
 Db 521 CNFSKNVWLSAVWMTWTFNFAKTGDPNPVQCTKFTKPNREEV 568

RESULT 15  
 ID AAE25020 standard; Protein: 835 AA.  
 AC AAE25020;  
 DT 30-OCT-2002 (first entry)

XX Human drug metabolizing enzyme (DME-5).

XX Human; drug metabolizing enzyme; autoimmune; inflammatory disorder;  
 KW acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;  
 KW proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;  
 KW asthma; neurological disorder; Alzheimer's disease; Huntington's disease;  
 KW dementia; Parkinson's disease; developmental disorder; anemia; adenoma;  
 KW drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;  
 KW renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;  
 KW anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;  
 KW goiter; gastrointestinal disorder; gene therapy; virucide; anticoagulant;  
 KW anticonvulsant; nootropic; enzyme; DME-5.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Peptide 1..14 /label= Signal\_peptide

FT Protein 5..835 /note= Mature human DME-5"

FT Peptide 1..16 /label= Signal\_peptide

FT Protein 17..835 /note= Mature human DME-5"

```

FC Domain 132..215
FT /note="Transmembrane domain"
FT 671..699
FT Domain /note="Transmembrane domain"
XX
XX WO030246426-A2.
XX
XX 13-JUN-2002.
XX
XX 04-DEC-2001; 2001WO-US47429.
XX
XX 08-DEC-2000; 2000US-25433AP.
XX
XX 15-DEC-2000; 2000US-25618BP.
XX
XX 21-DEC-2000; 2000US-257713P.
XX
XX 19-JAN-2001; 2001US-262736P.
XX
XX 02-FEB-2001; 2001US-266020P.
XX
XX (INCYTE GENOXICS INC.
XX
XX Sanjarnawa XM, Yao MG, Au-young J, Baughn XR, Arvizu C, Ring HZ,
XX Lee EA, Ding L, Hafalia AJA, Tang YF, Yue H, Tribouley CX,
XX Lu DM, Lai PG, Warren BA, Yang J, Walla NK, Nguyen DB,
XX Gandhi AR, Lu Y, Isori CH;
XX
XX WPI; 2002-519668/55.
XX
XX N-PSDB: AAD40563.
XX
XX Novel human drug metabolizing polypeptide, useful in diagnosis,
XX prevention or treatment of autoimmune/inflammatory, cell proliferative,
XX neurological, developmental, endocrine, metabolic and gastrointestinal
XX disorders.
XX
XX Claim 60; Page 147-149; 169pp; English.
XX
XX The invention relates to an isolated human drug metabolizing enzyme (DME)
XX and its nucleotide. DME is useful for diagnosing, treating or preventing
XX disorders associated with aberrant expression of DME, where the disorders
XX are selected from autoimmune/inflammatory disorder, such as acquired
XX immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,
XX cystitis; a cell proliferative disorder such as arteriosclerosis,
XX neuroblastoma, hepatoma, and cancer; a neurological disorder such as
XX Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
XX a developmental disorder such as renal tubular acidosis, epilepsy,
XX anemia; an endocrine disorder such as adenoma, thymosis and
XX infections; an eye disorder such as conjunctivitis, glaucoma, cataract;
XX metabolic disorder such as cystic fibrosis, diabetes and gout; a
XX gastrointestinal disorder such as anorexia, peptic ulcer, and liver
XX disorders. DME is useful in a number of drug screening techniques and to
XX analyze the proteome of a tissue or cell type. The invention is useful
XX for creating knock-in humanized animals or transgenic animals to model
XX human diseases, in somatic or germline gene therapy, to generate a
XX transcrip; page of a tissue or cell type, for detecting differences in
XX the chromosomal location due to translocation, inversion, etc. among
XX normal, carrier or affected individuals, and as hybridization probes for
XX mapping naturally occurring genomic sequences. The present sequence is
XX human DME-5.
XX
XX Sequence 835 AA:
XX
XX Query Match 5.9%; Score 48; DB 23; Length 835;
XX Best Local Similarity 100.0%; Pred. No. 8.4e-41;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 510 CNFSKNDVMSAVVMTWYNFAKTDFPNQPVQDTKFTHTKRNREEV 557
XX |||||
XX DB 521 CNFSKNDVMSAVVMTWYNFAKTDFPNQPVQDTKFTHTKRNREEV 568
XX
XX RESULT 16
XX ID ABB97215 standard; Protein; 835 AA.
XX
XX AC ABB97215;

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XX
XX 27-JUN-2002 (first entry)
XX
XX DE Novel human protein SEQ ID NO: 483.
XX
XX XX Human; anti-anemic; vulnerary; antiinflammatory; immunomodulator;
XX antiinfectivity; cerebroprotective; cytostatic; rheumatic; gene therapy;
XX neuroprotective; antiparkinsonian; protein therapy; EST;
XX expressed sequence tag.
XX
XX OS Homo sapiens.
XX
XX WO020222660-A2.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US26015.
XX
XX 11-SEP-2001; 2000US-0659671.
XX
XX (HYSEQ-) HYSEQ INC.
XX
XX Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F,
XX Xue AJ, Yang Y, Weinman T, Drmanac RT;
XX
XX WPI; 2002-292408/33.
XX
XX N-PSDB; ABB32401.
XX
XX Example 2; SEQ ID NO 483; 509pp; English.
XX
XX PS The present invention provides the protein and coding sequences of 444
XX CS novel human proteins. These were isolated from expressed sequences tags
XX CC (ESTs). They can be used to stimulate cell growth to regulate
XX CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
XX CC e.g. in burn treatment, to regulate the immune system e.g. to treat
XX CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
XX CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
XX CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
XX CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
XX CC Parkinson's disease. The present sequence is a protein of the invention.
XX
XX SQ Sequence 835 AA:
XX
XX Query Match 5.9%; Score 48; DB 23; Length 835;
XX Best Local Similarity 100.0%; Pred. No. 8.4e-41;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 510 CNFSKNDVMSAVVMTWYNFAKTDFPNQPVQDTKFTHTKRNREEV 557
XX |||||
XX DB 521 CNFSKNDVMSAVVMTWYNFAKTDFPNQPVQDTKFTHTKRNREEV 568
XX
XX RESULT 17
XX ID ABB07675 standard; Protein; 835 AA.
XX
XX AC ABB07675;
XX
XX 10-JUN-2002 (first entry)
XX
XX DE Human carboxylesterase family member, 33410 polypeptide.
XX
XX Carboxylesterase; 33410; cytostatic; cardiac; dermatologic; human;
XX antidiabetic; antirheumatic; antirheumatic; antirheumatic; vasotropic;
XX vulnerary; neuroprotective; antinflammatory; antitumor; antistatic;
XX antiallergic; antiviral; hepatocytic; nephrotoxic; anti-HIV; enzyme;
XX antiparkinsonian; tuberculostatic; hypotensive; antithrombotic;
XX nootropic; antisense therapy; angiogenesis; gene therapy.
XX
XX OS Homo sapiens.

```

XX W02002166:6-A2.  
 XX 28-FEB-2002.  
 PD  
 XX 21-AUG-2001; 2001WO-US26091.  
 XX 21-AUG-2000; 2000US-226774P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Curtis RAJ;  
 XX  
 XX WPI; 2002-257916/30.  
 DR N-PSDB; ABA955:99, ABA95230C.  
 XX  
 PT New carboxylesterase nucleic acid 33410, useful for the treatment and  
 PT diagnosis of immune, cardiovascular, reproductive and cancerous  
 PT disorders -  
 XX  
 XX Claim 1; Page 110; 123pp; English.  
 XX  
 XX The invention provides a novel carboxylesterase family member, designated  
 CC 33410. Compounds that bind to or modulate the activity or expression of  
 CC 33410, are useful for treating or preventing a disorder such as cellular  
 CC proliferative or differentiative, neural, cardiovascular, prostatic, skin  
 CC brain and skeletal muscular disorders, protein-protein interaction  
 CC disorders, signal transduction disorders, immune (e.g. diabetes and  
 CC rheumatoid arthritis), reproductive, cardiovascular (e.g. hypertension,  
 CC atherosclerosis, coronary artery disease, arrhythmia, ischemic heart  
 CC disease and angina pectoris), vascular disorders (e.g. varicose veins,  
 CC Wegener's granulomatosis and wound healing) or cancerous disorders.  
 CC Multiple sclerosis, Crohn's disease, ulcers, asthma, allergy, infection,  
 CC kidney disease (glomerulonephritis), idiopathic thrombocytopenic purpura,  
 CC hepatitis, tuberculosis, human immunodeficiency virus, Alzheimer's and  
 CC Parkinson's. The 33410 polynucleotide and polypeptide are useful for  
 CC diagnosis of a predisposition to a disorder, for evaluating the efficacy  
 CC of a therapeutic or prophylactic disorder, for chromosome mapping, as  
 CC immunogens, for drug screening, for the detection of mutations in the  
 CC gene and for tissue typing. The present sequence represents the human  
 CC carboxylesterase family member, 33410.  
 XX  
 XX Sequence 835 AA;  
 SC  
 Query Match 5.9%; Score 48; DB 23; Length 835;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-4;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 510 CNFSKNDVLSAVVMTYWTNFAKTGDPNQPVQDTKFIHTKRNREEV 557  
 DB 521 CNFSKNDVLSAVVMTYWTNFAKTGDPNQPVQDTKFIHTKRNREEV 568  
 RESULT 18  
 AAB62400  
 ID AAB62400 standard; Protein: 837 AA.  
 XX  
 XX AAB62400;  
 AC  
 XX  
 XX 29-JUN-2001 (first entry)  
 DT  
 XX  
 XX Human MBSP4 polypeptide (clone 21417374.0.9).  
 DE  
 XX  
 XX MBSPX; cancer; preclampsia; immune system; neurological; cytostatic;  
 KW gynecological; antiinflammatory; neuroproliferative; isotropic; relaxant;  
 KW cardiant; dermatological; gene therapy; human; MBSP4.  
 XX  
 XX Homo sapiens.  
 CS  
 XX  
 XX W0200127277-A2.  
 RN  
 XX  
 XX 19-APR-2001.  
 PD  
 XX

PF 13-OCT-2000; 2000WO-US26480.  
 XX  
 XX 13-OCT-1999; 99US-0159231.  
 PR 12-JAN-2000; 2000US-0175670.  
 PR 12-OCT-2000; 2000US-0159232.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Shimkete RA, Uchenstein H, Boldog FL;  
 XX  
 XX WPI; 2001-282030/29.  
 DR N-PSDB; AAF82996.  
 XX  
 XX Novel human polynucleotide sequences and the membrane bound or secreted  
 PT polypeptides encoded by these sequences, designated MBSPX -  
 XX  
 XX Claim 1; Page 26-29; 157pp; English.  
 XX  
 XX The invention relates to novel polypeptides, termed MBSPX and  
 CC polynucleotides encoding the MBSPX polypeptides. The MBSPX polypeptide,  
 CC nucleic acid and an MBSPX antibody are useful for treating or preventing  
 CC a pathology associated with the protein especially in humans. The MBSPX  
 CC nucleic acid can be used to express MBSPX protein (e.g. via a recombinant  
 CC expression vector in a host cell in gene therapy applications), or to  
 CC detect MBSPX mRNA in a biological sample or a genetic lesion in a MBSPX  
 CC gene. Disorders associated with insufficient or excessive production of  
 CC MBSPX protein include cancer, preclampsia, immune system disorders and  
 CC inflammation, neurological disorders, cardiovascular disorders and skin  
 CC and muscle abnormalities. The anti-MBSPX antibodies can be used to detect  
 CC and isolate MBSPX proteins and modulate MBSPX activity. The present  
 CC sequence represents the amino acid sequence of MBSP4, a human neurolygin  
 CC 2 homologue.  
 XX  
 XX Sequence 837 AA;  
 SC  
 Query Match 5.9%; Score 48; DB 22; Length 837;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-4;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 310 CNFSKNDVLSAVVMTYWTNFAKTGDPNQPVQDTKFIHTKRNREEV 557  
 DB 521 CNFSKNDVLSAVVMTYWTNFAKTGDPNQPVQDTKFIHTKRNREEV 568  
 RESULT 19  
 AAB51838  
 ID AAB51838 standard; Peptide; 49 AA.  
 XX  
 XX AAB51838;  
 AC  
 XX  
 XX 25-FEB-2003 (first entry)  
 DT  
 XX  
 XX Human liver peptide, SEQ ID No 30486.  
 DE  
 XX  
 XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 KW hypercholesterolaemia; coronary heart disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX W0200157273-A2.  
 PN  
 XX  
 XX 09-AUG-2001.  
 PD  
 XX  
 XX 30-JAN-2001; 2001WO-US00664.  
 PF  
 XX  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI; 2001-488896/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human adult liver.  
 XX  
 PS Claim 27; SEQ ID No 30486; 658bp; English.  
 CC  
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridizes at high  
 CC stringency to a nucleic acid molecule expressed in the human adult  
 CC liver. (I) may be used for predicting, measuring and displaying gene  
 CC expression in samples derived from human adult liver. The genes  
 CC identified may be involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which  
 CC is associated with coronary heart disease. AB047348-AB059930 represent  
 CC human liver single exon encoded peptides of the invention.  
 CC Note: The sequence information for this patent does not appear in the  
 CC printed specification but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 49 AA;  
 Query Match 5.6%; Score 46; DB 22; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-40;  
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 YY 163 QNSKKPVMVYIHGGSYMEGTGNNIDGSIILASYGIVIVITINRLGI 208  
 Db 4 QNSKKPVMVYIHGGSYMEGTGNNIDGSIILASYGIVIVITINRLGI 49  
 RESULT 20  
 ABG10270  
 ID ABG10270 standard; Protein; 1434 AA.  
 XX  
 AC ABG10270;  
 XX  
 CC 13-FEB-2002 (first entry);  
 XX  
 DE Novel human diagnostic protein #0261.  
 XX  
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US-8631.  
 XX  
 PR 31-MAR-2000; 2000US-0340217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 DR WPI; 2001-639362/73.  
 DR N-PSDB; AAS74457.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

PS Claim 20; SEQ ID No 40623; 103bp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on RNA and  
 CC amino acid sequences. ABG00010-AB030377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 1434 AA;  
 Query Match 5.3%; Score 43; DB 22; Length 1434;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-35;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 YY 515 NDVMSAVVMYIMTFKTDGPNQVPCDTGFIHKPKRFEV 557  
 Db 267 NDVMSAVVMYIMTFKTDGPNQVPCDTGFIHKPKRFEV 309  
 RESULT 21  
 ABP43803  
 ID ABP43803 standard; Protein; 826 AA.  
 XX  
 AC ABP43803;  
 XX  
 CC 26-FEB-2003 (first entry)  
 XX  
 DE 3 isoform protein.  
 XX  
 KM Neuroprotective; immunomodulator; cancer; chromosome Xq13.1;  
 KM cytoskeletal; anti-inflammatory; gene therapy; nutritional supplement;  
 KM wound; burn; ulcer; Alzheimer's disease; Huntington's disease;  
 KM amyotrophic lateral sclerosis; autoimmune disorder; inflammation;  
 KM vulvectomy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200221111-A2.  
 XX  
 PD 18-APR-2002.  
 XX  
 PF 11-OCT-2001; 2001WO-US27760.  
 XX  
 PR 12-OCT-2000; 2000US-0687527.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AC, Yang Y, Wehrman T, Drmanac RT;  
 DR WPI; 2002-426278/45.  
 DR N-PSDB; ABG61047.  
 XX  
 PT New polypeptides and their encoded proteins, useful as nutritional  
 PT sources or supplements, or in gene therapy, particularly for treating  
 PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or  
 PT inflammation.





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XX 12-MAR-1999; 99JUS-0124142.
PR 11-JUN-1999; 99JUS-0138597.
PR 03-DEC-1999; 99JUS-0168666.
XX
PA (HUMA-) HUMAN GEMOKE SCI INC.
XX
PI Rosen CA, Ruben SW, Kotsoulis G;
XX
XX WPI; 2000-638176/61.
XX
XX
XX Novel 49 human secreted proteoins useful for diagnosis, prevention and
PT treatment of disorders including neurological, cell proliferative,
PT cardiovascular, and autoimmune/inflammatory disorders and microbial
PT infections -
XX
XX
XX Disclosure; Page 402; 405pp; English.
XX
XX This invention describes a novel isolated polypeptide (I) comprising an
XX amino acid sequence at least 95 % identical to a polypeptide sequence
XX selected from 49 polypeptides encoded by polynucleotide sequences
XX included in American Type Culture Collection (ATCC) deposit number
XX 203917, defined in the specification. The products of the invention have
XX cytosolic, antiarthritic, antiasthmatic, immunosuppressive, neurologic,
XX antiarteriosclerotic, antiinflammatory, neuroprotective, antidiabetic,
XX tranquilizer, vulnerary, antibacterial, antiparasitic, antiarrhythmic,
XX antineoplastic, cardiant and anti-HIV activity. (I) or a nucleic acid (II)
XX encoding (I) is useful for preventing, treating or ameliorating a medical
XX condition and for diagnosing a pathological condition or susceptibility
XX to the condition. (I) is useful for identifying a binding partner which
XX affects the activity of the polypeptide and for identifying an activity
XX in a biological sample. (I), (II) or an antibody (IV) specific to (I) is
XX also useful for treating or preventing a disease, disorder or condition
XX associated with aberrant expression of (I). Diseases treated or diagnosed
XX include immune disorders such as autoimmune diseases, blood protein
XX disorders, anemia, allergic reactions and conditions such as asthma,
XX organ rejection or graft-versus-host disease, inflammation, hyper
XX proliferative disorders, cardiovascular disorders such as arteriosclerosis,
XX fistula, arrhythmias, arteriosclerosis, coronary thrombosis, organ
XX regeneration, cancer, neovascular glaucoma, diabetic retinopathy,
XX rheumatoid arthritis, psoriasis, diseases associated with increased
XX apoptosis that include acquired immunodeficiency syndrome (AIDS),
XX neurological diseases such as Parkinson's disease, viral, bacterial,
XX fungal or parasitic diseases. They are also used to repair, replace or
XX protect tissue damage by congenital defects, to treat trauma, in surgery,
XX including cosmetic plastic surgery, to treat fibrosis, reperfusion injury
XX or systemic cytokine damage, to stimulate chondrocyte growth, to prevent
XX skin aging due to sunburn, to change a mammal's mental state or physical
XX state by influencing biorythms, cardiac rhythms, depression, memory,
XX stress and for accelerating wound healing. (I), (II) and/or their agonist
XX or antagonist are useful as food additives or preservatives to increase
XX or decrease storage capabilities, fat content, lipid, protein,
XX carbohydrate, vitamin, mineral or other nutritional components. (I) is
XX useful for screening therapeutic compounds. (I) is useful in forensic
XX biology for detecting DNA sequences and as diagnostic probes for
XX detecting the presence of specific mRNA in a particular cell type.
XX
XX
XX Sequence 229 AA;
XX
XX Query Match 3.9%; Score 32; DB 21; Length 229;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-24;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 399 SVSNFVNLYGYPGSKCTLRATIKFMVTDMD 430
XX |||||
XX 108 SVSNFVNLYGYPGSKOTLRITIKFMVTDMD 139

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XX
XX 13-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #10255.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensics;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001-WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HUSE-) HUSEQ INC.
XX
XX Dymnac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639162/73.
XX N-PSDB; AAS74451.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 40623; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridization probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAG0010-AAG0377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 726 AA;
XX
XX Query Match 3.9%; Score 32; DB 22; Length 726;
XX Best Local Similarity 100.0%; Pred. No. 4.5e-24;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 510 CNFSKRWLWLSAVMTYTCNFAKTCPPQPPV 542
XX |||||
XX 272 CNFSKRWLWLSAVMTYTCNFAKTCPPQPPV 303

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RESULT 24  
 ABG10264  
 ID ABG10264 standard; Protein: 726 AA.  
 AC  
 XX  
 AC ABG10264;

RESULT 25  
 AAC01845  
 ID AAC01845 standard; Protein: 144 AA.  
 AC  
 AC AAC01845;  
 XX  
 AC  
 DT 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 15737.  
DZ  
XX  
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukemia;  
KW nervous system disorders; arthritis; inflammation.  
XX  
OS Homo sapiens.  
XX  
FN WO200164835-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 26-FEB-2001; 2001WO-US04927.  
XX  
PR 28-FEB-2000; 2000US-C515126.  
XX  
PR 18-MAY-2000; 2000US-C577409.  
XX  
PA (H5SE-) H5SEQ .NC.  
XX  
PI Targ YC, Liu C, Dermanac RJ;  
XX  
DR MPI; 2001-5:4835/56.  
XX  
N-PSDB; AA181776.  
XX  
PT Isolated nucleic acids and polypeptides, useful for preventing  
PT diagnosing and treating e.g. leukemia, inflammation and immune  
PT disorders -  
PS  
PS Claim 20; SEQ ID NO 15737; 1399pp + Sequence Listing; English.  
XX  
CC The invention relates to human polynucleotides (AA179941-AA193841) and  
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, hematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activity/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pat\_sequences.  
XX  
SQ Sequence 144 AA;  
Query Match 3.8%; Score 31; DB 22; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1,2e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 355 QLMGGEFLNYDMLGVNQGEGKXVDGIY 365  
DB 80 QLMGGEFLNYDMLGVNQGEGKXVDGIY 110  
RSDUT 26  
AAU87570  
ID AAU87570 standard; Protein; 8. AA.  
XX  
AC AAU87570;  
XX  
DT 05-JUN-2002 (first entry);  
XX  
DE Novel central nervous system protein #480.  
XX  
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischemia; angiosclerosis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;

KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO200155318-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JUN-2001; 2001WO-US01332.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
XX  
PR 04-FEB-2000; 2000US-0180628.  
XX  
PR 24-FEB-2000; 2000US-0184664.  
XX  
PR 02-MAR-2000; 2000US-0186350.  
XX  
PR 16-MAR-2000; 2000US-0189874.  
XX  
PR 17-MAR-2000; 2000US-0190776.  
XX  
PR 18-APR-2000; 2000US-0198123.  
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PR 19-MAY-2000; 2000US-0205515.  
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PR 07-JUN-2000; 2000US-0204967.  
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PR 28-JUN-2000; 2000US-0214886.  
XX  
PR 30-JUN-2000; 2000US-0215135.  
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PR 07-JUL-2000; 2000US-0216647.  
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PR 07-JUL-2000; 2000US-0216880.  
XX  
PR 11-JUL-2000; 2000US-0217487.  
XX  
PR 11-JUL-2000; 2000US-0217496.  
XX  
PR 14-JUL-2000; 2000US-0218290.  
XX  
PR 26-JUL-2000; 2000US-0220963.  
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PR 26-JUL-2000; 2000US-0220964.  
XX  
PR 14-AUG-2000; 2000US-0224518.  
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PR 14-AUG-2000; 2000US-0224519.  
XX  
PR 14-AUG-2000; 2000US-0225213.  
XX  
PR 14-AUG-2000; 2000US-0225214.  
XX  
PR 14-AUG-2000; 2000US-0225266.  
XX  
PR 14-AUG-2000; 2000US-0225267.  
XX  
PR 14-AUG-2000; 2000US-0225268.  
XX  
PR 14-AUG-2000; 2000US-0225270.  
XX  
PR 14-AUG-2000; 2000US-0225447.  
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PR 14-AUG-2000; 2000US-0225757.  
XX  
PR 14-AUG-2000; 2000US-0225758.  
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PR 14-AUG-2000; 2000US-0225759.  
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PR 18-AUG-2000; 2000US-0226279.  
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PR 22-AUG-2000; 2000US-0226681.  
XX  
PR 22-AUG-2000; 2000US-0226686.  
XX  
PR 23-AUG-2000; 2000US-0227182.  
XX  
PR 23-AUG-2000; 2000US-0227009.  
XX  
PR 30-AUG-2000; 2000US-0228924.  
XX  
PR 01-SEP-2000; 2000US-0229387.  
XX  
PR 01-SEP-2000; 2000US-0229343.  
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PR 01-SEP-2000; 2000US-0229344.  
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PR 01-SEP-2000; 2000US-0229345.  
XX  
PR 05-SEP-2000; 2000US-0229509.  
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PR 05-SEP-2000; 2000US-0229513.  
XX  
PR 06-SEP-2000; 2000US-0230437.  
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PR 06-SEP-2000; 2000US-0230438.  
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PR 08-SEP-2000; 2000US-0231242.  
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PR 08-SEP-2000; 2000US-0231243.  
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PR 08-SEP-2000; 2000US-0231244.  
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PR 08-SEP-2000; 2000US-0231414.  
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PR 08-SEP-2000; 2000US-0232080.  
XX  
PR 08-SEP-2000; 2000US-0232081.  
XX  
PR 12-SEP-2000; 2000US-0231968.  
XX  
PR 14-SEP-2000; 2000US-0232397.  
XX  
PR 14-SEP-2000; 2000US-0232398.  
XX  
PR 14-SEP-2000; 2000US-0232399.  
XX  
PR 14-SEP-2000; 2000US-0232400.  
XX  
PR 14-SEP-2000; 2000US-0232401.  
XX  
PR 14-SEP-2000; 2000US-0233063.  
XX  
PR 14-SEP-2000; 2000US-0233064.

	PR	14-SEP-2000	2000US-0233065.
	PR	21-SEP-2000	2000US-0234223.
	PR	21-SEP-2000	2000US-0234224.
	PR	25-SEP-2000	2000US-0234997.
	PR	25-SEP-2000	2000US-0234998.
	PR	26-SEP-2000	2000US-0235484.
	PR	27-SEP-2000	2000US-0235934.
	PR	27-SEP-2000	2000US-0235936.
	PR	29-SEP-2000	2000US-0236347.
	PR	29-SEP-2000	2000US-0236367.
	PR	29-SEP-2000	2000US-0236368.
	PR	29-SEP-2000	2000US-0236369.
	PR	29-SEP-2000	2000US-0236370.
	PR	02-OCT-2000	2000US-0236802.
	PR	02-OCT-2000	2000US-0237037.
	PR	02-OCT-2000	2000US-0237038.
	PR	02-OCT-2000	2000US-0237039.
	PR	13-OCT-2000	2000US-0239935.
	PR	13-OCT-2000	2000US-0240390.
	PR	20-OCT-2000	2000US-0241221.
	PR	20-OCT-2000	2000US-0241785.
	PR	20-OCT-2000	2000US-0241786.
	PR	20-OCT-2000	2000US-0241787.
	PR	20-OCT-2000	2000US-0241808.
	PR	20-OCT-2000	2000US-0241809.
	PR	20-OCT-2000	2000US-0241826.
	PR	01-NOV-2000	2000US-0244647.
	PR	08-NOV-2000	2000US-0246474.
	PR	08-NOV-2000	2000US-0246475.
	PR	08-NOV-2000	2000US-0246476.
	PR	08-NOV-2000	2000US-0246477.
	PR	08-NOV-2000	2000US-0246478.
	PR	08-NOV-2000	2000US-0246523.
	PR	08-NOV-2000	2000US-0246524.
	PR	08-NOV-2000	2000US-0246525.
	PR	08-NOV-2000	2000US-0246526.
	PR	08-NOV-2000	2000US-0246527.
	PR	08-NOV-2000	2000US-0246528.
	PR	08-NOV-2000	2000US-0246532.
	PR	08-NOV-2000	2000US-0246533.
	PR	08-NOV-2000	2000US-0246610.
	PR	08-NOV-2000	2000US-0246611.
	PR	08-NOV-2000	2000US-0246613.
	PR	17-NOV-2000	2000US-0249207.
	PR	17-NOV-2000	2000US-0249208.
	PR	17-NOV-2000	2000US-0249209.
	PR	17-NOV-2000	2000US-0249210.
	PR	17-NOV-2000	2000US-0249211.
	PR	17-NOV-2000	2000US-0249212.
	PR	17-NOV-2000	2000US-0249213.
	PR	17-NOV-2000	2000US-0249214.
	PR	17-NOV-2000	2000US-0249215.
	PR	17-NOV-2000	2000US-0249216.
	PR	17-NOV-2000	2000US-0249217.
	PR	17-NOV-2000	2000US-0249218.
	PR	17-NOV-2000	2000US-0249245.
	PR	17-NOV-2000	2000US-0249265.
	PR	17-NOV-2000	2000US-0249266.
	PR	17-NOV-2000	2000US-0249267.
	PR	17-NOV-2000	2000US-0249268.
	PR	17-NOV-2000	2000US-0249269.
	PR	17-NOV-2000	2000US-0249270.
	PR	17-NOV-2000	2000US-0249271.
	PR	17-NOV-2000	2000US-0249272.
	PR	17-NOV-2000	2000US-0249273.
	PR	17-NOV-2000	2000US-0249274.
	PR	17-NOV-2000	2000US-0249275.
	PR	17-NOV-2000	2000US-0249276.
	PR	17-NOV-2000	2000US-0249277.
	PR	17-NOV-2000	2000US-0249278.
	PR	17-NOV-2000	2000US-0249279.
	PR	17-NOV-2000	2000US-0249280.
	PR	17-NOV-2000	2000US-0249281.
	PR	17-NOV-2000	2000US-0249282.
	PR	17-NOV-2000	2000US-0249283.
	PR	17-NOV-2000	2000US-0249284.
	PR	17-NOV-2000	2000US-0249285.
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	PR	17-NOV-2000	2000US-0249287.
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	PR	17-NOV-2000	2000US-0249289.
	PR	17-NOV-2000	2000US-0249290.
	PR	17-NOV-2000	2000US-0249291.
	PR	17-NOV-2000	2000US-0249292.
	PR	17-NOV-2000	2000US-0249293.
	PR	17-NOV-2000	2000US-0249294.
	PR	17-NOV-2000	2000US-0249295.
	PR	17-NOV-2000	

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XX 17-JAN-2001; 2001WC-US01239.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249211.
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PR 05-JAN-2001; 2001US-0259678.
PR
XX
FA (HUGA-) HUMAN GENOME SCI INC.
XX
FI Rosen Ca, Barash SC, Ruben SM;
XX
DR WPI; 2001-465566/50.
DR N-PSDB; AAS41094.

```

XX Novel polypeptides and polynucleotides useful for diagnosing,  
 PT preventing, treating neural, immune system, muscular, reproductive,  
 PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous  
 PT diseases -

XX Claim 11; SEQ ID No 1220; 1180bp; English.

XX The present invention relates to the isolation of novel human enzyme  
 CC polypeptides, and the cDNA (AA540785-AAA51684) and genomic sequences  
 CC encoding them. The enzyme polypeptides of the invention may comprise the  
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 CC isomerases or ligases. The sequences of the invention are useful in the  
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
 CC disorders including hyperproliferative disorders (e.g. cancer),  
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders  
 CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),  
 CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders  
 CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),  
 CC blood-related disorders (e.g. haemophilia), reproductive disorders  
 CC (e.g. infertility) and infectious disorders (e.g. influenza). The  
 CC polynucleotides of the invention can also be used in gene therapy.

CC AAU22315-AAU23814 represent the novel human enzyme polypeptides of the  
 CC invention.

CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WFO  
 CC at ftp.wipo.int/pub/published\_pat\_sequences.

XX Sequence 81 AA;

XX Query Match 3.4%; Score 28; DB 22; Length 81;  
 XX Best Local Similarity 100.0%; Pred. No. 5,5e-21;  
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 46 EILGVECYLVSPYASPTGRRRQPE 73  
 XX |||||  
 XX 35 EILGVECYLVSPYASPTGRRRQPE 62

XX RESULT 28  
 XX AAM93345  
 XX ID AAM93345 standard; Protein: 335 AA.

XX AC AAM93345;  
 XX XX 06-NOV-2001 (first entry);  
 XX DT Human polypeptide, SEQ ID NO: 2889.  
 XX DE Human polypeptide, SEQ ID NO: 2889.  
 XX XX Human: full length cDNA; cDNA synthesis; oligo-capping.  
 XX OS Homo sapiens.  
 XX PN EP136094-A2.  
 XX PD 05-SEP-2001.  
 XX PF 07-JUL-2000; 2000EP-0114083.  
 XX PR 09-JUL-1999; 99JP-0194496.  
 XX PR 11-JAN-2000; 2000JP-0119774.  
 XX PR 02-MAY-2000; 2000JP-0169765.  
 XX XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.  
 XX DR N-PSDB; AAK94265.  
 XX PT 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -

XX Claim 8; SEQ ID NO 2889; 1380bp + sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5' and 3' ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a polypeptide  
 CC encoded by a full length human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 335 AA;

XX Query Match 3.4%; Score 28; DB 22; Length 335;  
 XX Best Local Similarity 100.0%; Pred. No. 3,5e-20;  
 XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 510 CFFSKNDVMSAVMTWYTPAKTGDPN 537  
 XX |||||  
 XX 31 CFFSKNDVMSAVMTWYTPAKTGDPN 58

XX RESULT 29  
 XX ABG16624  
 XX ID ABG16624 standard; Protein: 419 AA.

XX AC ABG16624;  
 XX DT 18-FEB-2002 (first entry)  
 XX DE Novel human diagnostic protein #16615.  
 XX DE Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX OS Homo sapiens.  
 XX PN WO200175067-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WC-US08631.  
 XX PR 31-MAR-2000; 2000US-0540217.  
 XX PR 23-MAY-2000; 2000US-0649167.  
 XX XX (HYSE-) HYSEQ INC.  
 XX FA Drmanac RT, Jin C, Tang YT;  
 XX F- WPI; 2001-639162/73.  
 XX DR N-PSDB; AAS60811.  
 XX XX New isolated polynucleotide and encoded polypeptides useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -

XX Claim 20; SEQ ID No 46983; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or



CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp://ipo.int/pub/published\_pat\_sequences.

XX Sequence 134 AA;

Query Match 2.6%; Score 21; E: 22; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-13;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 RDYSTELEVTIAVGASLLFLN 689  
 DB 50 RDYSTELEVTIAVGASLLFLN 70

RESULT 32  
 ABG64991

ID ABG64991 standard; Protein; 228 AA.

AC ABG64991;

DT 27-AUG-2002 (first entry)

DE Human albumin fusion protein; #1666.

XX Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 XX human serum albumin; HSA; cancer; reproductive disorder;  
 XX digestive disorder; immune disorder; endocrine disorder;  
 XX haematopoietic disorder; neural disorder; connective disorder;  
 XX cytostatic; antifertility; antiinflammatory; antitumor;  
 XX immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;  
 XX neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antithyroidic.

OS Homo sapiens.  
 OS Synthetic.

PN WO200177137-A1.

PD 18-OCT-2001.

PE 12-APR-2001; 2001WO-US-1988.

PR 12-APR-2000; 2000US-229358P.

PR 23-APR-2000; 2000US-199384P.

PR 21-DEC-2000; 2000US-256931P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Haseltine WA.

DR WPI; 2002-010886/C1.

PT New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein -

PS Claim 1; Page 1662-1663; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA), also known as human serum  
 CC albumin (HSA). The proteins are useful for treating a disease or  
 CC disorder that may be modulated by therapeutic protein X. The albumin  
 CC extends the shelf-life of protein X, and may increase its biological  
 CC in vitro/in vivo activity. The protein is useful for treating and  
 CC diagnosing disorders such as cancer, reproductive disorders, digestive  
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
 CC (e.g. diabetes), haematopoietic disorders, neural disorders  
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
 CC fusion proteins of the invention.

SQ Sequence 228 AA;

Query Match 2.2%; Score 18; E: 23; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 KPMVYIHGGSYMECTGN 184  
 DB 173 KPMVYIHGGSYMECTGN 190

RESULT 33  
 AAE21452

ID AAE21452 standard; Protein; 228 AA.

AC AAE21452;

DT 01-JUN-2002 (first entry)

DE Human gene 1 encoded secreted protein HAMH20, SEQ ID NO:68.

XX Human; secreted protein; gene therapy; autoimmune disease; vitamin;  
 XX rheumatoid arthritis; hyperproliferative disorder; neoplasia; breast;  
 KW liver; cardiovascular; cardiac arrest; cerebrovascular; infection;  
 KW cerebral ischaemia; angiogenesis; nervous system; Alzheimer's disease;  
 KW ocular; corneal infection; wound healing; neuroprotective; skin aging;  
 KW transplantation; chemotaxis; food additive; preservative; virotherapy;  
 KW storage capability; mineral; cofactor; immunosuppressive; cytostatic;  
 KW antiproliferative; cardiac; vasotropic; cerebroprotective; neurotropic;  
 KW fungicide; ophthalmological; sunburn; vitruicide; antibacterial.

OS Homo sapiens.

OS Homo sapiens.

OS Homo sapiens.

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OS Homo sapiens.



CC	disorders such as autoimmune diseases e.g. rheumatoid arthritis,
CC	hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC	cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC	e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC	Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC	and ocular disorders e.g. corneal infection. The polypeptides of the
CC	invention can also be used to aid wound healing and epithelial cell
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs
CC	before transplantation, for supporting cell culture of primary tissues,
CC	to regenerate tissues and in chemotaxis. They can also be used as a food
CC	additive or preservative to increase or decrease storage capabilities,
CC	fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC	and other nutritional components. The present sequence represents a
CC	human secreted protein of the invention.
XX	
SQ	Sequence 228 AA:
	Query Match 2.2%; Score 18; DB 23; Length 228;
	Best Local Similarity 100.0%; Pred. No. 7.6e-10;
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
CY	167 KPMWVTHGGSYVECTGN 184
D6	173 KPMWVTHGGSYVECTGN 190
RESULT 34	
AAE21516	ID AAE21516 standard; Protein; 161 AA.
XX	AAE21516;
AC	
XX	
DT	01-JUN-2002 (first entry);
XX	
DE	Human gene 1 encoded secreted protein fragment #1.
XX	
KM	Human: secreted protein; gene therapy; autoimmune disease; vitamin;
KM	rheumatoid arthritis; hyperproliferative disorder; neoplas; breast;
KM	liver; cardiovascular; cardiac arrest; cerebrovascular; infection;
KM	cerebral ischaemia; angiogenesis; nervous system; Alzheimer's disease;
KM	ocular; corneal infection; wound healing; neuroprotective; skin aging;
KM	transplantation; chemotaxis; food additive; preservative; vulnery;
KM	storage capability; mineral; cofactor; immunosuppressive; cytostatic;
KM	antiproliferative; cardiact; vasotrop;c; cerebroprotective; neuroprot;c;
KM	tungicide; optalmalogical; sunburn; vitruode; antibacterial.
OS	Homo sapiens.
GS	
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 133
FT	/label= Unknown
FT	Misc-difference 141
FT	/label= Unknown
FT	Misc-difference 153
FT	/label= Unknown
FT	Misc-difference 166
FT	/label= Unknown
XX	
PN	WO200224719-A1.
PD	28-MAR-2002.
XX	
XX	
PF	17-JAN-2001; 2001MO-US01565.
PR	20-SEP-2000; 2000US-224210P.
PA	(HUMA-) HUMAN GENOME SCI INC.
PI	Rosen CA, Komatsu SC, Baker KP, Birse CE, Soppet DR, Olsner HS;
P1	Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fischel N;
XX	Ni J;
DR	WPI, 2002-258042/39.

XX	New nucleic acid molecules encoding 21 human secreted proteins for
PT	diagnosing or treating e.g. autoimmune diseases, hyperproliferative
PT	disorders, and cardiovascular disorders, and used as food additives or
PT	preservatives -
XX	
PS	Disclosure, Page 8; 519pp; English.
XX	
CC	AAD3812-AD3868 represent cDNAs corresponding to 21 human secreted
CC	protein genes, and AAE21452-AAE21508 represent the proteins they encode.
CC	AAE21509-AAE21517 represent human secreted protein fragments. The genes
CC	and their corresponding secreted proteins are useful for preventing,
CC	treating or ameliorating medical conditions, e.g., by protein or gene
CC	therapy. Pathological conditions can be diagnosed by determining the
CC	amount of the new protein in a sample or by determining the presence of
CC	mutations in the new genes. Specific uses are described for each of the
CC	21 genes, based on the tissues in which they are most highly expressed,
CC	and include developing products for the diagnosis or treatment of
CC	disorders such as autoimmune diseases e.g. rheumatoid arthritis,
CC	hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC	cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC	e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC	Alzheimer's disease, infections caused by bacteria, viruses and fungi;
CC	and ocular disorders e.g. corneal infection. The polypeptides of the
CC	invention can also be used to aid wound healing and epithelial cell
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs
CC	before transplantation, for supporting cell culture of primary tissues,
CC	to regenerate tissues and in chemotaxis. They can also be used as a food
CC	additive or preservative to increase or decrease storage capabilities,
CC	fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC	and other nutritional components. The present sequence represents human
CC	secreted protein fragment referred to in the disclosure of the invention.
XX	
SQ	Sequence 161 AA:
XX	
CY	Query Match 1.8%; Score 15; EB 23; Length 161;
CV	Best Local Similarity 100.0%; Pctd. No. 7.9e-07;
Dc	Matches 15; Conservative 0; Mismatches 0; Indels C; Gaps 0.
XX	
62	PPTGERRRFPPEPPS 76
87	PPTGERRRFPPEPPS :01
XX	
RESULT 35	
ID	ABG64990 standard; Protein; 162 AA.
AS	ABG64990
XX	
AC	ABG64990;
XX	
DT	27-AUG-2002 (first entry)
XX	
DE	Human albumin fusion protein #1665.
XX	
KM	Albumin fusion protein; therapeutic protein X; human albumin; HA;
KM	human serum albumin; HSA; cancer; reproductive disorder;
KM	digestive disorder; immune disorder; endocrine disorder;
KM	haematopoietic disorder; neural disorder; connective disorder;
KM	cystostatic; antifertility; antiinflammatory; anticancer;
KM	immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KM	neuroprotective; antidepressant; antimicrobial; neuroleptic;
KM	osteopathic; antithrombotic.
OS	Homo sapiens.
GS	Synthetic.
XX	
PN	WC00017737-A1.
XX	
PD	15-OCT-2001.
XX	
PF	12-APR-2001, 2001WO-US11988.
PR	12-APR-2000, 2000US-229358P.

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PR 25-APR-2000; 2000US-199384P.
PR 21-DEC-2000; 2000US-255931P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX Rosen CA, Haseltine WA.
XX WPI; 2002-010886/01.
XX
XX New fusion protein for treating disease e.g. diabetes comprises an
XX albumin fused to a therapeutic protein.
XX
XX Claim 1; Page 1662; 2102pp; English.
XX
XX The present invention relates to albumin fusion proteins comprising a
XX therapeutic protein X and human albumin (HA), also known as human serum
XX albumin, HSA). The proteins are useful for treating a disease or
XX disorder that may be modulated by therapeutic protein X. The albumin
XX extends the shelf-life of protein X, and may increase its biological
XX in vitro/in vivo activity. The protein is useful for treating and
XX diagnosing disorders such as cancer, reproductive disorders, digestive
XX disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders
XX (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders
XX (e.g. diabetes), haematopoietic disorders, neural disorders
XX (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, and connective
XX tissue disorders), meningitis, schizophrenia, and connective disorders
XX (e.g. osteoporosis, arthritis). AAG53326-ABG55518 represent albumin
XX fusion proteins of the invention.
XX
XX Sequence 162 AA:
XX
XX Query Match 1.8%; Score 15; DB 23; Length 162;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-07;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 62 PPTGRRRFPPEPPS 76
XX |||||
XX 88 PPTGRRRFPPEPPS 102
XX
XX RESULT 36
XX AAE21473
XX ID AAE21473 standard; Protein; 162 AA.
XX AC AAE21473;
XX
XX 01-UTL-2002 (first entry)
XX
XX DE Human gene 1 encoded secreted protein HMMH20, SEQ ID NO:89.
XX
XX KM Human; secreted protein; gene therapy; autoimmune disease; vitamin;
XX rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast;
XX liver; cardiovascular; cardiac arrest; cerebrovascular; infection;
XX cerebral ischaemia; angioedema; nervous system; Alzheimer's disease;
XX ocular; corneal infection; wound healing; neuroprotective; skin aging;
XX transplantation; cholecystitis; food additives; preservative; vitamin;
XX storage capability; mineral; cofactor; immunosuppressive; cytotoxic;
XX antiproliferative; cardiac; vasodilator; cerebroprotective; neurotrophic;
XX fungicide; ophthalmological; sunburn; vitruole; antibacterial.
XX
XX OS Homo sapiens.
XX
XX FH Key location/Qualifiers
XX Peptide 1..45
XX /label= Signal_peptide
XX
XX Protein 46..162
XX /label= Mature_secreted_protein;
XX
XX Misc-difference 134
XX /label= Unknown
XX /note= "Encoded by NCG"
XX
XX Misc-difference 142
XX /label= Unknown
XX /note= "Encoded by GNT"

```

```

FT Misc-difference 154
FT /label= Unknown
FT /note= "Encoded by NCT"
FT Misc-difference 161
FT /label= Unknown
FT /note= "Encoded by NCC"
XX
XX MO200224719-A1.
XX
XX 28-MAR-2002.
XX
XX 17-JAN-2001; 2001WO-0501565.
XX
XX 20-SEP-2000; 2000US-234210P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Komatsu GA, Baker KP, Biese CE, Soppet DR, Olsen HS;
XX Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fischeia M;
XX N; 0;
XX
XX WPI; 2002-258042/30.
XX
XX DR N-PSDB; AAD33833.
XX
XX New nucleic acid molecules encoding 21 human secreted proteins for
XX diagnosing or treating e.g. autoimmune diseases, hyperproliferative
XX disorders, and cardiovascular disorders, and used as food additives or
XX preservatives.
XX
XX Claim 11; Page 483-484; 519pp; English.
XX
XX AAD33812-AAD33868 represent cDNAs corresponding to 21 human secreted
XX protein genes, and AAE21457-AAE21508 represent the proteins they encode.
XX CC AAE21509-AAE21517 represent human secreted protein fragments. The genes
XX and their corresponding secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 21 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX disorders such as autoimmune diseases e.g. rheumatoid arthritis,
XX hyperproliferative disorders e.g. neoplasms of the breast or liver,
XX cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
XX e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
XX Alzheimer's disease, infections caused by bacteria, viruses and fungi
XX and ocular disorders e.g. corneal infection. The polypeptides of the
XX invention can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues and in chemotaxis. They can also be used as a food
XX additive or preservative to increase or decrease storage capabilities,
XX fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
XX and other nutritional components. The present sequence represents a
XX human secreted protein of the invention.
XX
XX Sequence 162 AA:
XX
XX Query Match 1.8%; Score 15; DB 23; Length 162;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-07;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 62 PPTGRRRFPPEPPS 76
XX |||||
XX 88 PPTGRRRFPPEPPS 102
XX
XX RESULT 37
XX AAB54266
XX ID AAB54266 standard; Protein; 359 AA.
XX AC AAB54266;
XX

```

DT 09-MAR-2001 (first entry)  
 XX  
 DE Human pancreatic cancer antigen protein sequence SEQ ID NO:719.  
 XX  
 KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;  
 KW detection; diagnosis; identification; cytostatic; neuroprotective;  
 KW neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;  
 KW antinflammatory; cardiact; gene therapy; chromosome mapping;  
 KW linkage analysis; tissue identification; tissue typing; forensic;  
 KW neural; immune system; muscular; reproductive; gastrointestinal;  
 KW pulmonary; cardiovascular; renal; proliferative.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055320-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05989.  
 XX  
 FR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUKA-) HUKAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SY;  
 XX  
 DR WPI: 2000-579444/54.  
 DR N-PSDB: AAC99231.  
 XX  
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
 PT treating, or ameliorating a medical condition, particularly pancreatic  
 PT cancer, or for use in assays for diagnosing a pathological condition -  
 PS  
 PS Claim 1: Page 1159-1160; 1379pp; English.  
 XX  
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated  
 CC proteins, called pancreatic cancer antigens, given in AAB5406 to  
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
 CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,  
 CC gynaecological, cardiact and antinflammatory activities, and can be used  
 CC in gene therapy. The polynucleotide and proteins can be used for  
 CC preventing, treating, or ameliorating a medical condition or in assays  
 CC for diagnosing a pathological condition or a susceptibility to one in a  
 CC subject. Binding partners to the proteins and the activity of the  
 CC proteins can be identified. The pancreatic cancer antigens can be used to  
 CC detect, treat or prevent pancreatic disorders, especially cancer.  
 CC Agonists and antagonists to the antigens can be screened for. The  
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
 CC acid hybridisation probes that can be used in chromosome mapping, linkage  
 CC analysis, tissue identification and/or typing and a variety of forensic  
 CC and diagnostic methods. The proteins can be used to generate antibodies  
 CC which are used to purify, detect and target the polypeptides, including  
 CC both in vivo and in vitro diagnostic and therapeutic methods. The  
 CC proteins can be used to treat or prevent neural, immune system, muscular,  
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 359 AA;  
 XX  
 Query Match 1.5%; Score 12; DB 21; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 0.0023;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 526 YWTFNFAKTGDPN 537  
 DB 192 YWTFNFAKTGDPN 203  
 XX  
 RESULT 39  
 AAR58985  
 ID AAR58985 standard; protein; 535 AA.  
 XX

AC AAR58985;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 03-MAY-1995 (first entry)  
 XX  
 DE Bile salt-stimulated lipase (variant A).  
 XX  
 KW Bile salt stimulated lipase; BSSL; glycoprotein; esterase;  
 KW acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;  
 KW fat malabsorption; vitamins; dietary lipids; food supplement.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9420610-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 25-FEB-1994; 94WO-S000160.  
 XX  
 FR 01-MAR-1993; 93SE-0000686.  
 FR 04-MAR-1993; 93SE-0000722.  
 XX  
 PA (ASTR) ASTRA AB.  
 XX  
 PI Blaeckberg L, Edlund M, Hansson L, Hernell O, Lundberg L;  
 PI Strömqvist K, Toernell J;  
 XX  
 DR WPI: 1994-303018/37.  
 XX  
 PT Bile salt-stimulated lipase variants and coding sequences - used  
 PT to produce prods. for treatment of a pathological condition  
 PT related to exocrine pancreatic insufficiency  
 PS  
 PS Example 1.1.2: Page 57-58; 102pp; English.  
 XX  
 CC Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein  
 CC which is highly glycosylated. The N-terminal half of the protein  
 CC shows a homology to acetyl cholinesterase and some other esterases.  
 CC BSSL variant polypeptides can be used for the treatment of a  
 CC pathological condition related to exocrine pancreatic insufficiency  
 CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or  
 CC malabsorption of fat soluble vitamins for improvement of utilisation  
 CC of dietary lipids, particularly in preterm born infants. They can  
 CC also be used as supplements for infant food formulations. The BSSL  
 CC variants have maintained catalytic activity but contain less  
 CC glycosylation sites than native BSSL. This variant is a deletion  
 CC mutant lacking the C-terminal 187 amino acids of the wild-type  
 CC protein (See AAR58980).  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 535 AA;  
 XX  
 Query Match 1.5%; Score 12; DB 15; Length 535;  
 Best Local Similarity 100.0%; Pred. No. 0.0033;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 526 YWTFNFAKTGDPN 537  
 DB 467 YWTFNFAKTGDPN 478  
 XX  
 RESULT 39  
 AAR75098  
 ID AAR75098 standard; protein; 538 AA.  
 AC AAR75098;  
 XX  
 DT 25-JAN-1996 (first entry)  
 DT  
 XX  
 DE Recombinant bile salt-activated lipase.  
 XX  
 KW Bile salt activated lipase; BAL; C-terminal repeat.  
 KW

```

XX  Mammalia.
CS
XX
XX  JP07111891-A.
XX
XX  02-MAY-1995.
XX
XX  30-SEP-1993;  93JP-0245079.
XX
XX  30-SEP-1993;  93JP-0245079.
XX
XX  (MEIP ) MEIJI MILK PROD CO LTD.
XX
XX  WPI; 1995-196318/26.
XX
XX  N-PSDB; AAQ90569.
XX
XX  New recombinant bile salt-activated lipase(s); cDNA encoding them
XX  and vectors - useful for high level expression of the lipase(s) by
XX  fermenter-culturing.
XX
XX  Claim 1; Page 3-10; 31pp; Japanese.
XX
XX  New lipases are ones in which 1-15 repeats of any of the sequences
XX  AAR75099-R75105 (encoded by AAQ90570-Q90576) are attached to the C-
XX  terminus of the bile salt-activated lipase (BAL) of sequence AAR75098
XX  (encoded by AAQ90568) and/or in which the amino acid sequence SMTGS
XX  (encoded by AAQ90578) is attached to the N-terminus of the BAL. The
XX  recombinant lipases can be produced by fermentation in Pichia
XX  pastoris GS 115 transformed host cells.
XX
XX  Sequence 538 AA:
SQ
XX

Query Match      1.5%; Score 12; DB 16; Length 538;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY  526 YWTNPAKTGDPN 537
    |||||
DB  467 YWTNPAKTGDPN 478

RESULT 40
AAW10058
ID  AAW10058 standard; Protein; 538 AA.
XX
XX  AAW10058;
XX
XX  28-FEB-1997 (first entry);
XX
XX  Human wild-type bile salt-activated lipase.
XX
XX  BAL; bile salt-activated lipase; C-terminal repeat; recombinant;
XX  high yield; Pichia pastoris GS115; plasmid; transformation; pMT301;
XX  fermentation.
XX
XX  Homo sapiens.
XX
XX  JP09228779-A.
XX
XX  10-SEP-1996.
XX
XX  28-FEB-1995;  95TF-0039889.
XX
XX  28-FEB-1995;  95CP-0039889.
XX
XX  (MEIP ) MEIJI MILK PROD CO LTD.
XX
XX  WPI; 1996-453145/45.
XX
XX  N-PSDB; AAT47862.
XX
XX  High yield expression of recombinant bile salt activated lipase -
XX  in plasmid pMT301 transformed Pichia pastoris GS115

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FS  Disclosure; Page 6-8; 12pp; Japanese.
XX
XX  AAW10058 represents human wild-type mature bile salt-activated lipase
XX  (BAL). The invention is directed to the recombinant production of
XX  this enzyme at a high yield. This was achieved by the addition of
XX  cDNA encoding a repeat region consisting of 16 repeats of an 11
XX  amino acid sequence at the 3'-end of cDNA encoding the wild-type
XX  protein. Seven possible sequences are given in the specification
XX  for the 11 amino acid repeats (see AAW10050-W10057) expressed by
XX  the recombinant BAL cDNA (see AAT7961). Recombinant BAL, having
XX  the C-terminal repeats (see AAW10058) was expressed in Pichia pastoris
XX  that had been transformed by plasmid pMT301 and cultured at 15-30
XX  deg.C. at not more than 20% dissolved oxygen. This process resulted
XX  in a markedly high yield of BAL enzyme.
XX
XX  Sequence 538 AA:
SQ
XX

Query Match      1.5%; Score 12; DB 17; Length 538;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY  526 YWTNPAKTGDPN 537
    |||||
DB  467 YWTNPAKTGDPN 478

RESULT 41
AAR58981
ID  AAR58981 standard; protein; 546 AA.
XX
XX  AAR58981;
XX
XX  25-MAR-2003 (updated)
XX
XX  03-MAY-1995 (first entry)
XX
XX  Bile salt-stimulated lipase (variant B).
XX
XX  Bile salt-stimulated lipase; BSSL; glycoprotein; esterase;
XX  acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
XX  fat malabsorption; vitamins; dietary lipids; food supplement.
XX
XX  Homo sapiens.
XX
XX  WO9420610-A1.
XX
XX  15-SEP-1994.
XX
XX  25-FEB-1994;  94MO-SE06160.
XX
XX  01-MAR-1993;  93SE-0006686.
XX
XX  04-MAR-1993;  93SE-0006722.
XX
XX  (ASTR ) ASTRA AB.
XX
XX  Blackberg L, Edlund M, Hansson L, Hernell O, Lundberg L,
XX  Stroemyvist M, Toernell C;
XX
XX  WPI; 1994-303218/37.
XX
XX  Bile salt-stimulated lipase variants and coding sequences - used
XX  to produce prods. for treatment of a pathological condition
XX  related to exocrine pancreatic insufficiency
XX
XX  Claim 6; Page 58-60; 102pp; English.
XX
XX  Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
XX  which is highly glycosylated. The N-terminal half of the protein
XX  shows a homology to acetyl cholinesterase and some other esterases.
XX  BSSL variant polypeptides can be used for the treatment of a
XX  pathological condition related to exocrine pancreatic insufficiency
XX  such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
XX  malabsorption of fat soluble vitamins for improvement of utilisation
XX  of dietary lipids, particularly in preterm born infants. They can

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XX 01-MAR-1993; 93SE-0000686.
PR 04-MAR-1993; 93SE-0000722.
XX
XX (ASTR ) ASTRA AB.
XX
PI Blaeckberg L, Edlund M, Hansson L, Harnell O, Lundberg U,
PI Stenqvist M, Toernell U;
DR WPI; 1994-030308/37.
XX
XX Bile salt-stimulated lipase variants and coding sequences - used
PT to produce prods. for treatment of a pathological condition
PT related to exocrine pancreatic insufficiency
XX
PS Claim 8; Page 62-64; 102pp; English.
XX
CC Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
CC which is highly glycosylated. The N-terminal half of the protein
CC shows a homology to acetyl cholinesterase and some other esterases.
CC BSSL variant polypeptides can be used for the treatment of a
CC pathological condition related to exocrine pancreatic insufficiency
CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
CC malabsorption of fat soluble vitamins for improvement of utilization
CC of dietary lipids, particularly in preterm born infants. They can
CC also be used as supplements for infant food formulations. The BSSL
CC variants have maintained catalytic activity but contain less
CC glycosylation sites than native BSSL.
CC (Updated on 25-MAR-2003 to correct FN field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 722 AA;

Query Match 1.5%; Score 12; DB 15; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0243;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDDPN 537
   |||||
DQ 467 YWTFNFAKTGDDPN 478

RESULT 47
AA075107
ID AA075107 standard; Protein; 722 AA.
XX
AC AA075107;
XX
DT 01-FEB-1996 (first entry);
XX
DE Bile salt-activated lipase with 16 C-terminal 11-mer repeats.
XX
KW Bile salt activated lipase; BAL; C-terminal repeat.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Region 539..722
FT /note= "contains 16 copies of imperfect 11mer
FT repeats; the region is made up from a
FT combination of 7 different sequences"
XX
FN JPO7111991-A.
XX
PD 02-MAY-1995.
XX
PF 30-SEP-1993; 93JP-0245079.
XX
PR 30-SEP-1993; 93JP-0245079.
XX
PA (MEIP ) MEIJI MILK PROD CO LTD.
XX
DR WPI; 1995-196318/26.

```

```

DR N-PSDB; AA090579.
XX
XX New recombinant bile salt-activated lipase(s), DNA encoding them
PT and vectors - useful for high level expression of the lipase(s) by
PT fermenter-culturing.
XX
PS Disclosure; Page 10-13; 31pp; Japanese.
XX
CC New lipases are ones in which 1-15 repeats of any of the sequences
CC AA075093-R75105 (encoded by AA090570-090576) are attached to the C-
CC terminus of the bile salt-activated lipase (BAL) of sequence AA075098
CC (encoded by AA090569) and/or in which the amino acid sequence SWTGS
CC (encoded by AA090578) is attached to the N-terminus of the BAL. The
CC recombinant lipases can be produced by fermentation in Pichia
CC pastoris GS 115 transformed host cells. The present sequence
CC is a protein with 16 copies of the undecapeptide imperfect
CC repeats at the BAL C-terminus.
XX
SQ Sequence 722 AA;

Query Match 1.5%; Score 12; DB 16; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.0243;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDDPN 537
   |||||
DQ 467 YWTFNFAKTGDDPN 478

RESULT 48
AA010050
ID AA010050 standard; Protein; 722 AA.
XX
AC AA010050;
XX
DT 28-FEB-1997 (first entry);
XX
DE Human bile salt-activated lipase with C-terminal repeat region.
XX
KW BAL; bile salt-activated lipase; C-terminal repeat; recombinant;
XX high yield; Pichia pastoris GS115; plasmid; transformation; PH1301;
XX fermentation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 539..714
FT /label= repeat region
FT /note= "region of 16 repeated 11 amino acid
FT motifs, see also AA010051-57"
XX
FN JPC8228779-A.
XX
PD 10-SEP-1996.
XX
PF 28-FEB-1995; 95JP-0039869.
XX
PR 28-FEB-1995; 95JP-0039869.
XX
PA (MEIP ) MEIJI MILK PROD CO LTD.
XX
FN WPI; 1996-459145/46.
XX
DR N-PSDB; AA047861.
XX
XX High yield expression of recombinant bile salt activated lipase -
PT in plasmid PH1301 transformed Pichia pastoris GS115
XX
PS Disclosure; Page 9-11; 12pp; Japanese.
XX
CC AA010050 is human mature bile salt-activated lipase (BAL), which has a
CC repeat region consisting of 16 repeats of an 11 amino acid sequence
CC attached to its C-terminus. Seven possible sequences are given in the
CC specification for the 11 amino acid repeat sequence. The invention is

```

CC directed to the recombinant production of BAL at a high yield.  
 CC Recombinant BAL, having the C-terminal repeats (see AAW10051-K10357) was  
 CC expressed in *Pichia pastoris* that had been transformed by plasmid  
 CC PH1301 and cultured at 15-30 deg C. at not more than 20% dissolved  
 CC oxygen. This process resulted in a markedly high yield of BAL enzyme.

XX Sequence 722 AA:

Query Match 1:5% Score 12; DB 17; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 0.0043;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFPAKTGDPN 537  
 DB 467 YWTFPAKTGDPN 478

#### RESULT 49

AA898926 standard; Protein: 722 AA.

AC AA898926;

DT 31-OCT-1996 (first entry);

XX Human bile salt-activated lipase.

XX Bile salt-activated lipase; BAL; cholesterol; transgenic animal;

KW milk; hyperlipoproteinaemia; hypercholesterolaemia; atherosclerosis;

XX pancreatitis; therapy; drug delivery.

OS Homo sapiens.

Key	Location/Qualifiers
FT Region	539..722
FT	/label=C-tail
FT Region	539..549
FT	/label=Proline-rich_region
FT Region	550..560
FT	/label=Proline-rich_region
FT Region	561..571
FT	/label=Proline-rich_region
FT Region	572..582
FT	/label=Proline-rich_region
FT Region	583..593
FT	/label=Proline-rich_region
FT Region	594..604
FT	/label=Proline-rich_region
FT Region	605..615
FT	/label=Proline-rich_region
FT Region	616..626
FT	/label=Proline-rich_region
FT Region	627..637
FT	/label=Proline-rich_region
FT Region	638..648
FT	/label=Proline-rich_region
FT Region	649..659
FT	/label=Proline-rich_region
FT Region	660..670
FT	/label=Proline-rich_region
FT Region	671..681
FT	/label=Proline-rich_region
FT Region	682..692
FT	/label=Proline-rich_region
FT Region	693..703
FT	/label=Proline-rich_region
FT Region	704..714
FT	/label=Proline-rich_region

XX WO9617054-A1.  
 XX 06-JUN-1996.  
 XX

PF 01-DEC-1995; 95MO-0515647.  
 XX  
 XX 07-JUN-1995; 95US-0492262.  
 XX 01-DEC-1994; 94US-0347718.  
 PR 07-JUN-1995; 95US-0479160.  
 XX

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PI Tang JUN, Wang C;

XX WPI; 1996-277774/28.

XX Reducing intestinal absorption of cholesterol - by administering a  
 PT C-tail protein comprising the carboxy region of human bile salt  
 PT lipase or deriv.  
 XX

XX Claim 1: Page 79-81; 95pp; English.

XX The human bile salt-activated lipase (BAL) mature protein (AA898926)  
 CC includes a carboxy-terminal tail contg. 16 copies of a proline-  
 CC rich consensus repeat sequence (AA898928). The C-tail can compete  
 CC with BAL for binding to receptors on the intestinal surface  
 CC to inhibit uptake of cholesterol. It can be used to treat  
 CC hyperlipoproteinaemia and hypercholesterolaemia and associated  
 CC disease states and as a drug delivery agent. The C-tail can be  
 CC obtd. by protease digestion of natural BAL, expressed in eukaryotic  
 CC host cells (see also AAT34787), or secreted in the milk of  
 CC transgenic animals.

XX Sequence 722 AA;

Query Match 1:5% Score 12; DB 17; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 0.0043;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFPAKTGDPN 537  
 DB 467 YWTFPAKTGDPN 478

#### RESULT 50

AB804676 standard; Protein: 722 AA.

AC AB804676;

DT 06-MAR-2002 (first entry)

XX Human milk bile salt-stimulated lipase (BSL) protein SEQ ID NO:2.

XX Human; milk; bile salt-stimulated lipase; BSL; hypotensive; cardiant;  
 XX antidiabetic; nephrotropic; acetylcholinesterase inhibitor; food;  
 XX pharmaceutical; nutritional; hypertension; myocardial infarction;  
 KW left ventricular systolic dysfunction; diabetes mellitus;  
 KW progressive renal impairment; renal failure.

XX Homo sapiens.

XX WO200101368-A2.

XX 01-NOV-2001.

XX 19-APR-2001; 2001-WO-US12776.

XX 21-APR-2000; 2000US-19968CP.

XX (MOMS) VCN SANTO TECHNOLOGY LLC.

XX Kobzeff CM;

XX WPI; 2002-066434/09.

XX N-PSDB; AB804403.  
 XX



PT Producing the hypotensive tripeptide Val Pro Pro for use in  
 PT pharmaceutical, nutritional and food compositions, comprises first  
 PT producing recombinant Bile Salt Stimulated Lipase  
 XX  
 PS Disclosure, Page 26-29; 29pp; English.  
 XX  
 CC The present invention describes a method of producing polypeptides  
 CC containing VPP (Val Pro Pro). The method comprises: (a) obtaining a  
 CC recombinant expression vector containing a nucleic acid encoding  
 CC recombinant bile salt-stimulated lipase (BSSL) polypeptide;  
 CC (b) inserting the recombinant expression vector into a host cell;  
 CC (c) growing the host cell to express a protein encoded by the  
 CC recombinant vector; and (d) purifying the recombinant protein from the  
 CC host cell. BSSL has hypotensive, cardiant, antidiabetic and  
 CC nephrotropic activities, and is an acetylcholinesterase inhibitor. The  
 CC method is used to produce VPP which can be used in pharmaceutical, food  
 CC and nutritional compositions. The VPP produced by the method can be used  
 CC in the diagnosis, treatment and prophylaxis of hypertension and related  
 CC conditions such as left ventricular systolic dysfunction, myocardial  
 CC infarction, diabetes mellitus and progressive renal impairment/failure.  
 CC The present sequence represents human milk BSSL. The carboxy-terminal  
 CC region of human milk BSSL contains 16 proline-rich repeating units of  
 CC :1 amino acid, and each repeating unit contains the tripeptide VPP  
 CC. Taking the protein particularly advantageous for use in the present  
 CC invention.  
 XX  
 SQ Sequence 722 AA:  
 Query Match 1.5%; Score 12; DB 23; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 0.0043;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 526 YWTFNFAKTGDPN 537  
 |||||  
 DB 467 YWTFNFAKTGDPN 478  
 RESULT 51  
 AA009894  
 ID AA009894 standard; Protein: 722 AA.  
 AC  
 XX AA009894;  
 XX  
 CT 26-FEB-2002 (first entry)  
 XX  
 DE Bile Salt Stimulated Lipase (BSSL).  
 XX  
 KW Human; BSSL; hypotensive; cardiant; antidiabetic; nephrotropic;  
 KW bile salt stimulated lipase; antihypertensive tripeptide VPP; food;  
 KW transgenic animal; milk; pharmaceutical; nutritional; hypertension;  
 KW myocardial infarction; left ventricular systolic dysfunction;  
 KW diabetes mellitus; renal failure.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200181366-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 19-APR-2001; 2001WO-US12672.  
 XX  
 PR 21-APR-2000; 2000US-199675P.  
 XX  
 PA (MONS ) MONGSANTO TECHNOLOGY LLC.  
 XX  
 PI Kobzeff JM;  
 XX  
 DR MPI: 2002-041393/05.  
 XX  
 DR N-PSDB; AAS18538.  
 XX  
 PT Producing anti-hypertensive tripeptide, VPP, useful in pharmaceutical,  
 PT nutritional and food compositions, comprises purifying the polypeptide  
 PT from bile salt stimulated lipase expressed in the milk of a transgenic

PT nonhuman mammal  
 XX  
 PS Disclosure, Page 22-25; 25pp; English.  
 XX  
 CC The invention relates to a method of producing a polypeptide containing  
 CC antihypertensive tripeptide VPP (Val-Pro-Pro). The method comprises:  
 CC (a) collecting milk from a transgenic non-human mammal where the animal  
 CC has been engineered to express and secrete a recombinant Bile Salt  
 CC Stimulated Lipase (BSSL) polypeptide into their milk; and (b) purifying  
 CC the polypeptide from the milk. The method is used for production of a  
 CC polypeptide containing VPP which can be used in pharmaceutical, food and  
 CC nutritional compositions. The VPP produced can be used in the diagnosis,  
 CC treatment and prophylaxis of hypertension and related conditions such as  
 CC left ventricular systolic dysfunction, myocardial infarction, diabetes  
 CC mellitus and progressive renal impairment/failure. The method allows  
 CC industrial scale production of polypeptides containing VPP compared to  
 CC the low amounts present in the prior art fermentation of cow's milk.  
 CC Bile Salt Stimulated Lipase has a carboxy-terminal region which contains  
 CC 16 repeats of VPP and accumulates to 1% of the total milk protein. The  
 CC present sequence represents the amino acid sequence of bile salt  
 CC stimulated lipase.  
 XX  
 SQ Sequence 722 AA:  
 Query Match 1.5%; Score 12; DB 23; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 0.0043;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 526 YWTFNFAKTGDPN 537  
 |||||  
 DB 467 YWTFNFAKTGDPN 478  
 RESULT 52  
 ABP41901  
 ID ABP41901 standard; Protein: 725 AA.  
 AC  
 XX ABP41901;  
 XX  
 CT 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HTPFW87, SEQ ID NO:3033.  
 XX  
 DE Human ovarian antigen; ovary; ovarian; breast; cancer; tumor;  
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumor;  
 KW ovarian cancer; breast cancer; tumor; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200200677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 07-JUN-2001; 2001WO-US18569.  
 XX  
 PR 07-JUN-2000; 2000US-209467P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Birse CE, Rosen CA;  
 XX  
 DR WP1: 2002-147878/19.  
 XX  
 DR N-PSDB; ABO54978.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.

FT ovarian cancer), immune disorders, cardiovascular disorders and  
FT neurological diseases -  
PS Claim 11; SEQ ID NO 3033; 2222bp; English.  
XX  
CC The invention relates to 2:75 novel human ovarian antigens (ABP4-054-  
CC ABP4328) and to cDNAs encoding them (AB054131-AB054351), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovarian and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumors of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility), disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysendometriosis, endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic  
CC shock syndrome, inflammatory conditions (e.g., mastitis, gonorrhea and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents a human ovarian antigen of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIG  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 735 AA:  
  
Query Match 1.5%; Score 12; DB 23; Length 735;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 526 WTNFAKTGDPN 537  
DB 491 WTNFAKTGDPN 502  
  
RESULT 53  
AA:14311  
ID AAR4311 standard; Protein; 742 AA.  
XX  
AC AAR4311;  
XX  
DT 13-JAN-1992 (first entry)  
XX  
DE Human milk bile-salt activated lipase.  
XX  
KM premature baby; fat absorption; baby food.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 559..734  
FT /label= repeat\_region  
FT /note= "16 repeats of similar 11 amino acid motif"  
FT Peptide 1..20  
FT /label= signal\_peptide  
FT Modified-site 207  
FT /label= N-linked glycosylation site  
FT /note= "potential"  
FT Active-site 214  
FT /label= active site serine  
XX  
FN W09115234-A.

XX  
PD 17-OCT-1991.  
XX  
EF 04-APR-1991; 91WO-US02328.  
XX  
XX 12-JUN-1990; 90US-0537426.  
PR 04-APR-1990; 90US-0504635.  
XX  
PA (OKLA-) OKLAHOMA MED RES FO.  
XX  
FI Tang JLN, Wang CS;  
XX  
DR WPI: 1991-324964/44.  
DR N-PSDB: AA014186.  
XX  
PT New recombinant bile salt activated lipase(s) - used in improving  
PT infant nutrition, to treat diseases concerned with lipid  
PT digestion and as probes for studying BSL or related lipase(s);  
XX  
XX Claim 15; Fig 2; 36pp; English.  
XX  
XX This sequence is deduced from a combination of two cDNA clones  
XX (G10-2 and G10-3) isolated from a lactating human breast tissue  
XX cDNA library. Screening was with probes based on the 61-residue  
XX amino acid sequence of the N-terminal cleavage fragment of BSL.  
XX The C-terminal region consists of 16 similar 11 amino acid repeats;  
XX about a third of the residues in this region are proline. Human BSL  
XX is a glycoprotein and a potential N-glycosylation site has been  
XX identified.  
XX  
SQ Sequence 742 AA:  
  
Query Match 1.5%; Score 12; DB 12; Length 742;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 526 WTNFAKTGDPN 537  
DB 487 WTNFAKTGDPN 498  
  
RESULT 54  
AA:98927  
ID AAR98927 standard; Protein; 742 AA.  
XX  
AC AAR98927;  
XX  
DT 31-OCT-1996 (first entry)  
XX  
DE Human bile salt-activated lipase precursor.  
XX  
KM Bile salt-activated lipase; BSL; cholesterol; transgenic animal;  
KM milk; hyperlipoproteinaemia; hypercholesterolaemia; atherosclerosis;  
KM pancreatitis; therapy; drug delivery.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..26  
FT /label= sig\_peptide  
FT Modified-site 187  
FT /label= N-glycosylation site  
FT Modified-site 194  
FT /label= N-glycosylation site  
FT Region 559..742  
FT /label= C-tail  
FT Region 559..569  
FT /label= proline-rich\_region  
FT Region 570..580  
FT /label= proline-rich\_region  
FT Region 581..591  
FT /label= proline-rich\_region  
FT Region 592..602

FT /label= Proline-rich\_region  
 FT 603..623  
 FT /label= Proline-rich\_region  
 FT 614..624  
 FT /label= Proline-rich\_region  
 FT 625..635  
 FT /label= Proline-rich\_region  
 FT 636..646  
 FT /label= Proline-rich\_region  
 FT 647..657  
 FT /label= Proline-rich\_region  
 FT 658..668  
 FT /label= Proline-rich\_region  
 FT 669..679  
 FT /label= Proline-rich\_region  
 FT 680..690  
 FT /label= Proline-rich\_region  
 FT 691..701  
 FT /label= Proline-rich\_region  
 FT 702..712  
 FT /label= Proline-rich\_region  
 FT 713..723  
 FT /label= Proline-rich\_region  
 FT 724..734  
 FT /label= Proline-rich\_region

PN W09617054-A1.  
 PD 06-JUN-1996.  
 PF 01-DEC-1995; 95MO-US15647.  
 PR 07-JUN-1995; 95US-0482262.  
 PR 01-DEC-1994; 94US-0347718.  
 PR 07-JUN-1995; 95US-0479162.  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX Tang JCN, Wang C;  
 XX WPI; 1996-277774/28.  
 DR N-PCDB; AA734787.

XX Reducing intestinal absorption of cholesterol - by administering a C-tail protein comprising the carboxy region of human bile salt lipase or deriv.

XX Disclosure; Page 82-84; 99pp; English.

XX The human bile salt-activated lipase (BAL) precursor (AA98927) includes a carboxy-terminal tail consisting of a proline-rich consensus repeat sequence (AA98928). The C-tail can complete with BAL for binding to receptors on the intestinal surface to inhibit uptake of cholesterol. It can be used to treat hyperlipoproteinaemia and hypercholesterolaemia and associated disease states and as a drug delivery agent. BAL or its C-tail can be obtained by protease digestion of natural BAL expressed in eukaryotic host cells (see also AA134787), or secreted in the milk of transgenic animals.

XX Sequence 742 AA;

Query Match 1.5%; Score 12; DB 17; Length 742;  
 Best Local Similarity 100.0%; Pred. No. 0.0044;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537  
 |||||  
 DB 487 YWTFNFAKTGDPN 488

RESULT 55  
 AA945189.

ID AA945189 standard; Protein; 744 AA.  
 XX  
 AC AA945189;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 27-JUN-1994 (first entry)  
 DE BSSL/CEL.  
 XX  
 KM BSSL: biologically functional bile salt stimulated lipase; CE; carboxyl ester lipase; hybridisation; milk protein; transgenic; infant milk substitute; oral; specific; lipolysis; vitamin; bile; lipid malabsorption; cystic fibrosis; chronic pancreatitis; digestion.  
 XX  
 CS Homo sapiens.  
 XX  
 PN W09325669-A1.  
 PD 23-DEC-1993.  
 PF 03-JUN-1993; 93MO-SE00515.  
 PR 11-JUN-1992; 92SE-0001809.  
 PR 12-JUN-1992; 92SE-0001826.  
 PR 03-JUL-1992; 92SE-0002088.  
 PR 19-MAR-1993; 93SE-0000902.  
 PA (ASTRA) ASTRA AB.  
 XX  
 PE Bjurell KG, Carlsson PN, Enerback CSM, Hansson SU, Jaderberg JFF, Nilsson CA, Tornell UBF, Toerne-I UBF, Enerback CSM;  
 PI WPI; 1994-007527/01.  
 DR N-PCDB; AA054222.

XX DNA encoding bile salt-stimulated lipase/carboxyl ester lipase - expressed by transgenic non-human mammals and used as human milk substitute, contains intron sequences  
 FT  
 PS Claim 1; Page 43-51; 76pp; English.

XX The primers (AA054223-28) are used to amplify fragments of the BSSL / CEU gene, (AA054222), which encodes a bile salt-stimulated lipase / carboxyl ester lipase which when expressed by transgenic animals can be used as a human milk substitute. The BSSL is designed to pass through the stomach and is activated in the small intestine. As it has a broad substrate specificity it can mediate the complete digestion of most dietary lipids.  
 CC (updated on 25-MAR-2003 to correct PN field.)  
 CC  
 SC Sequence 744 AA;

Query Match 1.5%; Score 12; DB 15; Length 744;  
 Best Local Similarity 100.0%; Pred. No. 0.0044;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 526 YWTFNFAKTGDPN 537  
 |||||  
 DB 489 YWTFNFAKTGDPN 500

RESULT 56  
 AA920398  
 ID AA920398 standard; Protein; 745 AA.  
 XX  
 AC AA920398;  
 XX

DT 24-MAR-1992 (first entry)  
 XX  
 DE Bile-salt stimulated lipase.  
 XX

```

KW BSSL; fat malabsorption.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "signal peptide"
FT 24..745
FT Peptide /note= "mature peptide"
XX
XX MO9119923-A.
XX
XX -2-DEC-1991.
XX
XX 30-MAY-1991: 93WO-SE00381.
XX
XX 01-JUN-1990: 90SE-0001965.
XX
XX (ASTR ) ASTRA AB.
XX
XX Bjursett G, Blackberg L, Carlsson P, Enerback S, Hernell O,
XX Nilsson U, Olivecrona T;
XX WPL 1992-07429/C1.
XX
XX N-PSDB; AA02052.
XX
XX New human bile-salt stimulated lipase derivs. - useful to treat
XX pathological conditions related to chronic pancreatitis, cystic
XX fibrosis, etc.
XX
XX Claim 1; Fig 2: 54pp; English.
XX
XX The amino acid sequence is that of bile-salt stimulated lipase
XX (BSSL) which may be produced in large ants. through the use of
XX recombinant techniques. BSSL is used in pharmaceutical compns.
XX useful for the treatment of a condition related to exocrine
XX pancreatic insufficiency, cystic fibrosis, chronic pancreatitis,
XX fat malabsorption of any etiology, malabsorption of fat soluble
XX vitamins, fat malabsorption due to physiological reasons, e.g. in
XX new-born infants, etc. BSSL is suitable for oral admin.
XX
SQ Sequence 745 AA;
XX
XX Query Match 1.5%; Score 12; DB 13; Length 745;
XX Best Local Similarity 100.0%; Pred. No. 0.0044;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 526 YWTFNFAKTGDPK 537
XX |||||
XX 490 YWTFNFAKTGDPK 501
XX
XX
XX RESULT 57
XX AAR58980
XX ID AAR58980 standard; protein: 745 AA.
XX
XX AAR58980:
XX
XX 25-MAR-2003 (updated;
XX DT 03-MAY-1995 (first entry)
XX
XX Bile salt-stimulated lipase.
XX
XX Bile salt stimulated lipase; BSSL; glycoprotein; esterase;
XX acetyl; cholinesterase; cystic fibrosis; chronic pancreatitis;
XX fat malabsorption; vitamins; dietary lipids; food supplement.
XX
XX Homo sapiens.
XX
XX MO9420610-A.
XX
XX 15-SEP-1994.
XX
XX

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FH 25-FEB-1994; 94WO-SE00160.
XX
XX 01-MAR-1993; 93SE-C000636.
XX
XX 04-MAR-1993; 93SE-0000722.
XX
XX (ASTR ) ASTRA AB.
XX
XX Blackberg L, Edlund M, Hansson L, Hernell O, Lundberg L;
XX Stromqvist M, Toernell J;
XX WPL 1994-003018/37.
XX
XX N-PSDB; AA083221.
XX
XX Bile salt-stimulated lipase variants and coding sequences - used
XX to produce prods. for treatment of a pathological condition
XX related to exocrine pancreatic insufficiency
XX
XX Disclosure; Page 52-54; 102pp; English.
XX
XX Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
XX which is highly glycosylated. The N-terminal half of the protein
XX shows a homology to acetyl cholinesterase and some other esterases.
XX BSSL variant polypeptides can be used for the treatment of a
XX pathological condition related to exocrine pancreatic insufficiency
XX such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
XX malabsorption of fat soluble vitamins for improvement of utilisation
XX of dietary lipids, particularly in preterm born infants. They can
XX also be used as supplements for infant food formulations.
XX (updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 745 AA;
XX
XX Query Match 1.5%; Score 12; DB 15; Length 745;
XX Best Local Similarity 100.0%; Pred. No. 0.0044;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 526 YWTFNFAKTGDPK 537
XX |||||
XX 490 YWTFNFAKTGDPK 501
XX
XX
XX RESULT 58
XX AAR99257
XX ID AAR99257 standard; Protein: 745 AA.
XX
XX AAR99257:
XX
XX 05-DEC-1996 (first entry)
XX
XX Human bile salt-stimulated lipase.
XX
XX Bile salt-stimulated lipase; BSSL; lipid digestion; fat absorption;
XX infant feed; Pichia pastoris.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FH Peptide 1..23
XX FT /label= Sig_peptide
XX FT 24..745
XX FT Protein /label= Mat protein
XX FT /note= "Claim 5"
XX
XX Region 536..546
XX FT /label= Repeat_unit
XX FT 547..557
XX FT /label= Repeat_unit
XX FT 558..568
XX FT /label= Repeat_unit
XX FT 569..579
XX FT /label= Repeat_unit
XX FT 580..590
XX FT /label= Repeat_unit
XX

```

FT Region 591..601  
 FT /label= Repeat\_unit  
 FT Region 602..612  
 FT /label= Repeat\_unit  
 FT Region 613..623  
 FT /label= Repeat\_unit  
 FT Region 624..634  
 FT /label= Repeat\_unit  
 FT Region 635..645  
 FT /label= Repeat\_unit  
 FT Region 646..656  
 FT /label= Repeat\_unit  
 FT Region 657..667  
 FT /label= Repeat\_unit  
 FT Region 668..678  
 FT /label= Repeat\_unit  
 FT Region 679..689  
 FT /label= Repeat\_unit  
 FT Region 690..700  
 FT /label= Repeat\_unit  
 FT Region 701..711  
 FT /label= Repeat\_unit

XX GB2233085-A.

XX 25-SEP-1996.

XX 22-MAR-1995; 96GB-0006023.

XX 24-MAY-1995; 95SE-0001933.

XX 23-MAR-1995; 95IN-0000351.

XX (ASTR ) ASTRA AB.

XX Das G;

XX WPI: 1986-415384/42.

XX N-PSDB; AA135253.

XX New recombinant DNA coding for bile salt stimulated lipase and

XX secretory signal sequence - controlled by Pichia pastoris promoter

XX allows prodn. of correctly processed lipase in P. pastoris, useful

XX as additive for infant feeds to improve fat absorption

XX Claim 2; Page 27-29; 38pp; English.

XX Human bile salt-stimulated lipase (BSSL; EC-3.1.1.1) plays a

XX critical role in the digestion of milk lipids in breast-fed infants

XX and is believed to be the major rate-limiting factor in fat

XX absorption. Partic. in premature infants. Recombinant BSSL

XX can be produced cost-effectively, in properly processed form

XX in Pichia pastoris host cells utilizing vectors that incorporate

XX a BSSL nucleic acid (see also AA135250), an appropriate signal

XX sequence and pref. the P. pastoris methanol oxidase promoter.

XX The BSSL is useful in infant feed formulations.

XX Sequence 745 AA;

XX

Query Match 1:5%; Score 12; DB 17; Length 745;  
 Best Local Similarity 100.0%; Pred.No. 0.0044;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 YWTFNFAKTGDPN 537  
 |||||  
 Db 490 YWTFNFAKTGDPN 501

RESULT 59

AA132168

ID AA132168 standard; Protein; 745 AA.

XX AC AA132168;

XX

DT 01-FEB-2000 (first entry)

XX Human bile salt-stimulated lipase.

XX Bile salt-stimulated lipase; BSSL; human; transgenic sheep;

XX transgenic mammal; milk; pancreatic insufficiency; lipid;

XX preterm infant; nutrition; cystic fibrosis.

XX Homo sapiens.

XX Key

XX Reptide

XX Protein

XX Location/Qualifiers

XX 1..23

XX /note= "signal peptide"

XX 24..745

XX /note= "mature protein, specifically claimed in

XX Claim 10"

XX WO954443-A1.

XX 29-OCT-1999.

XX 21-APR-1999; 99WO-SE00648.

XX 22-APR-1999; 98SE-0001424.

XX (ASTR ) ASTRA AB.

XX (PPLT-) PPLTHERAPEUTICS.

XX Dairyville N. Lundberg L. Stromqvist M;

XX WPI: 1989-634002/54.

XX N-PSDB; AA220289; AA220300.

XX New recombinant human bile salt-stimulated lipase produced by

XX transgenic mammals, used for treating diseases related to exocrine

XX pancreatic insufficiency and improving utilization of dietary lipids in

XX preterm born infants

XX Claim 9; Page 56-58; 67pp; English.

XX The present sequence represents human bile salt-stimulated lipase

XX (BSSL). The invention relates to human recombinant BSSL obtainable

XX from transgenic sheep. The invention also relates to transgenic

XX sheep whose germ cells and somatic cells contain a recombinant

XX nucleotide molecule encoding BSSL. The nucleotide sequence can be

XX introduced as a BSSL genomic sequence including introns (see

XX AA220299) or as cDNA (see AA220300). Methods are provided for

XX producing the transgenic animals, and methods for producing human

XX BSSL derived from the transgenic animals. The recombinant BSSL,

XX produced in the sheep's milk, is glycosylated and fully active.

Query Match 1:5%; Score 12; DB 20; Length 745;  
 Best Local Similarity 100.0%; Pred.No. 0.0044;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 526 YWTFNFAKTGDPN 537  
 |||||  
 Db 490 YWTFNFAKTGDPN 501

RESULT 60

AA08201

ID AA08201 standard; Protein; 745 AA.

XX AC AA08201;

XX 04-DEC-2000 (first entry)



XX WPI: 1998-297929/26.  
 DR N-PSDB; AAV40764.  
 XX  
 PT New nucleic acid encoding carboxylesterase(s) from fleas - useful.  
 PT e.g. in vaccines, for preventing infestation by haematophagous  
 PT ectoparasites, particularly on cats and dogs  
 XX  
 PS Claim 1: Page 200-203; 230pp; English.  
 CC This sequence is the flea esterase protein, nfe:01590, of the invention.  
 CC When administered to animals, the protein induces a protective immune  
 CC (antibody) response against carboxylesterase (CE), so they, or  
 CC compositions containing CE proteins, are used, therapeutically or as  
 CC vaccines, to protect particularly mammals and birds, specifically cats  
 CC and dogs, against haematophagous ectoparasite infestation (HEP).  
 CC Specifically fleas. More generally the compositions can be used to treat  
 CC arthropods generally, including pests of agricultural crops, trees,  
 CC stored goods etc., also those that are vectors for identification or  
 CC the DNA can be used as probes and primers for identification or  
 CC production of nucleic acid. Antibodies against the protein can be used  
 CC for passive immunisation, to screen expression libraries, to isolate the  
 CC protein and to target cytotoxic compounds to HEP. The compounds  
 CC containing CE are effective against both adult and larval stages; they  
 CC target CEs, including juvenile hormone, that are involved in development,  
 CC metamorphosis, feeding, digestion and reproduction.  
 CC  
 SC Sequence 530 AA;  
 Query Match 1.3%; Score 11; DB 19; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 0.036;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCLYLNIVP 135  
 DB 81 EDCLYLNIVP 91  
 RESULT 63  
 ID ABB68593 standard; Protein: 1016 AA.  
 XX  
 AC ABB68593;  
 XX  
 DT 26-MAR-2002 (first entry);  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 32571.  
 XX  
 KM Drosophila developmental biology; cell signalling; insecticide;  
 KM pharmaceutical.  
 XX  
 CS Drosophila melanogaster.  
 XX  
 PN W020017042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEXE ) FE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI, 2001-656860/75.  
 DR N-PSDB; ABL12696.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -

PS Disclosure; SEQ ID NO 32571; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (AB857737-AB872072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SC Sequence 1016 AA;  
 Query Match 1.3%; Score 11; DB 22; Length 1016;  
 Best Local Similarity 100.0%; Pred. No. 0.066;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCLYLNIVP 135  
 DB 59 EDCLYLNIVP 69  
 RESULT 64  
 ID ABB61204 standard; Protein: 537 AA.  
 XX  
 AC ABB61204;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 10404.  
 XX  
 KM Drosophila developmental biology; cell signalling; insecticide;  
 KM pharmaceutical.  
 XX  
 CS Drosophila melanogaster.  
 XX  
 PN W020017042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEXE ) FE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI, 2001-656860/75.  
 DR N-PSDB; ABL05307.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 PS Disclosure; SEQ ID NO 10404; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL16176-ABL30511) and the encoded proteins  
 CC (AB857737-AB872072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 537 AA;  
 SQ Query Match 1.2%; Score 10; DB 22; Length 537;  
 Best Local Similarity 100.0%; Pred. No. 0.41;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 2y 203 NYRLOTIGSF 212  
 178 NYRLOTIGSF 167  
 Db  
 RESULT 65  
 AAO17545  
 ID AAO17545 standard; Protein; 92 AA.  
 AC AAO17545;  
 XX  
 DT 19-JUN-2002 (first entry)  
 XX  
 DE Human carboxylesterase-like enzyme #2.  
 XX  
 KW Human; carboxylesterase; organophosphorous compound; cancer;  
 KM inflammation; chronic obstructive pulmonary disease; COPD; cyclostatic;  
 KM extracellular matrix degradation; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200230969-A2.  
 XX  
 PD 18-APR-2002.  
 XX  
 PF 11-OCT-2002; 2001WO-EP11758.  
 XX  
 PR 13-OCT-2003; 2000US-239898P.  
 PR 31-AUG-2001; 2001US-315947P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 ZI Zhu Z;  
 XX  
 PS MPI; 2002-416856/44.  
 DR N-PSDB; AAU46412.  
 XX  
 27 New human carboxylesterase-like enzyme polypeptide, the regulation of  
 27 which is useful for treating diseases due to organophosphorus  
 27 intoxication, cancer or chronic obstructive pulmonary disease  
 XX  
 PS Claim 25; Fig 5; 92pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of a  
 CC human carboxylesterase-like enzyme. The sequences can be used in the  
 CC preparation of a medicament for modulating the activity of a  
 CC carboxylesterase-like enzyme in a disease due to organophosphorus  
 CC intoxication, cancer or chronic obstructive pulmonary disease (COPD). The  
 CC present sequence is a human carboxylesterase-like enzyme of the  
 CC invention.  
 XX  
 SQ Sequence 92 AA;  
 Query Match 1.1%; Score 9; DB 23; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 0.92;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCVLYNTY 133  
 29 EDCVLYNTY 36  
 Db  
 RESULT 66  
 ABP69056  
 ID ABP69056 standard; Protein; 266 AA.

AC ABP69056;  
 XX  
 DT 20-JAN-2003 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 1-03.  
 XX  
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 KW arthritis; cytostatic; immunomodulator; neotropic; neuroprotective;  
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatocologic;  
 KW haemostatic; vulnery; fungicide; antibacterial; virocid; protozoacide;  
 KW antiarthritic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200270539-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 05-MAR-2002; 2002WO-US05095.  
 XX  
 PR 05-MAR-2001; 2001US-0799451.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Zhou P, Goodrich RM, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,  
 PI Wehrman T, Kang J, Wang D, Drmanac RT.  
 XX  
 DR MPI; 2002-759812/82.  
 DR N-PSDB; ABZ11273.  
 XX  
 27 New polynucleotides comprising sequences assembled from expressed  
 27 sequence tags (ESTs), useful for treating cell-proliferative,  
 27 neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
 27 platelet or coagulation disorders  
 XX  
 PS Claim 9; SEQ ID NO 1103; 1012pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (I) comprising a  
 CC nucleotide sequence selected from any of 948 sequences  
 CC (ABZ1119-ABZ12066) or their mature protein coding portion, active domain  
 CC coding protein or complementary sequences. The polynucleotides are useful  
 CC for identifying expressed genes or for physical mapping of human genome.  
 CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular  
 CC weight markers, as a food supplement, for generating antibodies, in  
 CC medical imaging, screening and diagnostic assays and for treating  
 CC cell-proliferative disorders (cancer), neurodegenerative diseases  
 CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
 CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
 CC disorders, platelet or coagulation disorders, wound, burns, incision,  
 CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
 CC parasitic), arthritis, etc.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pat\_sequences.  
 XX  
 SQ Sequence 266 AA;  
 Query Match 1.1%; Score 9; DB 23; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCVLYNTY 133  
 148 EDCVLYNTY 156  
 Db  
 RESULT 67  
 ABB61993  
 ID ABB61993 standard; Protein; 507 AA.



```

XX AC ABB61993;
XX XX
XX DT 26-MAR-2002 (first entry)
XX XX
DE Drosophila melanogaster polypeptide SEQ ID NO 12771.
XX XX
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX XX
XX OS Drosophila melanogaster.
XX XX
XX PN WO200171042-A2.
XX XX
XX PD 27-SEP-2001.
XX XX
XX PF 23-MAR-2001; 2001WO-US09231.
XX XX
XX PR 23-MAR-2001; 2000US-191637P.
XX PR 11-JUL-2001; 2000US-0614150.
XX XX
XX PA (PEKE ) FE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL01892.
XX XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX XX
XX PS Disclosure; SEQ ID NO 12771; 21pp + Sequence Listing; English.
XX XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
XX CC sequences (AB101840-AB16175) and the encoded proteins
XX CC (ABBS7737-ABBS7072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pat_sequences.
XX CC
XX SQ Sequence 507 AA;

Query Match 1.1%; Score 9; DB 22; Length 507;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PWMVYTHGG 176
Db 118 PWMVYTHGG 126

RESULT 68
ABB57789
ID ABB57789 standard; Protein; 541 AA.
XX
XX AC ABB57789;
XX XX
XX DT 26-MAR-2002 (first entry)
XX XX
XX DE Drosophila melanogaster polypeptide SEQ ID NO 159.
XX XX
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX XX
XX OS Drosophila melanogaster.
XX OS
XX PI WO200171042-A2.
XX PR

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XX XX
XX PD 27-SEP-2001.
XX XX
XX PF 23-MAR-2001; 2001WO-US09231.
XX XX
XX PR 23-MAR-2001; 2000US-191637P.
XX PR 11-JUL-2001; 2000US-0614150.
XX XX
XX PA (PEKE ) FE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL01892.
XX XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX XX
XX PS Disclosure; SEQ ID NO 159; 21pp + Sequence Listing; English.
XX XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
XX CC sequences (AB101840-AB16175) and the encoded proteins
XX CC (ABBS7737-ABBS7072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pat_sequences.
XX CC
XX SQ Sequence 541 AA;

Query Match 1.1%; Score 9; DB 22; Length 541;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 PWMVYTHGG 176
Db 104 PWMVYTHGG 112

RESULT 69
AAV33146
ID AAV33146 standard; Protein; 543 AA.
XX
XX AC AAV33146;
XX XX
XX DT 16-NOV-1999 (first entry)
XX XX
XX DE Rabbit liver carboxylesterase protein fragment.
XX XX
XX KW Carboxylesterase; rabbit; liver; tumour cell; chemotherapy; prodrug;
XX KW disease-specific; responsive promoter; CRF-11; APC; resection;
XX KW recurrence; inhibition; bone marrow cell.
XX XX
XX OS Oryctolagus cuniculus.
XX OS
XX PN WO9942593-A1.
XX XX
XX PD 26-AUG-1999.
XX XX
XX PF 12-FEB-1999; 99WO-US03171.
XX XX
XX PR 19-FEB-1998; 98US-0075258.
XX XX
XX PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX XX
XX PI Danks MK, Potter PM, Houghton PJ;
XX XX
XX DR WPI; 1999-540311/45.

```

**New Carboxy-esterase polypeptide for treatment of tumors -**

Claim 3; Page 63-65; 70pp; English.

This invention describes a novel rabbit carboxylesterase polypeptide (**I**) capable of metabolizing a chemotherapeutic prodrug and its inactive metabolites into an active drug. The invention also describes a composition comprising (**i**) and a disease-specific responsive promoter. This composition is useful for sensitizing tumor cells to a chemotherapeutic prodrug (preferably CRT-III or APC) by transfecting into tumor cells, and contacting the sensitized cells with a chemotherapeutic prodrug to inhibit growth of the tumor cells. The composition can also be administered to the site of tumor resection to inhibit tumor recurrence, and be administered to bone marrow cells to remove tumor cells. The products of the invention are useful for identifying drugs that are inactivated by a carboxylesterase enzyme, and are also useful for identifying compounds containing a COOR ester linkage that are activated by a carboxylesterase enzyme. This sequence represents a rabbit liver carboxylesterase fragment which is described in the method of the invention.

Sequence    543 AA:

Query March                 118; Score 9; DS 20; Length 543;  
Best Local Similarity      100.0%; Pred. No. 4.6;  
Matches    9; Conservative    0; Mismatches    0; Indels    0; Gaps    0  
  
CY          :25 EDCYXENLY I33  
             |||||||  
Cb          :14 EDCLYNLY I22

RESULT 70

AAL018272  
ID AAL018272 standard: protein; 544 AA.  
XX  
AC AAO18272:  
DT  
D? 26-SEP-2002 (first entry)  
XX  
DE Recombinant porcine liver esterase protein subunit.  
KM XX P19: esterase; enzyme; PE3; carboxylic acid; ester; organic synthesis;  
KW pro-stereogenic compound.  
XS  
CS Sus scrofa.  
OS Synthetic.  
PN WC200248322-A2.  
PD 20-JUN-2002.  
PF 06-DEC-2002; 20CIMO-EPI4338.  
PR 12-DEC-2000; 20GODE-I061864.  
PA (DECS ) DEUSSA AG.  
Z1 Bornscheuer U., Musidlowska A., Schmidt-Barnert C., Lange S.;  
WI; 2002-547857/58.  
PT New recombinant porcine liver esterase subunit, useful for resolution  
of racemic carboxylic esters, is truncated at C-terminus -  
PS Claim 1; Page 3; 40pp; German.  
The present invention relates to a recombinant subunit of the porcine liver esterase (PLE) which lacks 1-50 amino acids from the C-terminus. The esterase enzyme can be used as a catalyst in organic synthesis, particularly in the esterase-catalysed racemate resolution of carboxylic acids or esters and for the reaction of pro-stereogenic compounds. The

CC present sequence is the esterase subunit of the invention.  
XX  
SQ Sequence 544 AA:  
  
Query Match 1.1k; Score 9; DB 23; Length 544;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 9; Conservative C; Mismatches 0; Indels 0; Gaps C;

OY 125 EDCLVNLNII 133  
|||  
De 97 EDCILNINII 105

RESULT 71  
ABP97364  
ID ABP97364 standard; Protein; 562 AA.

AC ABP97364;  
CT -0-MAY-2003 (first entry)  
XX  
DE Mouse acyl coenzyme A cholesterol acyltransferase-1.

KM Youse; murine; acyl coenzyme A cholesterol acyltransferase-1; ACAT;  
KM chromosome 1; cholesterol metabolism; free sterol regulation;  
KM cholesterol metabolism disorder; lipid metabolism disorder;  
KM atherosclerosis; cardiovascular disease; cardiac; expression inhibition;  
KM antisense therapy; enzyme.  
XX  
OS Mus musculus.  
PN MOZ003612144-A1.  
PD 13-FEB-2003.  
PF 17-JUL-2002; 2002W0-US22696.  
PR 01-AUG-2001; 2001US-0920394.  
PA (ISIS); ISIS PHARM INC.  
PI Crooke RM, Graham MJ, Lemonidis KM;  
DR WPE; 2003-239532/23.  
XX N-PSDB; A8274890.  
PT New antisense oligonucleotides targeted to a nucleic acid encoding acyl  
coenzyme A cholesterol acyltransferase-1, useful for treating a  
disease/condition involving abnormal lipid or cholesterol metabolism,  
e.g. atherosclerosis -  
XX  
PS Disclosure; Page 101:04; 117p; English.

XX This sequence represents murine acyl coenzyme A cholesterol  
acyltransferase-1. Acyl coenzyme A cholesterol ester transferase (ACAT)  
enzymes catalyze the synthesis of cholesterol esters from free  
cholesterol and fatty acyl-CoA, and are also involved in regulating the  
concentration of cellular free steroids. The murine acyl coenzyme A  
cholesterol acyltransferase-1 gene is located on chromosome 1. The  
invention relates to antisense oligonucleotides targeted to the human  
or mouse acyl coenzyme A cholesterol acyltransferase-1 gene, which  
inhibit its expression. A series of oligonucleotides (AB274897-AB274942)  
were designed to target different regions of the human or murine acyl  
coenzyme A cholesterol acyltransferase-1 RNA, and were analysed for their  
effect on mRNA levels by quantitative real-time PCR. The oligonucleotides  
of the invention are useful for the prevention and treatment of  
conditions associated with acyl coenzyme A cholesterol acyltransferase-1,  
such as disorders involving abnormal lipid or cholesterol metabolism,  
e.g., atherosclerosis or cardiovascular disease. They are also useful in  
research and diagnostics for modulating the expression of acyl coenzyme  
A cholesterol acyltransferase-1.

Sequence 562 AA;  
XX

Query Match 1.1%; Score 9; DB 24; Length 562;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 EDCLYLNIY 133  
DB 115 EDCLYLNIY 123

## RESULT 72

ABB60215

ID ABB60215 standard; Protein; 564 AA.

XX ABB60215;

XX 26-MAR-2002 (first entry);

XX Drosophila melanogaster polypeptide SEQ ID NO 7437.

XX Drosophila melanogaster developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX MO260171642-82.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WC-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 21-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams X, Li FWD, Myers EW;

XX WPI; 2001-656662/75.

XX N-PSDB; ABL04319.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

XX Disclosure; SEQ ID NO 7437; 21pp - Sequence listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (ABU16176-ABU35511), expressed DNA

XX sequences (ABU37737-ABU72072).

XX The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WFO

XX at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 564 AA;

QY 168 PMVYIHGG 176

DB 120 PMVYIHGG 128

## RESULT 73

ID AAY33145 standard; Protein; 565 AA.

XX AAY33145;  
XX 16-NOV-1999 (first entry);  
XX  
XX

DE Rabbit liver carboxylesterase protein.

XX Carboxylesterase; rabbit; liver; tumour cell; chemotherapy; prodrug;

XX disease-specific responsive promoter; CRT-11; APC; resection;

XX recurrence; inhibition; bone marrow cell.

XX Oryctolagus cuniculus.

XX Key Location/Qualifiers

XX MISC-difference 74 /note="Encoded by TTC"

XX MO9942593-A1.

XX 26-AUG-1999.

XX 12-FEB-1999; 99WO-US03171.

XX 19-FEB-1998; 98US-0075258.

XX (SCUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Danks WK, Potter PX, Houghton PJ;

XX WPI; 1999-54331/45.

XX N-PSDB; AA209683.

XX New carboxylesterase polypeptide for treatment of tumors -

XX Disclosure; Fig 4; 70pp; English.

XX This invention describes a novel rabbit carboxylesterase polypeptide (1)

XX capable of metabolizing a chemotherapeutic prodrug and its inactive

XX metabolites into an active drug. The invention also describes a

XX composition comprising (1) and a disease-specific responsive promoter.

XX This composition is useful for sensitizing tumor cells to a

XX chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into

XX tumor cells, and contacting the sensitized cells with a chemotherapeutic

XX prodrug to inhibit growth of the tumor cells. The composition can also be

XX administered to the site of tumor resection to inhibit tumor recurrence,

XX and be administered to bone marrow cells to remove tumor cells. The

XX products of the invention are useful for identifying drugs that are

XX inactivated by a carboxylesterase enzyme, and are also useful for

XX identifying compounds containing a COOC ester linkage that are activated

XX by a carboxylesterase enzyme. This sequence represents a rabbit liver

XX carboxylesterase which is described in the method of the invention.

XX Sequence 565 AA;

QY 125 EDCLYLNIY 133

DB 114 EDCLYLNIY 122

## RESULT 74

ID AAB08202 standard; Protein; 566 AA.

XX AAB08202;

XX 04-DEC-2000 (first entry)

DE Amino acid sequence of a rabbit liver esterase 3 designated R-E-3.

KW Rabbit; liver; esterase; RfE-3; pyridine herbicide;  
 KM pyridine resistant plant; herbicide tolerance; herbicide resistance.  
 OS Oryctolagus cuniculus.  
 XX  
 PN US6107549-A.  
 PD 22-AUG-2003.  
 XX  
 PF 09-MAR-1999; 99US-0264737.  
 XX  
 PR 10-MAR-1998; 98US-0077377.  
 XX  
 PA (MONS; WCN5A;70 CO.  
 XX  
 PI Feng FCC; Ruff TG;  
 XX  
 DR WPI: 2000-579555/54.  
 DR N-PDE: AAA63884.  
 XX  
 PT Recombinant polynucleotide molecule for generating pyridine resistant  
 PT transgenic plants, comprises plant functional promoter operably linked  
 PT to polynucleotide sequence encoding esterase.  
 XX  
 PS Claim 20; Column 31-36; 31pp; English.  
 XX  
 CC The present sequence represents a rabbit liver esterase, designated  
 CC RfE-3. The esterase catalyses the hydrolysis of a pyridine herbicide  
 CC compound. The esterase is linked to a plant functional promoter and  
 CC a 3' non-translated region that functions in plant cells to cause the  
 CC polydegradation of the 3' end of the RNA molecule produced by promoter.  
 CC The esterase construct is useful for production of pyridine resistant  
 CC transgenic plant. The esterase construct is also useful for genetic  
 CC manipulation of plants and confers herbicide tolerance and herbicide  
 CC resistance to the plants.  
 XX  
 SQ Sequence 566 AA;  
 SQ  
 Query Match: 1.1%; Score 9; DB 21; Length 566;  
 Best Local Similarity 100.0%; Pred. No. 4.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCYLYNLY 133  
 DB 115 EDCYLYNLY 123  
 DB  
 RESUME 75  
 AAB73263  
 CC AAB73263 standard; protein; 566 AA.  
 XX  
 AC AAB73263;  
 XX  
 DT 16-MAY-2001 (first entry)  
 XX  
 DE Human triacylglycerol hydrolase, TGH.  
 XX  
 KW Human; TGH; triacylglycerol hydrolase; carboxylesterase; EST-3; WLDL;  
 KW very low density lipoprotein; atherosclerosis; hypercholesterolaemia;  
 KW hyperlipoproteinaemia; non-insulin dependent diabetes mellitus;  
 KW coronary arterial disease; peripheral vascular disease; pancreatitis;  
 KW obesity; mixed dyslipidaemia; cerebro-vascular disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200116158-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000MC-EP08262.  
 XX  
 PR 28-AUG-1999; 99GB-0020334.  
 XX

PA (GLAX) GILKCO GROUP LTD.  
 PA (YVAL-1) UNIV ALBERTA.  
 XX  
 PI Borg-Capra CS, Lehner RJ, Vance DE;  
 XX  
 DR WPI: 2001-235119/24.  
 XX  
 PT Identifying compounds for treating elevated circulating levels of  
 PT triglyceride, very low density lipoprotein/low density  
 PT lipoprotein-cholesterol and ApoB-100, comprises identifying  
 PT triacylglycerol hydrolase inhibitors.  
 XX  
 PS Claim 2; Fig 1; 26pp; English.  
 XX  
 CC The present sequence is human triacylglycerol hydrolase (TGH). This  
 CC protein has previously been known as carboxylesterase EST-1. It is  
 CC thought that TGH may participate in the mobilisation of triacylglycerides  
 CC for assembly into very low density lipoproteins (VLDL). The present  
 CC invention relates to a method for identifying compounds which will be  
 CC useful in the treatment of conditions resulting from elevated circulating  
 CC levels of: triglycerides, apoB-100, and/or VLDL/LDL-cholesterol. The  
 CC method comprises determining whether the compound inhibits TGH activity.  
 CC Inhibitors of TGH are useful for treating atherosclerosis,  
 CC hypercholesterolaemia, hyperlipoproteinaemia, non-insulin dependent  
 CC diabetes mellitus (NIDDM), coronary arterial disease, peripheral vascular  
 CC disease, pancreatitis, obesity, mixed dyslipidaemia and cerebro-vascular  
 CC disease.  
 XX  
 SQ Sequence 566 AA;  
 SQ  
 Query Match: 1.1%; Score 9; DB 22; Length 566;  
 Best Local Similarity 100.0%; Pred. No. 4.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 125 EDCYLYNLY 133  
 DB 114 EDCYLYNLY 122  
 DB  
 Search completed: November 5, 2003, 15:24:19  
 Job time : 51 secs